## 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 comprising:

   c. at least one histone stem-loop.

3. The artificial nucleic acid molecule according to claim 1 or 2, wherein the 5'UTR element and the open reading frame are heterologous.

4. The artificial nucleic acid molecule according to any one of claims 1-3, wherein the 5'UTR element is suitable for increasing protein production from the artificial nucleic acid molecule.

5. The artificial nucleic acid molecule according to any one of claims 2-4, wherein the 5'UTR element and the histone stem-loop act together, preferably at least additively, to increase protein production from the artificial nucleic acid molecule.

6. The artificial nucleic acid molecule according to any one of claims 1-5, 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 polypyrimidine tract.

7. The artificial nucleic acid molecule according to any one of claims 1-6, 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 gene it is derived from.

8. The artificial nucleic acid molecule according to any one of claims 1-7, wherein the 5'UTR element does not comprise a start codon or an open reading frame.

9. The artificial nucleic acid molecule according to any one of claims 1-8, 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.

10. The artificial nucleic acid molecule according to any one of claims 2-9, wherein the at least one histone stem-loop is selected from following formulae (I) or (II):

formula (I) (stem-loop sequence without stem bordering elements):

$$\underbrace{[N_{0-2}GN_{3-5}]}_{\text{stem1}}\ \underbrace{[N_{0-4}(U/T)N_{0-4}]}_{\text{loop}}\ \underbrace{[N_{3-5}CN_{0-2}]}_{\text{stem2}}$$

formula (II) (stem-loop sequence with stem bordering elements):

$$\underbrace{N_{1-6}}_{\text{stem1 bordering element}}\ \underbrace{[N_{0-2}GN_{3-5}]}_{\text{stem1}}\ \underbrace{[N_{0-4}(U/T)N_{0-4}]}_{\text{loop}}\ \underbrace{[N_{3-5}CN_{0-2}]}_{\text{stem2}}\ \underbrace{N_{1-6}}_{\text{stem2 bordering element}}$$

wherein:

stem1 or stem2 bordering elements $N_{1-6}$ is a consecutive sequence of 1 to 6, preferably of 2 to 6, more preferably of 2 to 5, even more preferably of 3 to 5, most preferably of 4 to 5 or 5 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C, or a nucleotide analogue thereof;

stem1 $[N_{0-2}GN_{3-5}]$ is reverse complementary or partially reverse complementary with element stem2, and is a consecutive sequence between of 5 to 7 nucleotides;

wherein $N_{0-2}$ is a consecutive sequence of 0 to 2, preferably of 0 to 1, more preferably of 1 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C or a nucleotide analogue thereof;

wherein $N_{3-5}$ is a consecutive sequence of 3 to 5, preferably of 4 to 5, more preferably of 4 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C or a nucleotide analogue thereof, and

wherein G is guanosine or an analogue thereof, and may be optionally replaced by a cytidine or an analogue thereof, provided that its complementary nucleotide cytidine in stem2 is replaced by guanosine;

loop sequence $[N_{0-4}(U/T)N_{0-4}]$is located between elements stem1 and stem2, and is a consecutive sequence of 3 to 5 nucleotides, more preferably of 4 nucleotides;

wherein each $N_{0-4}$ is independent from another a consecutive sequence of 0 to 4, preferably of 1 to 3, more preferably of 1 to 2 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C or a nucleotide analogue thereof; and

wherein U/T represents uridine, or optionally thymidine;

stem2 [$N_{3-5}CN_{0-2}$] is reverse complementary or partially reverse complementary with element stem1, and is a consecutive sequence between of 5 to 7 nucleotides;

wherein $N_{3-5}$ is a consecutive sequence of 3 to 5, preferably of 4 to 5, more preferably of 4 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C or a nucleotide analogue thereof;

wherein $N_{0-2}$ is a consecutive sequence of 0 to 2, preferably of 0 to 1, more preferably of 1 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C or a nucleotide analogue thereof; and

wherein C is cytidine or an analogue thereof, and may be optionally replaced by a guanosine or an analogue thereof provided that its complementary nucleotide guanosine in stem1 is replaced by cytidine;

wherein

stem1 and stem2 are capable of base pairing with each other

forming a reverse complementary sequence, wherein base pairing may occur between stem1 and stem2, or

forming a partially reverse complementary sequence, wherein an incomplete base pairing may occur between stem1 and stem2.

