Claims

1. An artificial nucleic acid molecule comprising

a. at least one open reading frame (ORF); and

b. at least one 3'-untranslated region element (3'-UTR element) heterologous to the ORF, wherein the at least one 3'-UTR element:

prolongs and/or increases protein production from said artificial nucleic acid molecule; and

comprises or consists of a nucleic acid sequence from the 3'-UTR of a transcript of GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), wherein the 3' UTR element is selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 116, and a sequence having at least 90% sequence identity to SEQ ID NO: 1, 2, 3, 4, or 116.

2. The artificial nucleic acid molecule of claim 1, further comprising at least one 5'-untranslated region element (5'-UTR element), wherein ~~the at least one 3'-UTR element and/or~~ the at least one 5'-UTR element prolongs and/or increases protein production from said artificial nucleic acid molecule and wherein the at least one ~~3'-UTR element and/or the at least one~~ 5'-UTR element ~~is derived from a stable mRNA.~~

~~2. The artificial nucleic acid molecule according to claim 1, wherein the open reading frame is derived from a gene, which is distinct from a gene from which the at least one 3'-UTR element and/or the at least one 5'-UTR element is derived.~~

~~3. The artificial nucleic acid molecule according to claim 1 or 2 comprising at least one 3'-UTR element and at least one 5' UTR element.~~

~~4. The artificial nucleic acid molecule according to claim 3, wherein each of the at least one open reading frame, the at least one 3'-UTR element and the at least one 5'-UTR element are heterologous to each other.~~

~~5. The artificial nucleic acid molecule according to any of claims 1 to 4, wherein the stable mRNA from which the at least one 3'-UTR element and/or the at least one 5'-UTR element is derived is characterized by an mRNA decay wherein the ratio of the amount of said mRNA at a second point in time to the amount of said mRNA at a first point in time is at least 0.5 (50%), at least 0.6 (60%), at least 0.7 (70%), at least 0.75 (75%), at least 0.8 (80%), at least 0.85 (85%), at least 0.9 (90%), or at least 0.95 (95%).~~

~~6. The artificial nucleic acid molecule according to any of claims 1 to 5, wherein the artificial nucleic acid molecule does not comprise a 3' UTR and/or a 5' UTR of ribosomal protein S6, of RPL36AL, of rps16 or of ribosomal protein L9 and wherein the open reading frame of the artificial nucleic acid molecule does not code for a GFP protein.~~

~~7. The artificial nucleic acid molecule according to claim 6, wherein the open reading frame of the artificial nucleic acid molecule does not code for a reporter protein.~~

~~8. The artificial nucleic acid molecule according to any one of claims 1 to 7, wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element~~<u>additionally</u> comprises ~~or consists of~~ a nucleic acid sequence ~~which is derived from the 3' UTR and/or the 5'-UTR of a eukaryotic protein coding gene, preferably from the 3'-UTR and/or the 5'-UTR of a vertebrate protein coding gene, more preferably from the 3'-UTR and/or the 5'-UTR of a mammalian protein coding gene, even more preferably from the 3'-UTR and/or the 5'-UTR of a primate protein coding gene.~~

~~9. The artificial nucleic acid molecule according to claim 8, wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element comprises or consists of a nucleic acid sequence which is derived from the 3'-UTR and/or the 5'-UTR of a human or murine protein coding gene.~~

~~10. The artificial nucleic acid molecule according to claim 8 or 9, wherein:~~

~~(i) the nucleic acid molecule comprises at least one 3'-UTR element and at least one 5'-UTR element;~~

~~(ii) the at least one 3'-UTR element, the at least one 5'-UTR element and the at least one open reading frame are all heterologous to each other;~~

(iii) the at least one 3’ UTR element is derived from a gene selected from the group consisting of: housekeeping genes, genes coding for a membrane protein, genes involved in cellular metabolism, genes involved in transcription, translation and replication processes, genes involved in protein modification and genes involved in cell division; and

(iv) the 3’UTR is not derived from a gene coding for a ribosomal protein or from the Fig4 gene.

11. The artificial nucleic acid molecule according to any of claims 8 to 10, wherein:

(i) the nucleic acid molecule comprises at least one 3’-UTR element and at least one 5’-UTR element;

(ii) the at least one 3’-UTR element, the at least one 5’-UTR element and the at least one open reading frame are all heterologous to each other;

(iii) the at least one 5’-UTR element is derived from a gene selected from the group consisting of: housekeeping genes, genes coding for a membrane protein, genes involved in cellular metabolism, genes involved in transcription, translation and replication processes, genes involved in protein modification and genes involved in cell division;

(iv) the 5’-UTR is preferably not a 5’ TOP UTR; and

(v) the 3’-UTR is preferably not derived from a gene coding for a ribosomal protein or for albumin or from the Fig4 gene.

12. The artificial nucleic acid molecule according to claim 10 or 11, wherein:

(i) the nucleic acid molecule comprises at least one 3’-UTR element and at least one 5’-UTR element;

(ii) the at least one 3’-UTR element, the at least one 5’-UTR element and the at least one open reading frame are all heterologous to each other;

(iii) the at least one 3’ UTR element is derived from a human or a murine gene selected from the group consisting of: housekeeping genes, genes coding for a membrane protein, genes involved in cellular metabolism, genes involved in transcription, translation and replication processes, genes involved in protein modification and genes involved in cell division;

~~(iv) the 3'UTR is not derived from a gene coding for a ribosomal protein or for albumin or from the Fig4 gene;~~

~~(v) the at least one 5'-UTR element is derived from a human or a murine gene selected from the group consisting of: housekeeping genes, genes coding for a membrane protein, genes involved in cellular metabolism, genes involved in transcription, translation and replication processes, genes involved in protein modification and genes involved in cell division; and~~

~~(vi) the 5'-UTR is not a 5' TOP UTR.~~

~~13. The artificial nucleic acid molecule according to any of claims 10 to 12, wherein the 3'-UTR and the 5'-UTR are derived from a human or a murine housekeeping gene.~~

~~14. The artificial nucleic acid molecule according to claim 12, wherein the 3'-UTR and the 5'-UTR are derived from a human or a murine gene selected from the group consisting of: genes coding for a membrane protein, genes involved in cellular metabolism, genes involved in transcription, translation and replication processes, genes involved in protein modification and genes involved in cell division and wherein the 3'-UTR and the 5'-UTR are selected from distinct gene classes.~~

~~15. The artificial nucleic acid molecule according to any of claims 1 to 14, wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element prolongs protein production from said artificial nucleic acid molecule at least 1.2 fold, preferably at least 1.5 fold, more preferably at least 2 fold, even more preferably at least 2.5 fold, compared to the protein production from a reference nucleic acid molecule lacking a 3'-UTR and/or the at least one 5'-UTR, respectively, and/or wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element increases protein production from said artificial nucleic acid molecule at least 1.5 fold, preferably at least 2 fold, more preferably at least 2.5 fold, compared to the protein production from a reference nucleic acid molecule lacking a 3'-UTR and/or the at least one 5'-UTR, respectively.~~

~~16. The artificial nucleic acid molecule according to any one of claims 1 to 15, wherein the at least one 3' UTR element and/or the at least one 5' UTR element comprises or consists of a nucleic acid sequence which is derived from the 3'-UTR and/or~~from the the 5'-UTR of a

