Claims

1. An artificial nucleic acid molecule comprising:

a. at least one 5'-untranslated region element (5'UTR element) which comprises or consists of a nucleic acid sequence which is derived from the 5'UTR of a TOP gene or which is derived from a variant of the 5'UTR of a TOP gene; and

b. at least one open reading frame (ORF).

2. The artificial nucleic acid molecule according to claim 1 further comprisingc. at least one 3'UTR element which comprises or consists of a nucleic acid sequence derived from the 3'UTR of a chordate gene, preferably a vertebrate gene, more preferably a mammalian gene, most preferably a human gene, or from a variant of the 3'UTR of a chordate gene, preferably from a variant of the 3'UTR of a vertebrate gene, more preferably from a variant of the 3'UTR of a mammalian gene, most preferably from a variant of the 3'UTR of a human gene,

wherein the at least one 3'UTR element preferably comprises or consists of a nucleic acid sequence which is derived from a 3'UTR of a gene providing a stable mRNA or from a variant of the 3'UTR of a gene providing a stable mRNA.

3. The artificial nucleic acid molecule according to claim 1 or 2,

wherein the 3'UTR element comprises or consists of a nucleic acid sequence derived from a 3'UTR of a gene selected from the group consisting of an albumin gene, an α-globin gene, a β-globin gene, a tyrosine hydroxylase gene, a lipoxygenase gene, and a collagen alpha gene, or from a variant of a 3'UTR of a gene selected from the group consisting of an albumin gene, an α-globin gene, a β-globin gene, a tyrosine hydroxylase gene, a lipoxygenase gene, and a collagen alpha gene.

4. The artificial nucleic acid molecule according to any one of claims 1-3, wherein the at least one 3'UTR element comprises or consist of a nucleic acid sequence

which is derived from the 3'UTR of a vertebrate albumin gene or from a variant thereof, preferably from the 3'UTR of a mammalian albumin gene or from a variant thereof, more preferably from the 3'UTR of a human albumin gene or from a variant thereof, even more preferably from the 3'UTR of the human albumin gene according to GenBank Accession number NM_000477.5 or from a variant thereof.

5. The artificial nucleic acid molecule according to any one of claims 1-4, wherein the at least one 3'UTR element exhibits a length of at least about 50 nucleotides, preferably of at least about 75 nucleotides, more preferably of at least about 100 nucleotides, even more preferably of at least about 125 nucleotides, most preferably of at least about 150 nucleotides.

6. The artificial nucleic acid molecule according to claims 1-5, wherein the 5'UTR element and the open reading frame are heterologous and wherein the 5'UTR lacks the 5'TOP motif or the 5'UTR does not contain a functional 5'TOP motif, e.g. by insertions, deletions or substitutions of the 5'TOP motif..

7. The artificial nucleic acid molecule according to claim 1 to 6, wherein the 5'UTR element is suitable for increasing protein production from the artificial nucleic acid molecule.

8. The artificial nucleic acid molecule according to any one of claims 1-7, wherein the 5'UTR element does not comprise a TOP-motif, preferably wherein the nucleic acid sequence which is derived from a 5'UTR of a TOP gene, preferably the 5'UTR element, starts at its 5'-end with a nucleotide located at position 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 downstream of the TOP-motif of the 5'UTR of the TOP gene.

9. The artificial nucleic acid molecule according to any one of claims 1-8, wherein the nucleic acid sequence which is derived from a 5'UTR of a TOP gene, preferably the 5'UTR element terminates at its 3'-end with a nucleotide located at position 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 upstream of the start codon of the open reading frame of the gene or mRNA it is derived from.

10. The artificial nucleic acid molecule according to any one of claims 1-9, wherein the nucleic acid sequence which is derived from the 5'UTR of a TOP gene is derived from the 5'UTR of a eukaryotic TOP gene or from a variant thereof, preferably from the 5'UTR of a plant or animal TOP gene or from a variant thereof, more preferably from the 5'UTR of a chordate TOP gene or from a variant thereof, even more preferably from the 5'UTR of a vertebrate TOP gene or from a variant thereof, most preferably from the 5'UTR of a mammalian TOP gene, such as a human TOP gene, or from a variant thereof.