11. The artificial nucleic acid molecule according to any one of claims 2-10, wherein the at least one histone stem-loop is selected from at least one of following formulae (Ia) or (IIa):

$$\underbrace{[N_{0-1}GN_{3-5}]}_{\text{stem1}}\ \underbrace{[N_{1-3}(U/T)N_{0-2}]}_{\text{loop}}\ \underbrace{[N_{3-5}CN_{0-1}]}_{\text{stem2}}$$

formula (Ia) (stem-loop sequence without stem bordering elements)

$$\underbrace{N_{2-5}}_{\text{stem1 bordering element}}\ \underbrace{[N_{0-1}GN_{3-5}]}_{\text{stem1}}\ \underbrace{[N_{1-3}(U/T)N_{0-2}]}_{\text{loop}}\ \underbrace{[N_{3-5}CN_{0-1}]}_{\text{stem2}}\ \underbrace{N_{2-5}}_{\text{stem2 bordering element}}$$

formula (IIa) (stem-loop sequence with stem bordering elements)

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 poly(A) sequence comprises or consists of a sequence of about 25 to about 400 adenosine nucleotides, preferably a sequence of about 50 to about 400 adenosine nucleotides, more preferably a sequence of about 50 to about 300 adenosine nucleotides, even more preferably a sequence of about 50 to about 250 adenosine nucleotides, most preferably a sequence of about 60 to about 250 adenosine nucleotides.

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 of claims 1-14, further comprising:

e. a poly(C) sequence.

16. The artificial nucleic acid molecule according to claim 15, wherein the poly(C) sequence comprises, preferably consists of, about 10 to about 200 cytidine nucleotides, more preferably about 10 to about 100 cytidine nucleotides, more preferably about 10 to about 50 cytidine nucleotides, even more preferably about 20 to about 40 cytidine nucleotides.

17. The artificial nucleic acid molecule according to any one of claims 1-16, further comprising:

f. at least one 3'UTR element.

18. The artificial nucleic acid molecule according to claim 17, wherein the at least one 3'UTR element 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.

19. The artificial nucleic acid molecule according to claim 17 or 18, 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.

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 is derived from a nucleic acid sequence selected from the group consisting of SEQ ID NOs. 1-1363, SEQ ID NO. 1435, SEQ ID NO. 1461 or SEQ ID NO. 1462, , from the homologs of any of SEQ ID NOs. 1-1363, SEQ ID NO. 1435, SEQ ID NO. 1461 or SEQ ID NO. 1462, , or from a variant thereof.

21. The artificial nucleic acid molecule according to any one of claims 1-20, 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 nucleic acid sequence selected from SEQ ID NOs. 1-1363, SEQ ID NO. 1435, SEQ ID NO. 1461 or SEQ ID NO. 1462, 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 a nucleic acid sequence selected from SEQ ID NOs. 1-1363, SEQ ID NO. 1435, SEQ ID NO. 1461 or SEQ ID NO. 1462, or to a corresponding RNA sequence, preferably lacking the 5'TOP motif.

22. The artificial nucleic acid molecule according to any one of claims 1-21, 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 nucleic acid sequence according to any of SEQ ID NOs: 170, 232, 244, 259, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, or 1360;, a corresponding RNA sequence, a homolog thereof, or a variant thereof, preferably lacking the 5'TOP motif.

23. The artificial nucleic acid molecule according to any one of claims 1-22, 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 5'UTR of a nucleic acid sequence according to any of SEQ ID NOs: 170, 232, 244, 259, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, or 1360;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 NOs: 170, 232, 244, 259, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, or 1360;or to a corresponding RNA sequence, preferably lacking the 5'TOP motif.

24. The artificial nucleic acid molecule according to any one of claims 1-23, 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), preferably from a 5'UTR of a nucleic acid sequence according to any of SEQ ID NOs: 67, 259, 1284-1318, 1344, 1346, 1348-1354, 1357, 1461 and 1462, a corresponding RNA sequence, a homolog thereof, or a variant thereof, preferably lacking the 5'TOP motif.

25. The artificial nucleic acid molecule according to any one of claims 1-24, 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, 1461 and 1462, 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, 1461 and 1462 or to a corresponding RNA sequence, preferably lacking the 5'TOP motif.