transcript of a gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex~~), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus~~), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), LTA4H, SLC38A6, DECR1, PIGK, FAM175A, PHYH, TBC1D19, PIGB, ALG6, CRYZ, BRP44L, ACADSB, SUPT3H, TMEM14A, GRAMD1C, C11orf80, C9orf46, ANXA4, TBCK, IFI6, C2orf34, ALDH6A1, AGTPBP1, CCDC53, LRRC28, CCDC109B, PUS10, CCDC104, CASP1, SNX14, SKAP2, NDUFB6, EFHA1, BCKDHB, BBS2, LMBRD1, ITGA6, HERC5, NT5DC1, RAB7A, AGA, TPK1, MBNL3, HADHB, MCCC2, CAT, ANAPC4, PCCB, PHKB, ABCB7, PGCP, GPD2, TMEM38B, NFU1, OMA1, LOC128322/NUTF2, NUBPL, LANCL1, HHLA3, PIR, ACAA2, CTBS, GSTM4, ALG8, Ndufa1, Atp5e, Gstm5, Uqcr11, Ifi27l2a, Cbr2, Anapc13, Atp5I, Tmsb10, Nenf, Ndufa7, Atp5k, 1110008P14Rik, Cox4i1, Cox6a1, Ndufs6, Sec61b, Romo1, Gnas, Snrpd2, Mgst3, Aldh2, Ssr4, Myl6, Prdx4, Ubl5, 1110001J03Rik, Ndufa13, Ndufa3, Gstp2, Tmem160, Ergic3, Pgcp, Slpi, Myeov2, Ndufa4, Ndufs5, Gstm1, 1810027O10Rik, Atp5o, Shfm1, Tspo, S100a6, Taldo1, Bloc1s1, Hexa, Ndufb11, Map1lc3a, Morn2, Gpx4, Mif, Cox6b1, RIKEN cDNA2900010J23 (Swi5), Sec61g, 2900010M23Rik, Anapc5, Mars2, Phpt1, Ndufb8, Pfdn5, Arpc3, Ndufb7, Atp5h, Mrpl23, Uba52, Tomm6, Mtch1, Pcbd2, Ecm1, Hrsp12, Mecr, Uqcrq, Gstm3, Lsm4, Park7, Usmg5, Cox8a, Ly6c1, Cox7b, Ppib, Bag1, S100a4, Bcap31, Tecr, Rabac1, Robld3, Sod1, Nedd8, Higd2a, Trappc6a, Ldhb, Nme2, Snrpg, Ndufa2, Serf1, Oaz1, Rps4x, Rps13, Ybx1, Sepp1, Gaa, ACTR10, PIGF, MGST3, SCP2, HPRT1, ACSF2, VPS13A, CTH, NXT2, MGST2, C11orf67, PCCA, GLMN, DHRS1, PON2, NME7, ETFDH, ALG13, DDX60, DYNC2LI1, VPS8, ITFG1, CDK5, C1orf112, IFT52, CLYBL, FAM114A2, NUDT7, AKD1, MAGED2, HRSP12, STX8, ACAT1, IFT74, KIFAP3, CAPN1, COX11, GLT8D4, HACL1, IFT88, NDUFB3, ANO10, ARL6, LPCAT3, ABCD3, COPG2, MIPEP, LEPR, C2orf76, ABCA6, LY96, CROT, ENPP5, SERPINB7, TCP11L2, IRAK1BP1, CDKL2, GHR, KIAA1107, RPS6KA6, CLGN, TMEM45A, TBC1D8B, ACP6, RP6-213H19.1, SNRPN, GLRB, HERC6, CFH, GALC, PDE1A, GSTM5, CADPS2, AASS, TRIM6-TRIM34 (readthrough transcript), SEPP1, PDE5A, SATB1, CCPG1, CNTN1, LMBRD2, TLR3, BCAT1, TOM1L1, SLC35A1, GLYATL2, STAT4, GULP1, EHHADH, NBEAL1, KIAA1598, HFE, KIAA1324L, and MANSC1~~; preferably from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus~~.

3. The artificial nucleic acid molecule according to claim 2, wherein each of the at least one open reading frame, the at least one 3'-UTR element and the at least one 5'-UTR element are heterologous to each other.

4. The artificial nucleic acid molecule of claim 1, further comprising at least one 5'-untranslated region element (5'-UTR element), wherein the at least one 5'-UTR element prolongs and/or increases protein production from said artificial nucleic acid molecule and wherein the at least one 5'-UTR element comprises or consists of a nucleic acid sequence from the 5'-UTR of a transcript of GNAS (guanine nucleotide binding protein, alpha stimulating complex locus).

5. The artificial nucleic acid molecule according to any of claims 1 to 4, wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element are characterized by an mRNA decay wherein the ratio of the amount of said mRNA at a second point in time to the amount of said mRNA at a first point in time is at least 0.5 (50%), at least 0.6 (60%), at least 0.7 (70%), at least 0.75 (75%), at least 0.8 (80%), at least 0.85 (85%), at least 0.9 (90%), or at least 0.95 (95%).

6. The artificial nucleic acid molecule according to any of claims 1 to 5, wherein the artificial nucleic acid molecule does not comprise a 3'-UTR and/or a 5'-UTR of ribosomal protein S6, of RPL36AL, of rps16 or of ribosomal protein L9 and wherein the open reading frame of the artificial nucleic acid molecule does not code for a GFP protein and wherein the open reading frame of the artificial nucleic acid molecule does not code for a reporter protein.

7. The artificial nucleic acid molecule according to any of claims 1 to 6, wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element prolongs protein production from said artificial nucleic acid molecule at least 1.2 fold, or at least 1.5 fold, more preferably at least 2 fold, or at least 2.5 fold, compared to the protein production from a reference nucleic acid molecule lacking a 3'-UTR and/or the at least one 5'-UTR, respectively, and/or wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element increases protein production from said artificial nucleic acid molecule at least 1.5 fold, or at least 2 fold, or at least 2.5 fold, compared to the protein production from a reference nucleic acid molecule lacking a 3'-UTR and/or the at least one 5'-UTR, respectively.

8. The artificial nucleic acid molecule according to any one of claims 1 to 7 wherein the at least one 3'-UTR element additionally comprises a nucleic acid sequence which is derived from the 3'-UTR transcript of a gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), ~~Ybx1 (Y-Box binding protein 1), Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), and CNTN1 (contactin 1).~~

~~17. The artificial nucleic acid molecule according to claim 16, wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element comprises a nucleic acid sequence which is derived from the 3'-UTR and/or the 5'-UTR of a transcript of a human gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), Ybx1 (Y-Box binding protein 1), Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), CNTN1 (contactin 1),~~ LTA4H, SLC38A6, DECR1, PIGK, FAM175A, PHYH, TBC1D19, PIGB, ALG6, CRYZ, BRP44L, ACADSB, SUPT3H, TMEM14A, GRAMD1C, C11orf80, C9orf46, ANXA4, TBCK, IFI6, C2orf34, ALDH6A1, AGTPBP1, CCDC53, LRRC28, CCDC109B, PUS10, CCDC104, CASP1, SNX14, SKAP2, NDUFB6, EFHA1, BCKDHB, BBS2, LMBRD1, ITGA6, HERC5, NT5DC1, RAB7A, AGA, TPK1, MBNL3, HADHB, MCCC2, CAT, ANAPC4, PCCB, PHKB, ABCB7, PGCP, GPD2, TMEM38B, NFU1, OMA1, LOC128322/NUTF2, NUBPL, LANCL1, HHLA3, ~~, PIR, ACAA2, CTBS, GSTM4, ALG8, ACTR10, PIGF, MGST3, SCP2, HPRT1, ACSF2, VPS13A, CTH, NXT2, MGST2, C11orf67, PCCA, GLMN, DHRS1, PON2, NME7, ETFDH, ALG13, DDX60, DYNC2LI1, VPS8, ITFG1, CDK5, C1orf112, IFT52, CLYBL, FAM114A2, NUDT7, AKD1, MAGED2, HRSP12, STX8, ACAT1, IFT74, KIFAP3, CAPN1, COX11, GLT8D4, HACL1, IFT88, NDUFB3, ANO10, ARL6, LPCAT3, ABCD3, COPG2, MIPEP, LEPR, C2orf76, ABCA6, LY96, CROT, ENPP5, SERPINB7, TCP11L2, IRAK1BP1, CDKL2, GHR, KIAA1107, RPS6KA6, CLGN, TMEM45A, TBC1D8B, ACP6, RP6-213H19.1, SNRPN, GLRB, HERC6, CFH, GALC, PDE1A, GSTM5, CADPS2, AASS, TRIM6-TRIM34 (readthrough transcript), SEPP1, PDE5A, SATB1, CCPG1, LMBRD2,~~