11. The artificial nucleic acid molecule according to any of claims 1 to 10, wherein the at least one 3'UTR element and the at least one 5'UTR element act at least additively, preferably synergistically to increase protein production from said artificial nucleic acid molecule.

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

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

13. The artificial nucleic acid molecule according to claim 12, wherein the polyadenylation signal is located within the 3'UTR element.

14. The artificial nucleic acid molecule according to claim 12 or 13, 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.

15. The artificial nucleic acid molecule according to any one of claims 12-14, wherein the polyadenylation signal, preferably the consensus sequence NNUANA, is located less than about 50 nucleotides upstream of the 3'-end of the 3'UTR.

16. The artificial nucleic acid molecule according to any one of claims 12-15, 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.

17. The artificial nucleic acid molecule according to any one of claims 1-16, wherein the 5'UTR element is derived from a 5'UTR of a TOP gene encoding a ribosomal Large protein (RPL) or from a variant of a 5'UTR of a TOP gene encoding a ribosomal Large protein (RPL), wherein the 5'UTR lacks the 5'TOP motif or the 5'UTR does not contain a functional 5'TOP motif, e.g. by insertions, deletions or substitutions of the 5'TOP motif.

18. The artificial nucleic acid molecule according to any one of claims 1-17, wherein the 5'UTR element comprises or consists of a nucleic acid sequence having 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 the 5'UTR of a nucleic acid sequence according to any of SEQ ID NOs. 67, 259, 1284-1318, 1344, 1346, 1348-1354, 1357, 1358, 1421 or 1422 or to a corresponding RNA sequence, preferably lacking the 5'TOP motif, 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 the 5'UTR of a nucleic acid sequence according to SEQ ID No. SEQ ID NOs: 67, 259, 1284-1318, 1344, 1346, 1348-1354, 1357, and 1358, 1421 or 1422 or to a corresponding RNA sequence, preferably lacking the 5'TOP motif.

19. The artificial nucleic acid molecule according to any one of claims 1-18, wherein the 5'UTR element comprises or consists of a nucleic acid sequence which is derived from the 5'UTR a ribosomal protein Large 32 gene (RPL32), a ribosomal protein Large 35 gene (RPL35), a ribosomal protein Large 21 gene (RPL21), an ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle (ATP5A1) gene, an hydroxysteroid (17-beta) dehydrogenase 4 gene (HSD17B4), an androgen-induced 1 gene (AIG1),

cytochrome c oxidase subunit VIc gene (COX6C), or a N-acylsphingosine amidohydrolase (acid ceramidase) 1 gene (ASAH1) or from a variant thereof, preferably from a vertebrate ribosomal protein Large 32 gene (RPL32), a vertebrate ribosomal protein Large 35 gene (RPL35), a vertebrate ribosomal protein Large 21 gene (RPL21), a vertebrate ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle (ATP5A1) gene, a vertebrate hydroxysteroid (17-beta) dehydrogenase 4 gene (HSD17B4), a vertebrate androgen-induced 1 gene (AIG1), a vertebrate cytochrome c oxidase subunit VIc gene (COX6C), or a vertebrate N-acylsphingosine amidohydrolase (acid ceramidase) 1 gene (ASAH1) or from a variant thereof, more preferably from a mammalian ribosomal protein Large 32 gene (RPL32), a ribosomal protein Large 35 gene (RPL35), a ribosomal protein Large 21 gene (RPL21), a mammalian ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle (ATP5A1) gene, a mammalian hydroxysteroid (17-beta) dehydrogenase 4 gene (HSD17B4), a mammalian androgen-induced 1 gene (AIG1), a mammalian cytochrome c oxidase subunit VIc gene (COX6C), or a mammalian N-acylsphingosine amidohydrolase (acid ceramidase) 1 gene (ASAH1) or from a variant thereof, most preferably from a human ribosomal protein Large 32 gene (RPL32), a human ribosomal protein Large 35 gene (RPL35), a human ribosomal protein Large 21 gene (RPL21), a human ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle (ATP5A1) gene, a human hydroxysteroid (17-beta) dehydrogenase 4 gene (HSD17B4), a human androgen-induced 1 gene (AIG1), a human cytochrome c oxidase subunit VIc gene (COX6C), or a human N-acylsphingosine amidohydrolase (acid ceramidase) 1 gene (ASAH1) or from a variant thereof, wherein preferably the 5'UTR element does not comprise the 5'TOP motif of said gene.