26. The artificial nucleic acid molecule according to any one of claims 1-25, wherein the 5'UTR element comprises or consists of a nucleic acid sequence which is derived from the 5'UTR of a ribosomal protein Large 32 gene or from a variant thereof, preferably from the 5'UTR of a vertebrate ribosomal protein Large 32 (L32) gene or from a variant thereof, more preferably from the 5'UTR of

a mammalian ribosomal protein Large 32 (L32) gene or from a variant thereof, most preferably from the 5'UTR of a human ribosomal protein Large 32 (L32) gene or from a variant thereof, wherein preferably the 5'UTR element, preferably the artificial nucleic acid molecule does not comprise the 5'TOP of said gene.

27. The artificial nucleic acid molecule according to any one of claims 1-26, 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 NOs. 1368 or 1452-1460, or 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 NOs. 1368 or 1452-1460, or to a corresponding RNA sequence.

28. The artificial nucleic acid molecule according to any one of claims 21, 23, 25 and 27, 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.

29. The artificial nucleic acid molecule according to any one of claims 1-28, 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.

30. The artificial nucleic acid molecule according to any one of claims 1-29, wherein the 5'UTR element comprises or consists of a nucleic acid sequence which is derived from the 5'UTR of a TOP gene 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 or from a variant thereof.

31. The artificial nucleic acid molecule according to any one of claims 2-30, wherein the at least one histone stem-loop comprises or consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs. 1391-1433, preferably from the group consisting of SEQ ID NOs. 1403-1433.

32. The artificial nucleic acid molecule according to any one of claims 2-31, wherein the histone stem-loop comprises or consists of a nucleic acid sequence having a sequence identity of at least about 75%, preferably of at least about 80%, preferably of at least about 85%, more preferably of at least about 90%, even more preferably of at least about 95% to the sequence according to SEQ ID NO. 1433 or to the corresponding RNA sequence, wherein preferably positions 6, 13 and 20 of the sequence having a sequence identity of at least about 75%,

preferably of at least about 80%, preferably at least about 85%, more preferably at least about 90%, even more preferably at least about 95% to the sequence according to SEQ ID NO. 1433 or to the corresponding RNA sequence are conserved, i.e. are identical to the nucleotides at positions 6, 13 and 20 of SEQ ID NO. 1433 or to the corresponding RNA nucleotides.

33. The artificial nucleic acid molecule according to any one of claims 17-32, 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.

34. The artificial nucleic acid molecule according to any one of claims 17-33, wherein the at least one 3'UTR element comprises or consists 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.

35. The artificial nucleic acid molecule according to any one of claims 17-33, wherein the at least one 3'UTR element comprises or consists of a nucleic acid sequence which is derived from the 3'UTR of a vertebrate α-globin gene or from a variant thereof, preferably from the 3'UTR of a mammalian α-globin gene or

from a variant thereof, more preferably from the 3'UTR of a human α-globin gene or from a variant thereof.

36. The artificial nucleic acid molecule according to any one of claims 17-33, 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. 1369-1377 and 1434 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. 1369-1377 and 1434 or to a corresponding RNA sequence.

37. The artificial nucleic acid molecule according to claim 36, 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.

38. The artificial nucleic acid molecule according to any one of claims 17-37, wherein the 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.

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.

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 artificial nucleic acid molecule according to any one of claims 1-40, which is an RNA, preferably an mRNA molecule.

42. 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.

43. The vector according to claim 42, further comprising:

c. at least one histone-stem loop.

44. The vector according to claim 42 or 43, wherein the 5'UTR element and the open reading frame are heterologous.

45. The vector according to any one of claims 42-44, wherein the 5'UTR element is suitable for increasing protein production from the vector.

46. The vector to any one of claims 43-45, wherein the 5'UTR element and the histone stem-loop act together, preferably at least additively, to increase protein production from the vector.

47. The vector according to any one of claims 42-46, 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 polypyrimidine tract.

48. The vector according to any one of claims 42-47, 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 gene it is derived from.

49. The vector according to any one of claims 42-48, wherein the 5'UTR element does not comprise a start codon or an open reading frame.