~~TLR3, BCAT1, TOM1L1, SLC35A1, GLYATL2, STAT4, GULP1, EHHADH, NBEAL1, KIAA1598, HFE, KIAA1324L, and MANSC1.~~

~~18. The artificial nucleic acid molecule according to claim 16, wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element comprises a nucleic acid sequence which is derived from the 3'-UTR and/or the 5'-UTR of a transcript of a murine gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), Ybx1 (Y-Box binding protein 1), Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), CNTN1 (contactin 1), Atp5e, Gstm5, Uqcr11, Ifi27l2a~~PIR, ACAA2, CTBS, GSTM4, ALG8, Ndufa1, Atp5e, Gstm5, Uqcr11, Ifi27l2a, Cbr2, Anapc13, Atp5I, Tmsb10, Nenf, Ndufa7, Atp5k, 1110008P14Rik, Cox4i1, Cox6a1, Ndufs6, Sec61b, Romo1, ~~Snrpd2, Mgst3, Aldh2, Ssr4, Myl6, Prdx4, Ubl5, 1110001J03Rik, Ndufa13, Ndufa3, Gstp2, Tmem160, Ergic3, Pgcp, Slpi, Myeov2, Ndufs5, 1810027O10Rik, Atp5o, Shfm1, Tspo, S100a6, Taldo1, Bloc1s1, Hexa, Ndufb11, Map1lc3a, Gpx4, Mif, Cox6b1, RIKEN cDNA2900010J23 (Swi5), Sec61g, 2900010M23Rik, Anapc5, Mars2, Phpt1, Pfdn5, Arpc3, Ndufb7, Atp5h, Mrpl23, Uba52, Tomm6, Mtch1, Pcbd2, Ecm1, Hrsp12, Mecr, Uqcrq, Gstm3, Lsm4, Park7, Usmg5, Cox8a, Ly6c1, Cox7b, Ppib, Bag1, S100a4, Bcap31, Tecr, Rabac1, Robld3, Sod1, Nedd8, Higd2a, Trappc6a, Ldhb, Nme2, Snrpg, Ndufa2, Serf1, Oaz1, Rps4x, Rps13, Sepp1, and Gaa.~~

~~19. The artificial nucleic acid molecule according to any one of claims 16 to 18, wherein the at least one 3'-UTR element comprises a nucleic acid sequence which is derived from the 3'-UTR of a transcript of a gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), SLC38A6, DECR1, PIGK, FAM175A, PHYH, TBC1D19, PIGB, ALG6, CRYZ, BRP44L, ACADSB, TMEM14A, GRAMD1C, C11orf80, ANXA4, TBCK, IFI6, C2orf34, ALDH6A1, AGTPBP1, CCDC53, LRRC28, CCDC109B, PUS10, CCDC104, CASP1, SNX14, SKAP2, NDUFB6, EFHA1, BCKDHB, BBS2, LMBRD1, ITGA6, HERC5, HADHB, ANAPC4, PCCB, ABCB7, PGCP, NFU1, OMA1, HHLA3, ACAA2, GSTM4, ALG8,~~

~~Ndufa1, Atp5e, Gstm5, Uqcr11, Ifi27l2a, Cbr2, Atp5l, Tmsb10, Nenf, Atp5k, 1110008P14Rik, Cox4i1, Cox6a1, Ndufs6, Sec61b, Romo1,~~ Gnas, Snrpd2, Mgst3, Aldh2, Ssr4, Myl6, Prdx4, Ubl5, 1110001J03Rik, Ndufa13, Ndufa3, Gstp2, Tmem160, Ergic3, Pgcp, Slpi, Myeov2, Ndufa4, Ndufs5, Gstm1, 1810027O10Rik, Atp5o, Shfm1, Tspo, S100a6, Taldo1, Bloc1s1, Hexa, Ndufb11, Map1lc3a, Morn2, Gpx4, Mif, Cox6b1, RIKEN cDNA2900010J23 (Swi5), Sec61g, 2900010M23Rik, Anapc5, Mars2, Phpt1, Ndufb8, Pfdn5, Arpc3, Ndufb7, Atp5h, Mrpl23, Uba52, Tomm6, Mtch1, Pcbd2, Ecm1, Hrsp12, Mecr, Uqcrq, Gstm3, Lsm4, Park7, Usmg5, Cox8a, Ly6c1, Cox7b, Ppib, Bag1, S100a4, Bcap31, Tecr, Rabac1, Robld3, Sod1, Nedd8, Higd2a, Trappc6a, Ldhb, Nme2, Snrpg, Ndufa2, Serf1, Oaz1, Rps4x, Rps13, Ybx1, Sepp1, Gaa, ACTR10, PIGF, MGST3, SCP2, HPRT1, ACSF2, VPS13A, CTH, NXT2, MGST2, C11orf67, PCCA, GLMN, DHRS1, PON2, NME7, ETFDH, ALG13, DDX60, DYNC2LI1, VPS8, ITFG1, CDK5, C1orf112, IFT52, CLYBL, FAM114A2, NUDT7, AKD1, MAGED2, HRSP12, STX8, ACAT1, IFT74, KIFAP3, CAPN1, COX11, GLT8D4, HACL1, IFT88, NDUFB3, ANO10, ARL6, LPCAT3, ABCD3, COPG2, MIPEP, LEPR, C2orf76, ABCA6, LY96, CROT, ENPP5, SERPINB7, TCP11L2, IRAK1BP1, CDKL2, GHR, KIAA1107, RPS6KA6, CLGN, TMEM45A, TBC1D8B, ACP6, RP6-213H19.1, SNRPN, GLRB, HERC6, CFH, GALC, PDE1A, GSTM5, CADPS2, AASS, TRIM6-TRIM34 (readthrough transcript), SEPP1, PDE5A, SATB1, CCPG1, CNTN1, LMBRD2, TLR3, BCAT1, TOM1L1, SLC35A1, GLYATL2, STAT4, GULP1, EHHADH, NBEAL1, KIAA1598, HFE, KIAA1324L, and MANSC1; ~~preferably, the at least one 3'-UTR element comprises or consists of a nucleic acid sequence which is derived from the 3'-UTR of a transcript of a gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), Ybx1 (Y-Box binding protein 1), Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), and CNTN1 (contactin 1).~~

~~20~~9. The artificial nucleic acid molecule according to claim ~~19,~~8 wherein the at least one 3'-UTR element additionally comprises a nucleic acid sequence ~~which is derived~~ from the 3'-UTR ~~of a~~ transcript of a ~~human~~ gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), ~~SLC38A6, DECR1, PIGK,~~

~~FAM175A, PHYH, TBC1D19, PIGB, ALG6, CRYZ, BRP44L, ACADSB, TMEM14A, GRAMD1C, C11orf80, ANXA4, TBCK, IFI6, C2orf34, ALDH6A1, AGTPBP1, CCDC53, LRRC28, CCDC109B, PUS10, CCDC104, CASP1, SNX14, SKAP2, NDUFB6, EFHA1, BCKDHB, BBS2, LMBRD1, ITGA6, HERC5, HADHB, ANAPC4, PCCB, ABCB7, PGCP, NFU1, OMA1, HHLA3, ACAA2, GSTM4, ALG8, ACTR10, PIGF, MGST3, SCP2, HPRT1, ACSF2, VPS13A, CTH, NXT2, MGST2, C11orf67, PCCA, GLMN, DHRS1, PON2, NME7, ETFDH, ALG13, DDX60, DYNC2LI1, VPS8, ITFG1, CDK5, C1orf112, IFT52, CLYBL, FAM114A2, NUDT7, AKD1, MAGED2, HRSP12, STX8, ACAT1, IFT74, KIFAP3, CAPN1, COX11, GLT8D4, HACL1, IFT88, NDUFB3, ANO10, ARL6, LPCAT3, ABCD3, COPG2, MIPEP, LEPR, C2orf76, ABCA6, LY96, CROT, ENPP5, SERPINB7, TCP11L2, IRAK1BP1, CDKL2, GHR, KIAA1107, RPS6KA6, CLGN, TMEM45A, TBC1D8B, ACP6, RP6-213H19.1, SNRPN, GLRB, HERC6, CFH, GALC, PDE1A, GSTM5, CADPS2, AASS, TRIM6-TRIM34 (readthrough transcript), SEPP1, PDE5A, SATB1, CCPG1, CNTN1, LMBRD2, TLR3, BCAT1, TOM1L1, SLC35A1, GLYATL2, STAT4, GULP1, EHHADH, NBEAL1, KIAA1598, HFE, KIAA1324L, and MANSC1; preferably, the at least one 3'-UTR element comprises or consists of a nucleic acid sequence which is derived from the 3'-UTR of a transcript of a human gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2),~~MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), Ybx1 (Y-Box binding protein 1), Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), and CNTN1 (contactin 1).