20. The artificial nucleic acid molecule according to any one of claims 1-19, 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 the nucleic acid sequence according to SEQ ID NO. 1368 or SEQ ID NOs 1412-1420, or to a corresponding RNA sequence, 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 the nucleic acid sequence according to SEQ ID No. 1368 or SEQ ID NOs 1412-1420, or to a corresponding RNA sequence.

21. The artificial nucleic acid molecule according to any one of claims 18 or 20, , wherein the fragment consists of a continuous stretch of nucleotides corresponding to a continuous stretch of nucleotides in the full-length sequence, which represents at least 20%, preferably at least 30%, more preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, even more preferably at least 70%, even more preferably at least 80%, and most preferably at least 90% of the full-length sequence the fragment is derived from.

22. The artificial nucleic acid molecule according to any one of claims 1-21, wherein the at least one 5'UTR element exhibits a length of at least about 20 nucleotides, preferably of at least about 30 nucleotides, more preferably of at least about 40 nucleotides.

23. The artificial nucleic acid molecule according to any one of claims 1-22, wherein the at least one 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 nucleic acid sequence selected from SEQ ID NOs. 1369-1393 or to a corresponding RNA sequence, 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 a nucleic acid sequence selected from SEQ ID NOs. 1369-1393 or to a corresponding RNA sequence.

24. The artificial nucleic acid molecule according to claim 23, wherein the fragment consists of a continuous stretch of nucleotides corresponding to a continuous stretch of nucleotides in the full-length sequence, which represents at least 20%, preferably at least 30%, more preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, even more preferably at least 70%, even more preferably at least 80%, and most preferably at least 90% of the full-length sequence the fragment is derived from.

25. The artificial nucleic acid molecule according to claim 23 or 24, wherein the fragment exhibits a length of at least about 50 nucleotides, preferably of at least about 75 nucleotides, more preferably of at least about 100 nucleotides, even more preferably of at least about 125 nucleotides, most preferably of at least about 150 nucleotides.

26. The artificial nucleic acid molecule according to any one of claims 1-25, wherein the at least one 3'UTR element exhibits a length of at least about 50 nucleotides, preferably of at least about 75 nucleotides, more preferably of at least about 100 nucleotides, even more preferably of at least about 125 nucleotides, most preferably of at least about 150 nucleotides.

27. The artificial nucleic acid molecule according to any one of claims 1-26, wherein the open reading frame does not code for a reporter protein, such as a GFP protein, a luciferase protein, a globin protein, human growth hormon, or human albumin, preferably not for albumin.

28. The artificial nucleic acid molecule according to any one of claims 1-27, further comprising a 5'-cap structure, a poly(C) sequence and/or an IRES-motif.

29. The artificial nucleic acid molecule according to any one of claims 1-28, further comprising a promoter containing-sequence.

30. The artificial nucleic acid molecule according to any one of claims 1-29, 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.

31. The artificial nucleic acid molecule according to any one of claims 1-30, wherein the open reading frame comprises a codon-optimized region, preferably, wherein the open reading frame is codon-optimized.

32. The artificial nucleic acid molecule according to any one of claims 1-31, which is an RNA, preferably an mRNA molecule.

33. A vector comprising:

a. at least one 5'-untranslated region element (5'UTR element) which comprises or consists of a nucleic acid sequence which is derived from the 5'UTR of a TOP gene or which is derived from a variant of the 5'UTR of a TOP gene; and

b. at least one open reading frame (ORF) and/or at least one cloning site.