50. The vector according to any one of claims 42-49, 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.

51. The vector according to any one of claims 43-50, wherein the at least one histone stem-loop is selected from following formulae (I) or (II):

formula (I) (stem-loop sequence without stem bordering elements):

$$\underbrace{[N_{0-2}GN_{3-5}]}_{\text{stem1}}\ \underbrace{[N_{0-4}(U/T)N_{0-4}]}_{\text{loop}}\ \underbrace{[N_{3-5}CN_{0-2}]}_{\text{stem2}}$$

formula (II) (stem-loop sequence with stem bordering elements):

$$\underbrace{N_{1-6}}_{\text{stem1 bordering element}}\ \underbrace{[N_{0-2}GN_{3-5}]}_{\text{stem1}}\ \underbrace{[N_{0-4}(U/T)N_{0-4}]}_{\text{loop}}\ \underbrace{[N_{3-5}CN_{0-2}]}_{\text{stem2}}\ \underbrace{N_{1-6}}_{\text{stem2 bordering element}}$$

wherein:

stem1 or stem2 bordering elements $N_{1-6}$ is a consecutive sequence of 1 to 6, preferably of 2 to 6, more preferably of 2 to 5, even more preferably of 3 to 5, most preferably of

4 to 5 or 5 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C, or a nucleotide analogue thereof;

stem1 [$N_{0-2}GN_{3-5}$] is reverse complementary or partially reverse complementary with element stem2, and is a consecutive sequence between of 5 to 7 nucleotides;

wherein $N_{0-2}$ is a consecutive sequence of 0 to 2, preferably of 0 to 1, more preferably of 1 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C or a nucleotide analogue thereof;

wherein $N_{3-5}$ is a consecutive sequence of 3 to 5, preferably of 4 to 5, more preferably of 4 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C or a nucleotide analogue thereof, and

wherein G is guanosine or an analogue thereof, and may be optionally replaced by a cytidine or an analogue thereof, provided that its complementary nucleotide cytidine in stem2 is replaced by guanosine;

loop sequence [$N_{0-4}(U/T)N_{0-4}$]is located between elements stem1 and stem2, and is a consecutive sequence of 3 to 5 nucleotides, more preferably of 4 nucleotides;

wherein each $N_{0-4}$ is independent from another a consecutive sequence of 0 to 4, preferably of 1 to 3, more preferably of 1 to 2 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C or a nucleotide analogue thereof; and

wherein U/T represents uridine, or optionally thymidine;

stem2 [$N_{3-5}CN_{0-2}$] is reverse complementary or partially reverse complementary with element stem1, and is a consecutive sequence between of 5 to 7 nucleotides;

wherein $N_{3-5}$ is a consecutive sequence of 3 to 5, preferably of 4 to 5, more preferably of 4 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C or a nucleotide analogue thereof;

wherein $N_{0-2}$ is a consecutive sequence of 0 to 2, preferably of 0 to 1, more preferably of 1 N, wherein each N is independently from another selected from a nucleotide selected from A, U, T, G and C or a nucleotide analogue thereof; and

wherein C is cytidine or an analogue thereof, and may be optionally replaced by a guanosine or an analogue thereof provided that its complementary nucleotide guanosine in stem1 is replaced by cytidine;

wherein

stem1 and stem2 are capable of base pairing with each other

forming a reverse complementary sequence, wherein base pairing may occur between stem1 and stem2, or

forming a partially reverse complementary sequence, wherein an incomplete base pairing may occur between stem1 and stem2.

52. The vector according to any one of claims 43-51, wherein the at least one histone stem-loop is selected from at least one of following formulae (Ia) or (IIa):

$$\underbrace{[N_{0-1}GN_{3-5}]}_{\text{stem1}}\ \underbrace{[N_{1-3}(U/T)N_{0-2}]}_{\text{loop}}\ \underbrace{[N_{3-5}CN_{0-1}]}_{\text{stem2}}$$

formula (Ia) (stem-loop sequence without stem bordering elements)

$$\underbrace{N_{2-5}}_{\substack{\text{stem1}\\\text{bordering element}}}\ \underbrace{[N_{0-1}GN_{3-5}]}_{\text{stem1}}\ \underbrace{[N_{1-3}(U/T)N_{0-2}]}_{\text{loop}}\ \underbrace{[N_{3-5}CN_{0-1}]}_{\text{stem2}}\ \underbrace{N_{2-5}}_{\substack{\text{stem2}\\\text{bordering element}}}$$

formula (IIa) (stem-loop sequence with stem bordering elements)

53. The vector according to any one of claims 42-52, further comprising

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

54. The vector according to claim 53, wherein the poly(A) sequence comprises or consists of a sequence of about 25 to about 400 adenosine nucleotides, preferably a sequence of about 50 to about 400 adenosine nucleotides, more preferably a sequence of about 50 to about 300 adenosine nucleotides, even more preferably a sequence of about 50 to about 250 adenosine nucleotides, most preferably a sequence of about 60 to about 250 adenosine nucleotides.