~~21~~10. The artificial nucleic acid molecule according to ~~claim 19,~~any one of claims 1 to 9 wherein the at least one ~~3'~~5'-UTR element comprises a nucleic acid sequence ~~which is derived~~ from the ~~3'~~5'-UTR of a transcript of a ~~murine~~ gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), Ybx1 (Y-Box binding protein 1), Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), and CNTN1 (contactin 1~~), Ndufa1, Atp5e, Gstm5, Uqcr11, Ifi27l2a, Cbr2, Atp5l, Tmsb10, Nenf, Atp5k, 1110008P14Rik,~~

~~Cox4i1, Cox6a1, Ndufs6, Sec61b, Romo1, Gnas, Snrpd2, Mgst3, Aldh2, Ssr4, Myl6, Prdx4, Ubl5, 1110001J03Rik, Ndufa13, Ndufa3, Gstp2, Tmem160, Ergic3, Pgcp, Slpi, Myeov2, Ndufa4, Ndufs5, Gstm1, 1810027O10Rik, Atp5o, Shfm1, Tspo, S100a6, Taldo1, Bloc1s1, Ndufb11, Map1lc3a, Morn2, Gpx4, Mif, Cox6b1, RIKEN cDNA2900010J23 (Swi5), Sec61g, 2900010M23Rik, Anapc5, Mars2, Phpt1, Ndufb8, Pfdn5, Arpc3, Ndufb7, Atp5h, Mrpl23, Uba52, Tomm6, Mtch1, Pcbd2, Ecm1, Hrsp12, Mecr, Uqcrq, Gstm3, Lsm4, Park7, Usmg5, Cox8a, Ly6c1, Cox7b, Ppib, Bag1, S100a4, Bcap31, Tecr, Rabac1, Robld3, Sod1, Nedd8, Higd2a, Trappc6a, Ldhb, Nme2, Snrpg, Ndufa2, Serf1, Oaz1, Rps4x, Rps13, Ybx1, Sepp1, and Gaa; preferably, the at least one 3'-UTR element comprises or consists of a nucleic acid sequence which is derived from the 3'-UTR of a transcript of a murine gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), Ybx1 (Y-Box binding protein 1), Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), and CNTN1 (contactin 1).~~

~~22. The artificial nucleic acid molecule according to any one of claims 16 to 18, wherein the at least one 5'-UTR element comprises a nucleic acid sequence which is derived from the 5'-UTR of a transcript of a gene selected from the group consisting of MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4),~~) LTA4H, DECR1, PIGK, TBC1D19, BRP44L, ACADSB, SUPT3H, TMEM14A, C9orf46, ANXA4, IFI6, C2orf34, ALDH6A1, CCDC53, CCDC104, CASP1, NDUFB6, BCKDHB, BBS2, HERC5, FAM175A, NT5DC1, RAB7A, AGA, TPK1, MBNL3, MCCC2, CAT, ANAPC4, PHKB, ABCB7, GPD2, TMEM38B, NFU1, LOC128322/NUTF2, NUBPL, LANCL1, PIR, CTBS, GSTM4, Ndufa1, Atp5e, Gstm5, ~~Cbr2,~~ Anapc13, Ndufa7, Atp5k, 1110008P14Rik, Cox4i1, Ndufs6, Sec61b, Snrpd2, Mgst3, Prdx4; Pgcp; Myeov2; Ndufa4; Ndufs5; Gstm1; Atp5o; Tspo; Taldo1; Bloc1s1; and Hexa~~; preferably, the at least one 5'-UTR element comprises or consists of a nucleic acid sequence which is derived from the 5'-UTR of a transcript of MP68 (RIKEN cDNA 2010107E04 gene) or NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4).~~ .

~~23~~11. The artificial nucleic acid molecule according to claim ~~22,~~10 wherein ~~the at least one 5'-UTR element comprises a nucleic acid sequence which is derived from the 5'-UTR of a~~

~~transcript of a human gene selected from the group consisting of MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), LTA4H, DECR1, PIGK, TBC1D19, BRP44L, ACADSB, SUPT3H, TMEM14A, C9orf46, ANXA4, IFI6, C2orf34, ALDH6A1, CCDC53, CCDC104, CASP1, NDUFB6, BCKDHB, BBS2, HERC5, FAM175A, NT5DC1, RAB7A, AGA, TPK1, MBNL3, MCCC2, CAT, ANAPC4, PHKB, ABCB7, GPD2, TMEM38B, NFU1, LOC128322/NUTF2, NUBPL, LANCL1, PIR, CTBS, and GSTM4; preferably,~~ the at least one 5'-UTR element comprises or consists of a nucleic acid sequence which is derived from the 5'-UTR of a ~~human~~ transcript of MP68 (RIKEN cDNA 2010107E04 gene) or NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4).

~~24. The artificial nucleic acid molecule according to claim 22, wherein the at least one 5'-UTR element comprises a nucleic acid sequence which is derived from the 5'-UTR of a transcript of a murine gene selected from the group consisting of MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), Ndufa1, Atp5e, Gstm5, Cbr2, Anapc13, Ndufa7, Atp5k, 1110008P14Rik, Cox4i1, Ndufs6, Sec61b, Snrpd2, Mgst3, Prdx4; Pgcp; Myeov2; Ndufa4; Ndufs5; Gstm1; Atp5o; Tspo; Taldo1; Bloc1s1; and Hexa; preferably, the at least one 5'-UTR element comprises or consists of a nucleic acid sequence which is derived from the 5'-UTR of a murine transcript of MP68 (RIKEN cDNA 2010107E04 gene) or NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4).~~

~~25. The artificial nucleic acid molecule according to any one of claims 1 – 21, wherein the at least one 3'-UTR element comprises or consists of a nucleic acid sequence which has an identity of at least about 50%, preferably of at least about 60%, preferably of at least about 70%, more preferably of at least about 80%, more preferably of at least about 90%, even more preferably of at least about 95%, even more preferably of at least about 99% to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1 to 24 and SEQ ID NOs: 49 to 318 or wherein the at least one 3'-UTR element comprises or consists of a fragment of a nucleic acid sequence which has an identity of at least about 40%, preferably of at least about 50%, preferably of at least about 60%, preferably of at least about 70%, more preferably of at least about 80%, more preferably of at least about 90%, even more preferably of at least about 95%, even~~

~~more preferably of at least about 99% to fragment of a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1 to 24 and SEQ ID NOs: 49 to 318.~~

~~26. The artificial nucleic acid molecule according to any one of claims 1 – 18 and 22 to 24, wherein the at least one 5'-UTR element comprises or consists of a nucleic acid sequence which has an identity of at least about 50%, preferably of at least about 60%, preferably of at least about 70%, more preferably of at least about 80%, more preferably of at least about 90%, even more preferably of at least about 95%, even more preferably of at least about 99% to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 25 to 30 and SEQ ID NOs: 319 to 382 or wherein the at least one 5'-UTR element comprises or consists of a fragment of a nucleic acid sequence which has an identity of at least about 40%, preferably of at least about 50%, preferably of at least about 60%, preferably of at least about 70%, more preferably of at least about 80%, more preferably of at least about 90%, even more preferably of at least about 95%, even more preferably of at least about 99% to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 25 to 30 and SEQ ID NOs: 319 to 382.~~

~~27. The artificial nucleic acid molecule according to claim 25 or 26, wherein the fragment exhibits a length of between 3 and about 500 nucleotides, preferably of between 5 and about 150 nucleotides, more preferably of between 10 and 100 nucleotides, even more preferably of between 15 and 90, most preferably of between 20 and 70.~~

~~28. The artificial nucleic acid molecule according to any one of claims 1 – 27, wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element exhibits a length of between 3 and about 500 nucleotides, preferably of between 5 and about 150 nucleotides, more preferably of between 10 and 100 nucleotides, even more preferably of between 15 and 90, most preferably of between 20 and 70.~~

~~29. The artificial nucleic acid molecule according to any one of claims 1 – 28 further comprising~~

12. The artificial nucleic acid molecule according to any one of claims 1 to 11 further comprising:

c. a poly(A) sequence and/or a polyadenylation signal.