34. The vector according to claim 33 further comprising

c. at least one 3'UTR element which comprises or consists of a nucleic acid sequence derived from the 3'UTR of a chordate gene, preferably a vertebrate gene, more preferably a mammalian gene, most preferably a human gene, or from a variant of the 3'UTR of a chordate gene, preferably from a variant of the 3'UTR of a vertebrate gene, more preferably from a variant of the 3'UTR of a mammalian gene, most preferably from a variant of the 3'UTR of a human gene,

wherein the at least one 3'UTR element preferably comprises or consists of a nucleic acid sequence which is derived from a 3'UTR of a gene providing a stable mRNA or from a variant of the 3'UTR of a gene providing a stable mRNA.

35. The vector according to any one of claims 33 or 34, wherein the 3'UTR element comprises or consists of a nucleic acid sequence derived from a 3'UTR of a gene

selected from the group consisting of an albumin gene, an α-globin gene, a β-globin gene, a tyrosine hydroxylase gene, a lipoxygenase gene, and a collagen alpha gene, or from a variant of a 3'UTR of a gene selected from the group consisting of an albumin gene, an α-globin gene, a β-globin gene, a tyrosine hydroxylase gene, a lipoxygenase gene, and a collagen alpha gene.

36. The vector according to any one of claims 33-35, wherein the at least one 3'UTR element comprises or consist of a nucleic acid sequence which is derived from the 3'UTR of a vertebrate albumin gene or from a variant thereof, preferably from the 3'UTR of a mammalian albumin gene or from a variant thereof, more preferably from the 3'UTR of a human albumin gene or from a variant thereof, even more preferably from the 3'UTR of the human albumin gene according to GenBank Accession number NM_000477.5 or from a variant thereof.

37. The vector according to any of claims 33 to 36, wherein the 5'UTR element and the open reading frame are heterologous.

38. The vector according to any of claims 33 to 37, wherein the 5'UTR element is suitable for increasing protein production from the vector.

39. The vector according to any one of claims 33 to 38, wherein the 5'UTR element does not comprise a TOP-motif, preferably wherein the nucleic acid sequence which is derived from a 5'UTR of a TOP gene, preferably the 5'UTR element, starts at its 5'-end with a nucleotide located at position 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 downstream of the TOP-motif of the 5'UTR of the TOP gene.

40. The vector according to any one of claims 33-39, wherein the nucleic acid sequence which is derived from a 5'UTR of a TOP gene, preferably the 5'UTR element terminates at its 3'-end with a nucleotide located at position 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 upstream of the start codon of the open reading frame of the gene or mRNA it is derived from.

41. The vector according to any one of claims 33-40, wherein the nucleic acid sequence which is derived from the 5'UTR of a TOP gene is derived from a eukaryotic TOP gene, preferably a plant or animal TOP gene, more preferably a chordate TOP gene, even more preferably a vertebrate TOP gene, most preferably a mammalian TOP gene, such as a human TOP gene.

42. The vector according to any of claims 34 to 41, wherein the at least one 3'UTR element and the at least one 5'UTR element act at least additively, preferably synergistically to increase protein production from said artificial nucleic acid molecule.

43. The vector according to any one of claims 33-42, further comprising

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

44. The vector according to claim 43, wherein the polyadenylation signal is located within the 3'UTR element.

45. The vector according to claim 43 or 44, 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.

46. The vector according to any one of claims 43-45, wherein the polyadenylation signal, preferably the consensus sequence NNUANA, is located less than about 50 nucleotides upstream of the 3'-end of the 3'UTR.