55. The vector according to claim 53 or 54, 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.

56. The vector according to any one of claims 42-55, further comprising:

e. a poly(C) sequence.

57. The vector according to claim 56, wherein the poly(C) sequence comprises, preferably consists of, about 10 to about 200 cytidine nucleotides, more preferably about 10 to about 100 cytidine nucleotides, more preferably about 10 to about 50 cytidine nucleotides, even more preferably about 20 to about 40 cytidine nucleotides.

58. The vector according to any one of claims 42-57, further comprising:

f. at least one 3'UTR element.

59. The vector according to claim 58, wherein the at least one 3'UTR element 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.

60. The vector according to claim 58 or 59, 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 vector.

61. The vector according to any one of claims 42-60, wherein the 5'UTR element comprises or consists of a nucleic acid sequence which is derived from a nucleic acid sequence selected from the group consisting of SEQ ID NOs. 1-1363, SEQ ID NO. 1435, SEQ ID NO. 1461 or SEQ ID NO. 1462, , from the homologs of any of SEQ ID NOs. 1-1363, SEQ ID NO. 1435, SEQ ID NO. 1461 or SEQ ID NO. 1462, , or from a variant thereof.

62. The vector according to any one of claims 42-61, 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 nucleic acid sequence selected from SEQ ID NOs. 1-1363, SEQ ID NO. 1435, SEQ ID NO. 1461 or SEQ ID NO. 1462, 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 a nucleic acid sequence selected from SEQ ID NOs. 1-1363, SEQ ID NO. 1435, SEQ ID NO. 1461 or SEQ ID NO. 1462, or to a corresponding RNA sequence, preferably lacking the 5'TOP motif.

63. The vector according to any one of claims 42-62, 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 nucleic acid sequence according to any of SEQ ID NOs: 170, 232, 244, 259, 1284,

1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, or 1360, a corresponding RNA sequence, a homolog thereof, or a variant thereof as described herein, preferably lacking the 5'TOP motif.

64. The vector according to any one of claims 42-63, 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 5'UTR of a nucleic acid sequence according to any of SEQ ID NOs: 170, 232, 244, 259, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, or 1360 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 NOs: 170, 232, 244, 259, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310,

1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, or 1360 or to a corresponding RNA sequence, preferably lacking the 5'TOP motif.

65. The vector according to any one of claims 42-64, 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), preferably from a 5'UTR of a nucleic acid sequence according to any of SEQ ID NOs: 67, 259, 1284-1318, 1344, 1346, 1348-1354, 1357, 1461 and 1462, a corresponding RNA sequence, a homolog thereof, or a variant thereof, preferably lacking the 5'TOP motif.

66. The vector according to any one of claims 42-65, 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, 1461 and 1462 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, 1461 and 1462 or to a corresponding RNA sequence, preferably lacking the 5'TOP motif.

67. The vector according to any one of claims 42-66, wherein the 5'UTR element comprises or consists of a nucleic acid sequence which is derived from the 5'UTR of a ribosomal protein Large 32 gene, preferably from the 5'UTR of a vertebrate ribosomal protein Large 32 (L32) gene or from a variant thereof, more preferably from the 5'UTR of a mammalian ribosomal protein Large 32 (L32) gene or from a variant thereof, most preferably from the 5'UTR of a human ribosomal protein Large 32 (L32) gene or from a variant thereof, wherein preferably the 5'UTR element does not comprise the 5'TOP of said gene.

68. The vector according to any one of claims 42-67, 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 NOs. 1368 or 1452-1460 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 NOs. 1368 or 1452-1460 or to a corresponding RNA sequence.

69. The vector according to any one of claims 62, 64, 66 and 68, 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.

70. The vector according to any one of claims 42-69, 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.

71. The vector according to any one of claims 42-70, wherein the 5'UTR element comprises or consists of a nucleic acid sequence which is derived from the 5'UTR of a TOP gene 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, UBA52or from a variant thereof.