~~30~~13. The artificial nucleic acid molecule according to claim ~~29~~12, wherein the poly(A) sequence or the polyadenylation signal is located 3' of the 3'-UTR element~~.~~

~~31. The artificial nucleic acid molecule according to claim 29 or 30,~~ and/or wherein the polyadenylation signal comprises the consensus sequence NN(U/T)ANA, with N = A or U, ~~preferably~~ AA(U/T)AAA or A(U/T)(U/T)AAA~~.~~

~~32. The artificial nucleic acid molecule according to any one of claims 29 – 31,~~ and/or wherein the polyadenylation signal,~~ preferably~~ the consensus sequence NNUANA, is located less than about 50 nucleotides downstream of the 3'-end of the 3'-UTR element~~.~~ and/or wherein the poly(A) sequence has a length of about 20 to about 300 adenine nucleotides, or of about 40 to about 200 adenine nucleotides, or of about 50 to about 100 adenine nucleotides, or of about 60 to about 70 adenine nucleotides.

~~33. The artificial nucleic acid molecule according to any one of claims 29 – 32, wherein the poly(A) sequence has a length of about 20 to about 300 adenine nucleotides, preferably of about 40 to about 200 adenine nucleotides, more preferably of about 50 to about 100 adenine nucleotides, even more preferably of about 60 to about 70 adenine nucleotides.~~

~~34~~14. The artificial nucleic acid molecule according to any one of claims 1 ~~– 33~~to 13, further comprising a 5'-cap structure, a poly(C) sequence, a histone stem-loop, and/or an IRES-motif~~.~~, wherein the histone stem-loop comprises a sequence according to SEQ ID NO: 34.

~~35~~15. The artificial nucleic acid molecule according to any one of claims 1 ~~– 34, wherein the histone stem-loop comprises a sequence according to SEQ ID NO: 34.~~

~~36. The artificial nucleic acid molecule according to any one of claims 1 – 35, wherein the nucleic acid comprises a promoter.~~

~~37. The artificial nucleic acid molecule according to any one of claims 1 – 36~~to 14, wherein the nucleic acid comprises a 5'-TOP UTR~~.~~

~~38. The artificial nucleic acid molecule according to any one of claims 1 – 37, wherein the nucleic acid comprises a 3'-UTR, which comprises~~ and/or ~~consists of a nucleic acid sequence which is derived from a 3'-UTR of an albumin gene.~~

~~39. The artificial nucleic acid molecule according to any one of claims 1 – 38,~~ wherein the artificial nucleic acid molecule, ~~preferably~~ the open reading frame, is at least partially G/C modified, ~~preferably~~ wherein the G/C content of the open reading frame is increased compared to the wild type open reading frame~~.~~ and/or

~~40. The artificial nucleic acid molecule according to any one of claims 1 – 39,~~ wherein the open reading frame comprises a codon-optimized region, ~~preferably,~~ wherein the open reading frame is codon-optimized.

~~41. The~~ 16. The artificial nucleic acid molecule according to claim 15 wherein the artificial nucleic acid molecule ~~according to any one of claims 1 – 40, which~~ is an RNA~~, preferably~~ or an mRNA molecule.

~~42~~17. A vector comprising an artificial nucleic acid molecule according to any one of claims 1 ~~–~~ ~~41.~~ to 16.

~~43. The vector according to claim 42, which is a DNA vector.~~

~~44~~18. The vector according to claim ~~42 or 43, which is~~17 selected from the group consisting of a DNA vector, a plasmid vector ~~or~~, and a viral vector~~, preferably a plasmid vector.~~.

~~45. The vector according to any one of claims 42 – 44, which is a circular molecule.~~

~~46~~19. The vector according to claim ~~42~~18, wherein the ~~poly(A) sequence, the poly(C) sequence, the histone stem-loop or the 3'-UTR element of the coding strand is followed in 5'→3' direction by a restriction site for linearization of the circular vector molecule.~~vetor is a plasmid vector.

~~47~~20. A cell comprising the artificial nucleic acid molecule according to any one of claims 1 ~~– 39~~to 16 or the vector according to any one of claims 17 to ~~any one of claims 42 – 46~~19.

~~48~~21. The cell according to claim ~~47, which~~20, wherein the cell is a mammalian cell.

~~49. The cell according to claim 47 or 48, which is a cell of a mammalian subject, preferably an isolated cell of a mammalian subject, preferably of a human subject.~~

~~50~~22. A pharmaceutical composition comprising the artificial nucleic acid molecule according to any one of claims 1 ~~– 41~~to 16, the vector according to any one of claims ~~42 – 46~~17 to 19, or the cell according to ~~any one of claims 47 – 49~~claim 20 or 21.

~~51~~23. The pharmaceutical composition according to claim ~~50,~~22 further comprising one or more pharmaceutically acceptable vehicles, diluents~~ and/or,~~ excipients~~ and/,~~ or ~~one or more~~ adjuvants.

~~52. The~~24. Use of the artificial nucleic acid molecule according to any one of claims 1 ~~– 41~~to 16, the vector according to any one of claims ~~42 – 46~~17 to 19, the cell according to ~~any one of claims 47 – 49, or the pharmaceutical composition according to~~ claim ~~50 or 51 for use as a medicament.~~

~~53. The artificial nucleic acid molecule according to any one of claims 1 – 41, the vector according to any one of claims 42 - 46, the cell according to any one of claims 47 - 49~~20 or 21, or the pharmaceutical composition according to claim ~~50~~22 or ~~51~~23 for ~~use as~~the manufacture of a ~~vaccine or for use in gene therapy~~medicament.

~~54. A method for treating or preventing a disorder comprising administering the artificial nucleic acid molecule according to any one of claims 1 – 41, the vector according to any one of claims 42 – 46, the cell according to any one of claims 47 – 49, or the pharmaceutical composition according to claim 50 or 51 to a subject in need thereof.~~

~~55. A method of treating or preventing a disorder comprising transfection of a cell with an artificial nucleic acid molecule according to any one of claims 1 – 41 or the vector according to any one of claims 42 – 46.~~

~~56. The method according to claim 55, wherein transfection of a cell is performed *in vitro/ex vivo* and the transfected cell is administered to a subject in need thereof, preferably to a human patient.~~

~~57. The method according to claim 56, wherein the cell which is to be transfected *in vitro* is an isolated cell of the subject, preferably of the human patient.~~

~~58. The method according to any one of claims 54 – 57, which is a vaccination method or a gene therapy method.~~

~~59~~25. The use according to claim 24 wherein the medicament is for a vaccine or for gene therapy.

26. A method for increasing and/or prolonging protein production from an artificial nucleic acid molecule, ~~preferably~~ from an mRNA molecule or a vector, the method comprising the step of associating an open reading frame with a 3'-UTR element and/or a 5'-UTR element, wherein the 3'-UTR element and/or the 5'-UTR element prolongs and/or increases protein production from a resulting artificial nucleic acid molecule and wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element is ~~derived~~ from a stable mRNA, to obtain an artificial nucleic acid molecule, ~~preferably~~or an mRNA molecule, according to any of claims 1 ~~– 41~~to 16 or a vector according to any one of claims ~~42 – 46~~17 to 19.

~~60. A method for increasing and/or prolonging protein production from an artificial nucleic acid molecule, preferably from an mRNA molecule or a vector, according to claim 59, wherein the 3'-UTR element and/or the 5'-UTR element comprises or consists of a nucleic acid sequence which is derived from the 3'-UTR and/or the 5'-UTR of a transcript of a gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), LTA4H, SLC38A6, DECR1, PIGK, FAM175A, PHYH, TBC1D19, PIGB, ALG6, CRYZ, BRP44L, ACADSB, SUPT3H, TMEM14A, GRAMD1C, C11orf80, C9orf46, ANXA4, TBCK, IFI6, C2orf34, ALDH6A1, AGTPBP1, CCDC53, LRRC28, CCDC109B, PUS10, CCDC104, CASP1, SNX14, SKAP2, NDUFB6, EFHA1, BCKDHB, BBS2, LMBRD1, ITGA6, HERC5, NT5DC1, RAB7A, AGA, TPK1, MBNL3, HADHB, MCCC2, CAT, ANAPC4, PCCB, PHKB, ABCB7, PGCP, GPD2, TMEM38B, NFU1, OMA1, LOC128322/NUTF2, NUBPL, LANCL1, HHLA3, PIR, ACAA2, CTBS, GSTM4, ALG8, Atp5e, Gstm5, Uqcr11, Ifi27l2a, Anapc13, Atp5l, Tmsb10, Nenf, Ndufa7, Atp5k, 1110008P14Rik, Cox4i1, Cox6a1,~~