47. The vector according to any one of claims 43-46, 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.

48. The vector according to any one of claims 33-47, wherein the 5'UTR element comprises or consists of a nucleic acid sequence which is derived from a 5'UTR of a TOP gene encoding a ribosomal protein or from a variant of a 5'UTR of a TOP gene encoding a ribosomal protein, preferably from a 5'UTR of a ribosomal protein selected from RPSA, RPS2, RPS3, RPS3A, RPS4, RPS5, RPS6, RPS7,

RPS8, RPS9, RPS10, RPS11, RPS12, RPS13, RPS14, RPS15, RPS15A, RPS16, RPS17, RPS18, RPS19, RPS20, RPS21, RPS23, RPS24, RPS25, RPS26, RPS27, RPS27A, RPS28, RPS29, RPS30, RPL3, RPL4, RPL5, RPL6, RPL7, RPL7A, RPL8, RPL9, RPL10, RPL10A, RPL11, RPL12, RPL13, RPL13A, RPL14, RPL15, RPL17, RPL18, RPL18A, RPL19, RPL21, RPL22, RPL23, RPL23A, RPL24, RPL26, RPL27, RPL27A, RPL28, RPL29, RPL30, RPL31, RPL32, RPL34, RPL35, RPL35A, RPL36, RPL36A, RPL37, RPL37A, RPL38, RPL39, RPL40, RPL41, RPLP0, RPLP1, RPLP2, RPLP3, UBA52 ,more preferably from a 5'UTR of a nucleic acid sequence according to any of SEQ ID NOs: 67, 170, 193, 244, 259, 554, 650, 675, 700, 721, 913, 1016, 1063, 1120, 1138, and 1284-1360, a corresponding RNA sequence, a homolog thereof, or a variant thereof as described herein, preferably lacking the 5'TOP motif.

49. The vector according to any one of claims 33-48, wherein the 5'UTR element comprises or consists of a nucleic acid sequence which is derived from the 5'UTR a ribosomal protein Large 32 gene (RPL32), a ribosomal protein Large 35 gene (RPL35), a ribosomal protein Large 21 gene (RPL21), an ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle (ATP5A1) gene, an hydroxysteroid (17-beta) dehydrogenase 4 gene (HSD17B4), an androgen-induced 1 gene (AIG1), cytochrome c oxidase subunit VIc gene (COX6C), or a N-acylsphingosine amidohydrolase (acid ceramidase) 1 gene (ASAH1) or from a variant thereof, preferably from a vertebrate ribosomal protein Large 32 gene (RPL32), a ribosomal protein Large 35 gene (RPL35), a ribosomal protein Large 21 gene (RPL21), an ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle (ATP5A1) gene, an hydroxysteroid (17-beta) dehydrogenase 4 gene (HSD17B4), an androgen-induced 1 gene (AIG1), cytochrome c oxidase subunit VIc gene (COX6C), or a N-acylsphingosine amidohydrolase (acid ceramidase) 1 gene (ASAH1) or from a variant thereof, more preferably from a mammalian ribosomal protein Large 32 gene (RPL32), a ribosomal protein Large 35 gene (RPL35), a ribosomal protein Large 21 gene (RPL21), an ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle (ATP5A1) gene, an hydroxysteroid

(17-beta) dehydrogenase 4 gene (HSD17B4), an androgen-induced 1 gene (AIG1), cytochrome c oxidase subunit VIc gene (COX6C), or a N-acylsphingosine amidohydrolase (acid ceramidase) 1 gene (ASAH1) or from a variant thereof, most preferably from a human ribosomal protein Large 32 gene (RPL32), a ribosomal protein Large 35 gene (RPL35), a ribosomal protein Large 21 gene (RPL21), an ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle (ATP5A1) gene, an hydroxysteroid (17-beta) dehydrogenase 4 gene (HSD17B4), an androgen-induced 1 gene (AIG1), cytochrome c oxidase subunit VIc gene (COX6C), or a N-acylsphingosine amidohydrolase (acid ceramidase) 1 gene (ASAH1) or from a variant thereof, wherein preferably the 5'UTR element does not comprise the 5'TOP of said gene.

50. The vector according to any one of claims 33-49, 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 the nucleic acid sequence according to SEQ ID No. 1368 or SEQ ID NOs 1412-1420, or to a corresponding RNA sequence, 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 the nucleic acid sequence according to SEQ ID No. 1368 or SEQ ID NOs 1412-1420, or to a corresponding RNA sequence.