72. The vector according to any one of claims 43-71, wherein the at least one histone stem-loop comprises or consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs. 1391-1433, preferably from the group consisting of SEQ ID NOs. 1403-1433.

73. The vector according to any one of claims 43-72, wherein the histone stem-loop comprises or consists of a nucleic acid sequence having a sequence identity of at least about 75%, preferably of at least about 80%, preferably at least about 85%, more preferably at least about 90%, even more preferably at least about

95% to the sequence according to SEQ ID NO. 1433 or to the corresponding RNA sequence, wherein preferably positions 6, 13 and 20 of the sequence having a sequence identity of at least about 75%, preferably of at least about 80%, preferably at least about 85%, more preferably at least about 90%, even more preferably at least about 95% to the sequence according to SEQ ID NO. 1433 or to the corresponding RNA sequence are conserved, i.e. are identical to the nucleotides at positions 6, 13 and 20 of SEQ ID NO. 1433 or to the corresponding RNA nucleotides.

74. The vector according to any one of claims 58-73, 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.

75. The vector according to any one of claims 58-74, wherein the at least one 3'UTR element comprises or consists 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.

76. The vector according to any one of claims 58-74, wherein the at least one 3'UTR element comprises or consists of a nucleic acid sequence which is derived from the 3'UTR of a vertebrate α-globin gene or from a variant thereof,

preferably from the 3'UTR of a mammalian α-globin gene or from a variant thereof, more preferably from the 3'UTR of a human α-globin gene or from a variant thereof.

77. The vector according to any one of claims 58-74, 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. 1369-1377 and 1434 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. 1369-1377 and 1434 or to a corresponding RNA sequence.

78. The vector according to claim 77, 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.

79. The vector according to any one of claims 58-78, wherein the 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.

80. The vector according to any one of claims 42-79, 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.

81. The vector according to any one of claims 42-80, wherein the open reading frame comprises a codon-optimized region, preferably, wherein the open reading frame is codon-optimized.

82. The vector according to any one of claims 42-81, which is a DNA vector.

83. The vector according to any one of claims 42-82, which is a plasmid vector or a viral vector, preferably a plasmid vector.

84. The vector according to any one of claims 42-83, which comprises or codes for an artificial nucleic acid molecule according to any one of claims 1-41.

85. The vector according to any one of claims 42-84, which is a circular molecule.

86. A cell comprising the artificial nucleic acid molecule according to any one of claims 1-41 or the vector according to any one of claims 42-85.

87. The cell according to claim 86, which is a mammalian cell.

88. The cell according to claim 86 or 87, which is a cell of a mammalian subject, preferably an isolated cell of a mammalian subject, preferably of a human subject.

89. A pharmaceutical composition comprising the artificial nucleic acid molecule according to any one of claims 1-41, the vector according to any one of claims 42-85, or the cell according to any one of claims 86-88.

90. The pharmaceutical composition according to claim 89, further comprising one or more pharmaceutically acceptable diluents and/or excipients and/or one or more adjuvants.

91. The artificial nucleic acid molecule according to any one of claims 1-41, the vector according to any one of claims 42-85, the cell according to any one of claims 86-88, or the pharmaceutical composition according to claim 89 or 90 for use as a medicament.

92. The artificial nucleic acid molecule according to any one of claims 1-41, the vector according to any one of claims 42-85, the cell according to any one of claims 86-88, or the pharmaceutical composition according to claim 89 or 90 for use as a vaccine or for use in gene therapy.

93. 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 42-85, the cell according to any one of claims 86-88, or the pharmaceutical composition according to claim 89 or 90 to a subject in need thereof.

94. 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 1-41 or the vector according to any one of claims 42-85.

95. The method according to claim 94, 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.

96. The method according to claim 95, wherein the cell which is to be transfected *in vitro* is an isolated cell of the subject, preferably of the human patient.

97. The method according to any one of claims 93-96, which is a vaccination method or a gene therapy method.

98. 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;

ii. preferably at least one histone stem-loop; and

iii. optionally, a poly(A) sequence and/or a polyadenylation signal.

99. 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 and preferably at least one histone stem-loop for increasing protein production from a nucleic acid molecule.

100. A kit or kit of parts comprising an artificial nucleic acid molecule according to any one of claims 1-41, the vector according to any one of claims 42-85, the cell according to any one of claims 86-88, and/or the pharmaceutical composition according to claim 89 or 90.

101. The kit according to claim 100, 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.