~~Ndufs6, Sec61b, Romo1, Snrpd2, Mgst3, Aldh2, , Ssr4, Myl6, Prdx4, Ubl5, 1110001J03Rik, Ndufa13, Ndufa3, Gstp2, Tmem160, Ergic3, Pgcp, Slpi, Myeov2, Ndufs5, 1810027O10Rik, Atp5o, Shfm1, Tspo, S100a6, Taldo1, Bloc1s1, Hexa, Ndufb11, Map1lc3a, Gpx4, Mif, Cox6b1, RIKEN cDNA2900010J23 (Swi5), Sec61g, 2900010M23Rik, Anapc5, Mars2, Phpt1, Ndufb8, Pfdn5, Arpc3, Ndufb7, Atp5h, Mrpl23, Uba52, Tomm6, Mtch1, Pcbd2, Ecm1, Hrsp12, Mecr, Uqcrq, Gstm3, Lsm4, Park7, Usmg5, Cox8a, Ly6c1, Cox7b, Ppib, Bag1, S100a4, Bcap31, Tecr, Rabac1, Robld3, Sod1, Nedd8, Higd2a, Trappc6a, Ldhb, Nme2, Snrpg, Ndufa2, Serf1, Oaz1, Rps4x, Rps13, Ybx1, Sepp1, Gaa, ACTR10, PIGF, MGST3, SCP2, HPRT1, ACSF2, VPS13A, CTH, NXT2, MGST2, C11orf67, PCCA, GLMN, DHRS1, PON2, NME7, ETFDH, ALG13, DDX60, DYNC2LI1, VPS8, ITFG1, CDK5, C1orf112, IFT52, CLYBL, FAM114A2, NUDT7, AKD1, MAGED2, HRSP12, STX8, ACAT1, IFT74, KIFAP3, CAPN1, COX11, GLT8D4, HACL1, IFT88, NDUFB3, ANO10, ARL6, LPCAT3, ABCD3, COPG2, MIPEP, LEPR, C2orf76, ABCA6, LY96, CROT, ENPP5, SERPINB7, TCP11L2, IRAK1BP1, CDKL2, GHR, KIAA1107, RPS6KA6, CLGN, TMEM45A, TBC1D8B, ACP6, RP6-213H19.1, SNRPN, GLRB, HERC6, CFH, GALC, PDE1A, GSTM5, CADPS2, AASS, TRIM6-TRIM34 (readthrough transcript), SEPP1, PDE5A, SATB1, CCPG1, CNTN1, LMBRD2, TLR3, BCAT1, TOM1L1, SLC35A1, GLYATL2, STAT4, GULP1, EHHADH, NBEAL1, KIAA1598, HFE, KIAA1324L, and MANSC1; preferably from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), Ybx1 (Y-Box binding protein 1), Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), and CNTN1 (contactin 1).~~

61. ~~Use of a 3'-UTR element and/or a 5'-UTR element for increasing and/or prolonging protein production from an artificial nucleic acid molecule, preferably from an mRNA molecule or a vector, wherein the 3'-UTR element and/or the 5'-UTR element comprises or consists of a nucleic acid sequence which is derived from the 3'-UTR and/or the 5'-UTR of a transcript of a gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat~~

~~containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), LTA4H, SLC38A6, DECR1, PIGK, FAM175A, PHYH, TBC1D19, PIGB, ALG6, CRYZ, BRP44L, ACADSB, SUPT3H, TMEM14A, GRAMD1C, C11orf80, C9orf46, ANXA4, TBCK, IFI6, C2orf34, ALDH6A1, AGTPBP1, CCDC53, LRRC28, CCDC109B, PUS10, CCDC104, CASP1, SNX14, SKAP2, NDUFB6, EFHA1, BCKDHB, BBS2, LMBRD1, ITGA6, HERC5, NT5DC1, RAB7A, AGA, TPK1, MBNL3, HADHB, MCCC2, CAT, ANAPC4, PCCB, PHKB, ABCB7, PGCP, GPD2, TMEM38B, NFU1, OMA1, LOC128322/NUTF2, NUBPL, LANCL1, HHLA3, PIR, ACAA2, CTBS, GSTM4, ALG8, Atp5e, Gstm5, Uqcr11, Ifi27l2a, Anapc13, Atp5l, Tmsb10, Nenf, Ndufa7, Atp5k, 1110008P14Rik, Cox4i1, Cox6a1, Ndufs6, Sec61b, Romo1, Snrpd2, Mgst3, Aldh2, Ssr4, Myl6, Prdx4, Ubl5, 1110001J03Rik, Ndufa13, Ndufa3, Gstp2, Tmem160, Ergic3, Pgcp, Slpi, Myeov2, Ndufs5, 1810027O10Rik, Atp5o, Shfm1, Tspo, S100a6, Taldo1, Bloc1s1, Hexa, Ndufb11, Map1lc3a, Gpx4, Mif, Cox6b1, RIKEN cDNA2900010J23 (Swi5), Sec61g, 2900010M23Rik, Anapc5, Mars2, Phpt1, Ndufb8, Pfdn5, Arpc3, Ndufb7, Atp5h, Mrpl23, Uba52, Tomm6, Mtch1, Pcbd2, Ecm1, Hrsp12, Mecr, Uqcrq, Gstm3, Lsm4, Park7, Usmg5, Cox8a, Ly6c1, Cox7b, Ppib, Bag1, S100a4, Bcap31, Tecr, Rabac1, Robld3, Sod1, Nedd8, Higd2a, Trappc6a, Ldhb, Nme2, Snrpg, Ndufa2, Serf1, Oaz1, Rps4x, Rps13, Ybx1, Sepp1, Gaa, ACTR10, PIGF, MGST3, SCP2, HPRT1, ACSF2, VPS13A, CTH, NXT2, MGST2, C11orf67, PCCA, GLMN, DHRS1, PON2, NME7, ETFDH, ALG13, DDX60, DYNC2LI1, VPS8, ITFG1, CDK5, C1orf112, IFT52, CLYBL, FAM114A2, NUDT7, AKD1, MAGED2, HRSP12, STX8, ACAT1, IFT74, KIFAP3, CAPN1, COX11, GLT8D4, HACL1, IFT88, NDUFB3, ANO10, ARL6, LPCAT3, ABCD3, COPG2, MIPEP, LEPR, C2orf76, ABCA6, LY96, CROT, ENPP5, SERPINB7, TCP11L2, IRAK1BP1, CDKL2, GHR, KIAA1107, RPS6KA6, CLGN, TMEM45A, TBC1D8B, ACP6, RP6-213H19.1, SNRPN, GLRB, HERC6, CFH, GALC, PDE1A, GSTM5, CADPS2, AASS, TRIM6-TRIM34 (readthrough transcript), SEPP1, PDE5A, SATB1, CCPG1, CNTN1, LMBRD2, TLR3, BCAT1, TOM1L1, SLC35A1, GLYATL2, STAT4, GULP1, EHHADH, NBEAL1, KIAA1598, HFE, KIAA1324L, and MANSC1; preferably from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), Ybx1 (Y Box binding protein 1),~~

Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), and CNTN1 (contactin 1).

62. The method according to claim 60 or the use according to claim 61, wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element comprises a nucleic acid sequence which is derived from the 3'-UTR and/or the 5'-UTR of a transcript of a human gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), Ybx1 (Y-Box binding protein 1), Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), CNTN1 (contactin 1), LTA4H, SLC38A6, DECR1, PIGK, FAM175A, PHYH, TBC1D19, PIGB, ALG6, CRYZ, BRP44L, ACADSB, SUPT3H, TMEM14A, GRAMD1C, C11orf80, C9orf46, ANXA4, TBCK, IFI6, C2orf34, ALDH6A1, AGTPBP1, CCDC53, LRRC28, CCDC109B, PUS10, CCDC104, CASP1, SNX14, SKAP2, NDUFB6, EFHA1, BCKDHB, BBS2, LMBRD1, ITGA6, HERC5, NT5DC1, RAB7A, AGA, TPK1, MBNL3, HADHB, MCCC2, CAT, ANAPC4, PCCB, PHKB, ABCB7, PGCP, GPD2, TMEM38B, NFU1, OMA1, LOC128322/NUTF2, NUBPL, LANCL1, HHLA3, PIR, ACAA2, CTBS, GSTM4, ALG8, ACTR10, PIGF, MGST3, SCP2, HPRT1, ACSF2, VPS13A, CTH, NXT2, MGST2, C11orf67, PCCA, GLMN, DHRS1, PON2, NME7, ETFDH, ALG13, DDX60, DYNC2LI1, VPS8, ITFG1, CDK5, C1orf112, IFT52, CLYBL, FAM114A2, NUDT7, AKD1, MAGED2, HRSP12, STX8, ACAT1, IFT74, KIFAP3, CAPN1, COX11, GLT8D4, HACL1, IFT88, NDUFB3, ANO10, ARL6, LPCAT3, ABCD3, COPG2, MIPEP, LEPR, C2orf76, ABCA6, LY96, CROT, ENPP5, SERPINB7, TCP11L2, IRAK1BP1, CDKL2, GHR, KIAA1107, RPS6KA6, CLGN, TMEM45A, TBC1D8B, ACP6, RP6-213H19.1, SNRPN, GLRB, HERC6, CFH, GALC, PDE1A, GSTM5, CADPS2, AASS, TRIM6-TRIM34 (readthrough transcript), SEPP1, PDE5A, SATB1, CCPG1, LMBRD2, TLR3, BCAT1, TOM1L1, SLC35A1, GLYATL2, STAT4, GULP1, EHHADH, NBEAL1, KIAA1598, HFE, KIAA1324L, and MANSC1.