51. The vector according to claim 50, wherein the fragment consists of a continuous stretch of nucleotides corresponding to a continuous stretch of nucleotides in the full-length sequence, which represents at least 20%, preferably at least 30%, more preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, even more preferably at least 70%, even more

preferably at least 80%, and most preferably at least 90% of the full-length sequence the fragment is derived from.

52. The vector according to any one of claims 33-51, wherein the at least one 5'UTR element exhibits a length of at least about 20 nucleotides, preferably of at least about 30 nucleotides, more preferably of at least about 40 nucleotides.

53. The vector according to any one of claims 34-52, wherein the at least one 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 nucleic acid sequence selected from SEQ ID NOs. 1369-1393 or to a corresponding RNA sequence, 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 a nucleic acid sequence selected from SEQ ID NOs. 1369-1393 or to a corresponding RNA sequence.

54. The vector according to claim 53, wherein the fragment consists of a continuous stretch of nucleotides corresponding to a continuous stretch of nucleotides in the full-length sequence, which represents at least 20%, preferably at least 30%, more preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, even more preferably at least 70%, even more preferably at least 80%, and most preferably at least 90% of the full-length sequence the fragment is derived from.

55. The vector according to claim 53 or 54, wherein the fragment exhibits a length of at least about 40 nucleotides, preferably of at least about 50 nucleotides, preferably of at least about 75 nucleotides, more preferably of at least about 100 nucleotides, even more preferably of at least about 125 nucleotides, most preferably of at least about 150 nucleotides.

56. The vector according to any one of claims 34-55, wherein the at least one 3'UTR element exhibits a length of at least about 40 nucleotides, preferably of at least about 50 nucleotides, preferably of at least about 75 nucleotides, more preferably of at least about 100 nucleotides, even more preferably of at least about 125 nucleotides, most preferably of at least about 150 nucleotides.

57. The vector according to any one of claims 33-56, wherein the open reading frame does not code for a reporter protein, such as a GFP protein, a luciferase protein, a globin protein, human growth factor or human albumin, preferably not for albumin.

58. The vector according to any one of claims 33-57, further comprising a 5'-cap structure, a poly(C) sequence and/or an IRES-motif.

59. The vector according to any one of claims 33-58, further comprising a promoter containing-sequence.

60. The vector according to any one of claims 33-59, wherein the vector, 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.

61. The vector according to any one of claims 33-60, wherein the open reading frame comprises a codon-optimized region, preferably, wherein the open reading frame is codon-optimized.

62. The vector according to any one of claims 33-61, which is an RNA vector.

63. The vector according to any one of claims 33-62, which is a DNA vector.

64. The vector according to any one of claims 33-63, which is a plasmid vector or a viral vector, preferably a plasmid vector.

65. The vector according to any one of claims 33-64, which comprises or codes for an artificial nucleic acid molecule according to any one of claims 1-39.

66. The vector according to any one of claims 33-65, which is a circular molecule.

67. The vector according to claim 66, wherein the ORF, the poly(A) sequence 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.

68. A cell comprising the artificial nucleic acid molecule according to any one of claims 1-32 or the vector according to any one of claims 33-67.

69. The cell according to claim 68, which is a mammalian cell.

70. The cell according to claim 68 or 69, which is a cell of a mammalian subject, preferably an isolated cell of a mammalian subject, preferably of a human subject.

71. A pharmaceutical composition comprising the artificial nucleic acid molecule according to any one of claims 1-32, the vector according to any one of claims 33-67, or the cell according to any one of claims 68-70.

72. The pharmaceutical composition according to claim 71, further comprising one or more pharmaceutically acceptable diluents and/or excipients and/or one or more adjuvants.

73. The artificial nucleic acid molecule according to any one of claims 1-32, the vector according to any one of claims 33-67, the cell according to any one of claims 68-70, or the pharmaceutical composition according to claim 71 or 72 for use as a medicament.