63. The method according to claim 60 or the use according to claim 61, wherein the at least one 3'-UTR element and/or the at least one 5'-UTR element comprises a nucleic acid sequence which is derived from the 3'-UTR and/or the 5'-UTR of a transcript of a murine gene selected from the group consisting of NDUFA1 (NADH dehydrogenase

(ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), Ybx1 (Y-Box binding protein 1), Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), CNTN1 (contactin 1), Atp5e, Gstm5, Uqcr11, Ifi27l2a, Anapc13, Atp5l, Tmsb10, Nenf, Ndufa7, Atp5k, 1110008P14Rik, Cox4i1, Cox6a1, Ndufs6, Sec61b, Romo1, Snrpd2, Mgst3, Aldh2, Ssr4, Myl6, Prdx4, Ubl5, 1110001J03Rik, Ndufa13, Ndufa3, Gstp2, Tmem160, Ergic3, Pgcp, Slpi, Myeov2, Ndufs5, 1810027O10Rik, Atp5o, Shfm1, Tspo, S100a6, Taldo1, Bloc1s1, Hexa, Ndufb11, Map1lc3a, Gpx4, Mif, Cox6b1, RIKEN cDNA2900010J23 (Swi5), Sec61g, 2900010M23Rik, Anapc5, Mars2, Phpt1, Pfdn5, Arpc3, Ndufb7, Atp5h, Mrpl23, Uba52, Tomm6, Mtch1, Pcbd2, Ecm1, Hrsp12, Mecr, Uqcrq, Gstm3, Lsm4, Park7, Usmg5, Cox8a, Ly6c1, Cox7b, Ppib, Bag1, S100a4, Bcap31, Tecr, Rabac1, Robld3, Sod1, Nedd8, Higd2a, Trappc6a, Ldhb, Nme2, Snrpg, Ndufa2, Serf1, Oaz1, Rps4x, Rps13, Sepp1, and Gaa.

64. The method or the use according to any one of the claims 60 – 63, wherein the at least one 3'-UTR element comprises a nucleic acid sequence which is derived from the 3'-UTR of a transcript of a gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), SLC38A6, DECR1, PIGK, FAM175A, PHYH, TBC1D19, PIGB, ALG6, CRYZ, BRP44L, ACADSB, TMEM14A, GRAMD1C, C11orf80, ANXA4, TBCK, IFI6, C2orf34, ALDH6A1, AGTPBP1, CCDC53, LRRC28, CCDC109B, PUS10, CCDC104, CASP1, SNX14, SKAP2, NDUFB6, EFHA1, BCKDHB, BBS2, LMBRD1, ITGA6, HERC5, HADHB, ANAPC4, PCCB, ABCB7, PGCP, NFU1, OMA1, HHLA3, ACAA2, GSTM4, ALG8, Ndufa1, Atp5e, Gstm5, Uqcr11, Ifi27l2a, Cbr2, Atp5l, Tmsb10, Nenf, Atp5k, 1110008P14Rik, Cox4i1, Cox6a1, Ndufs6, Sec61b, Romo1, Gnas, Snrpd2, Mgst3, Aldh2, Ssr4, Myl6, Prdx4, Ubl5, 1110001J03Rik, Ndufa13, Ndufa3, Gstp2, Tmem160, Ergic3, Pgcp, Slpi, Myeov2, Ndufa4, Ndufs5, Gstm1, 1810027O10Rik, Atp5o, Shfm1, Tspo, S100a6, Taldo1, Bloc1s1, Ndufb11, Map1lc3a, Morn2, Gpx4, Mif, Cox6b1, RIKEN cDNA2900010J23 (Swi5), Sec61g, 2900010M23Rik, Anapc5, Mars2, Phpt1, Ndufb8, Pfdn5, Arpc3, Ndufb7, Atp5h, Mrpl23, Uba52, Tomm6,

~~Mtch1, Pcbd2, Ecm1, Hrsp12, Mecr, Uqcrq, Gstm3, Lsm4, Park7, Usmg5, Cox8a, Ly6c1, Cox7b, Ppib, Bag1, S100a4, Bcap31, Tecr, Rabac1, Robld3, Sod1, Nedd8, Higd2a, Trappc6a, Ldhb, Nme2, Snrpg, Ndufa2, Serf1, Oaz1, Rps4x, Rps13, Ybx1, Sepp1, Gaa, ACTR10, PIGF, MGST3, SCP2, HPRT1, ACSF2, VPS13A, CTH, NXT2, MGST2, C11orf67, PCCA, GLMN, DHRS1, PON2, NME7, ETFDH, ALG13, DDX60, DYNC2LI1, VPS8, ITFG1, CDK5, C1orf112, IFT52, CLYBL, FAM114A2, NUDT7, AKD1, MAGED2, HRSP12, STX8, ACAT1, IFT74, KIFAP3, CAPN1, COX11, GLT8D4, HACL1, IFT88, NDUFB3, ANO10, ARL6, LPCAT3, ABCD3, COPG2, MIPEP, LEPR, C2orf76, ABCA6, LY96, CROT, ENPP5, SERPINB7, TCP11L2, IRAK1BP1, CDKL2, GHR, KIAA1107, RPS6KA6, CLGN, TMEM45A, TBC1D8B, ACP6, RP6-213H19.1, SNRPN, GLRB, HERC6, CFH, GALC, PDE1A, GSTM5, CADPS2, AASS, TRIM6-TRIM34 (readthrough transcript), SEPP1, PDE5A, SATB1, CCPG1, CNTN1, LMBRD2, TLR3, BCAT1, TOM1L1, SLC35A1, GLYATL2, STAT4, GULP1, EHHADH, NBEAL1, KIAA1598, HFE, KIAA1324L, and MANSC1; preferably, the at least one 3'-UTR element comprises or consists of a nucleic acid sequence which is derived from the 3'-UTR of a transcript of a gene selected from the group consisting of NDUFA1 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex), GNAS (guanine nucleotide binding protein, alpha stimulating complex locus), MORN2 (MORN repeat containing 2), GSTM1 (glutathione S-transferase, mu 1), CBR2 (carbonyl reductase 2), Ybx1 (Y-Box binding protein 1), Ndufb8 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8), and CNTN1 (contactin 1).~~

65. ~~The method or the use according to any one of the claims 60 – 63, wherein the at least one 5'-UTR element comprises a nucleic acid sequence which is derived from the 5'-UTR of a transcript of a gene selected from the group consisting of MP68 (RIKEN cDNA 2010107E04 gene), NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4), LTA4H, DECR1, PIGK, TBC1D19, BRP44L, ACADSB, SUPT3H, TMEM14A, C9orf46, ANXA4, IFI6, C2orf34, ALDH6A1, CCDC53, CCDC104, CASP1, NDUFB6, BCKDHB, BBS2, HERC5, FAM175A, NT5DC1, RAB7A, AGA, TPK1, MBNL3, MCCC2, CAT, ANAPC4, PHKB, ABCB7, GPD2, TMEM38B, NFU1, LOC128322/NUTF2, NUBPL, LANCL1, PIR, CTBS, GSTM4, Ndufa1, Atp5e, Gstm5, Cbr2, Anapc13, Ndufa7, Atp5k, 1110008P14Rik, Cox4i1, Ndufs6, Sec61b, Snrpd2, Mgst3, , Prdx4; Pgcp; Myeov2; Ndufa4; Ndufs5; Gstm1; Atp5o; Tspo; Taldo1; Bloc1s1; and Hexa; preferably, the at least one 5'-UTR element comprises or consists of a nucleic acid sequence which is derived from the 5'-~~

~~UTR of a transcript of MP68 (RIKEN cDNA 2010107E04 gene) or NDUFA4 (NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4).~~

~~66. The method or the use according to any one of the claims 60 – 64, wherein the 3'-UTR element comprises or consists of a nucleic acid sequence which has an identity of at least about 40%, preferably of at least about 50%, preferably of at least about 60%, preferably of at least about 70%, more preferably of at least about 80%, more preferably of at least about 90%, even more preferably of at least about 95%, even more preferably of at least about 99% to a sequence selected from the group consisting of SEQ ID NOs: 1 to 24 and SEQ ID NOs: 49 to 318 or wherein the 3'-UTR element comprises or consists of a fragment of a nucleic acid sequence that has an identity of at least about 40%, preferably of at least about 50%, preferably of at least about 60%, preferably of at least about 70%, more preferably of at least about 80%, more preferably of at least about 90%, even more preferably of at least about 95%, even more preferably of at least about 99% to a sequence selected from the group consisting of SEQ ID NOs: 1 to 24 and SEQ ID NOs: 49 to 318.~~

~~67. The method or the use according to any one of the claims 60 – 63 and 65, wherein the 5'-UTR element comprises or consists of a nucleic acid sequence which has an identity of at least about 40%, preferably of at least about 50%, preferably of at least about 60%, preferably of at least about 70%, more preferably of at least about 80%, more preferably of at least about 90%, even more preferably of at least about 95%, even more preferably of at least about 99% to a sequence selected from the group consisting of SEQ ID NOs: 25 to 30 and SEQ ID NOs: 319 to 382 or wherein the 5'-UTR element comprises or consists of a fragment of a nucleic acid sequence that has an identity of at least about 40%, preferably of at least about 50%, preferably of at least about 60%, preferably of at least about 70%, more preferably of at least about 80%, more preferably of at least about 90%, even more preferably of at least about 95%, even more preferably of at least about 99% to a sequence selected from the group consisting of SEQ ID NOs: 25 to 30 and SEQ ID NOs: 319 to 382.~~

~~68. The method or the use according to claim 66 or 67, wherein the fragment exhibits a length of between 3 and about 500 nucleotides, preferably of between 5 and about~~

~~150 nucleotides, more preferably of between 10 and 100 nucleotides, even more preferably of between 15 and 90, most preferably of between 20 and 70.~~

~~69. The method or the use according to any one of claims 60 – 68, wherein the 3'-UTR element and/or the 5'-UTR element exhibits a length of between 3 and about 500 nucleotides, preferably of between 5 and about 150 nucleotides, more preferably of between 10 and 100 nucleotides, even more preferably of between 15 and 90, most preferably of between 20 and 70.~~

~~70. A kit or kit of parts comprising an artificial nucleic acid molecule according to any one of claims 1 – 41, a vector according to any one of claims 42 – 46, a cell according to any one of claims 47 – 49, and/or a pharmaceutical composition according to claim 50 or 51.~~

~~71. The kit according to claim 70~~27. Use of a 3'-UTR element for increasing and/or prolonging protein production from an artificial nucleic acid molecule, from an mRNA molecule or a vector, wherein the 3'-UTR element comprises or consists of a nucleic acid sequence from the 3'-UTR of a transcript of GNAS (guanine nucleotide binding protein, alpha stimulating complex locus).

28. A kit comprising any one or more of an artificial nucleic acid molecule according to any one of claims 1 to 16, a vector according to any one of claims 17 to 19, a cell according to claim 20 or 21, and a pharmaceutical composition according to claim 22 or 23.

29. The kit according to claim 28 further comprising any one or more of instructions for use, cells for transfection, an adjuvant, a means for administration of the pharmaceutical composition, a pharmaceutically acceptable carrier ~~and/or,~~ a pharmaceutically acceptable solution for dissolution or dilution of the artificial nucleic acid molecule, the vector, the cells ~~or,~~ and the pharmaceutical composition.

~~72. A method for identifying a 3'-untranslated region element (3'-UTR element) and/or a 5'-untranslated region element (5'-UTR element), which is derived from a stable mRNA comprising the following steps:~~

~~a) Analyzing the stability of a plurality of mRNA species comprising the following sub-steps:~~

i. Determining the amount of each mRNA species of said plurality of mRNA species at a first point in time during a decay process of said mRNA species,

ii. Determining the amount of each mRNA species of said plurality of mRNA species at a second point in time during a decay process of said mRNA species, and

iii. Calculating for each mRNA species of said plurality of mRNA species the ratio of the amount of said mRNA species determined in step (i) to the the amount of said mRNA species determined in step (ii);

b) Ranking of the mRNA species of the plurality of mRNA species according to the ratio calculated in sub-step (iii) for each mRNA species;

c) Selecting one or more mRNA species having the highest ratio or the highest ratios calculated in sub-step (iii); and

d) Determining the nucleotide sequence of a 3'- and/or 5'-UTR element of said mRNA.

7330. The method for identifying a 3'-UTR element and/or a 5'-UTR element according to claim 72, wherein the time period between the first point in time and the second point in time is at least 5h, preferably at least 6h, preferably at least 7h, more preferably at least 8h, more preferably at least 9h, even more preferably at least 10h, even more preferably at least 11h, and particularly preferably at least 12h.

74. The method for identifying a 3'-UTR element and/or a 5'-UTR element according to any of claims 72 – 73, wherein the stability of an mRNA is analysed by pulse labelling, preferably using a pulse-chase methodology.

75. A method for identifying a 3'-untranslated region element (3'-UTR element) and/or a 5'-untranslated region element (5'-UTR element), which prolongs and/or increases protein production from an artificial nucleic acid molecule and which is derived from a stable mRNA comprising the following steps:

a) identifying a 3'-UTR element and/or a 5'-UTR element which is derived from a stable mRNA by a method for identifying a 3'-UTR element and/or a 5'-UTR element according to any one of claims 72 – 74;

b) synthesizing an artificial nucleic acid molecule comprising at least one open reading frame and at least one 3'-UTR element and/or at least one 5'-UTR element

~~which corresponds~~1 to ~~or is comprised by the 3'-UTR element and/or the 5'-UTR element identified in step a);~~

~~c) analyzing the expression of the protein encoded by the at least one open reading frame of the artificial nucleic acid molecule synthesized in step b);~~

~~d) analyzing the expression of a protein encoded by at least one open reading frame (ORF) of a reference artificial nucleic acid molecule lacking a 3'-UTR element and/or a 5'-UTR element;~~

~~e) comparing the protein expression from the artificial nucleic acid molecule analysed in step c) to the protein expression from the reference artificial nucleic acid molecule analysed in step d); and~~

~~f) selecting the 3'-UTR element and/or the 5'-UTR element if the protein expression from the artificial nucleic acid molecule analysed in step c) is prolonged and/or increased in comparison to the protein expression from the reference artificial nucleic acid molecule analysed in step d).~~

~~76. A method for generating an artificial nucleic acid molecule, wherein an artificial nucleic acid molecule comprising at least one open reading frame and at least one 3'-UTR element and/or at least one 5'-UTR element identified by a method for identifying a 3'-UTR element and/or a 5'-UTR element according to any of claims 72 – 75 is synthesized.~~

~~77. The method for generating an artificial nucleic acid molecule according to claim 76, wherein a~~ 16, the vector according to any ~~of claims 42 – 46 is used for synthesizing the artificial nucleic acid molecule.~~one of claims 17 to 19, the cell according to claim 20 or 21, or the pharmaceutical composition according to claim 22 or 23, for use as a medicament.

~~78~~31. The ~~method for generating an artificial nucleic acid molecule~~use according to claim ~~76 or 77,~~30 wherein the ~~artificial nucleic acid molecule~~medicament is ~~an artificial nucleic acid molecule according to any of claims 1 to 41.~~vaccination or gene therapy.

~~79. An artificial nucleic acid molecule obtainable by a method for generating an artificial nucleic acid molecule according to any of claims 76 – 78.~~