74. The artificial nucleic acid molecule according to any one of claims 1-32, the vector according to any one of claims 33-67, the cell according to any one of claims 68-70, or the pharmaceutical composition according to claim 71 or 72 for use as a vaccine or for use in gene therapy.

75. A method for treating or preventing a disorder comprising administering the artificial nucleic acid molecule according to any one of claims 1-32, the vector according to any one of claims 33-67, the cell according to any one of claims 68-70, or the pharmaceutical composition according to claim 71 or 72 to a subject in need thereof.

76. A method of treating or preventing a disorder comprising transfection of a cell with the artificial nucleic acid molecule according to any one of claims 1-32 or the vector according to any one of claims 33-67.

77. The method according to claim 76, 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.

78. The method according to claim 77, wherein the cell which is to be transfected *in vitro* is an isolated cell of the subject, preferably of the human patient.

79. The method according to any one of claims 75-78, which is a vaccination method or a gene therapy method.

80. A method for increasing protein production from an artificial nucleic acid molecule, comprising the step of providing the artificial nucleic acid molecule with:

i. at least one 5'-untranslated region element (5'UTR element) which comprises or consists of a nucleic acid sequence which is derived from the 5'UTR of a TOP gene or which is derived from a variant of the 5'UTR of a TOP gene.

81. The method according to claim 80, wherein the 5'UTR element does not comprise a TOP-motif, preferably wherein the nucleic acid sequence which is derived from a 5'UTR of a TOP gene, preferably the 5'UTR element, starts at its 5'-end with a nucleotide located at position 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 downstream of the TOP-motif of the 5'UTR of the TOP gene.

82. The method according to claim 80 or 81, wherein the 5'UTR lacks the 5'TOP motif or the 5'UTR does not contain a functional 5'TOP motif, e.g. by insertions, deletions or substitutions of the 5'TOP motif.

83. The method according to any of claims 80 to 82, further comprising providing the artificial nucleic acid molecule with:

ii. at least one 3'UTR element which comprises or consists of a nucleic acid sequence derived from the 3'UTR of a chordate gene, preferably a vertebrate

gene, more preferably a mammalian gene, most preferably a human gene, or from a variant of the 3'UTR of a chordate gene, preferably from a variant of the 3'UTR of a vertebrate gene, more preferably from a variant of the 3'UTR of a mammalian gene, most preferably from a variant of the 3'UTR of a human gene.

84. Use of a 5'UTR element which comprises or consists of a nucleic acid sequence which is derived from the 5'UTR of a TOP gene or which is derived from a variant of the 5'UTR of a TOP gene for increasing protein production from a nucleic acid molecule.

85. Use according to claim 84, wherein the 5'UTR element does not comprise a TOP-motif, preferably wherein the nucleic acid sequence which is derived from a 5'UTR of a TOP gene, preferably the 5'UTR element, starts at its 5'-end with a nucleotide located at position 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 downstream of the TOP-motif of the 5'UTR of the TOP gene.

86. The use according to claim 84 or 85, wherein the 5'UTR lacks the 5'TOP motif or the 5'UTR does not contain a functional 5'TOP motif, e.g. by insertions, deletions or substitutions of the 5'TOP motif.

87. Use according to any of claims 84 to 86, wherein the 5'UTR element is used in combination with a 3'UTR element which comprises or consists of a nucleic acid sequence derived from the 3'UTR of a chordate gene, preferably a vertebrate gene, more preferably a mammalian gene, most preferably a human gene, or from a variant of the 3'UTR of a chordate gene, preferably from a variant of the 3'UTR of a vertebrate gene, more preferably from a variant of the 3'UTR of a mammalian gene, most preferably from a variant of the 3'UTR of a human gene.

88. A kit or kit of parts comprising an artificial nucleic acid molecule according to any one of claims 1-32, the vector according to any one of claims 34-67, or the cell according to any one of claims 68-70, and/or the pharmaceutical composition according to claim 71 or 72.

89. The kit according to claim 88, further comprising 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 or the pharmaceutical composition.

Claims:

1. An invention not claimed in any divisional application.