11477

Schematic

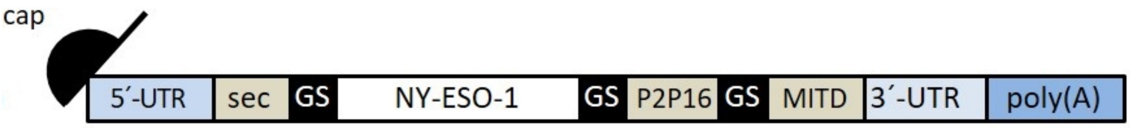


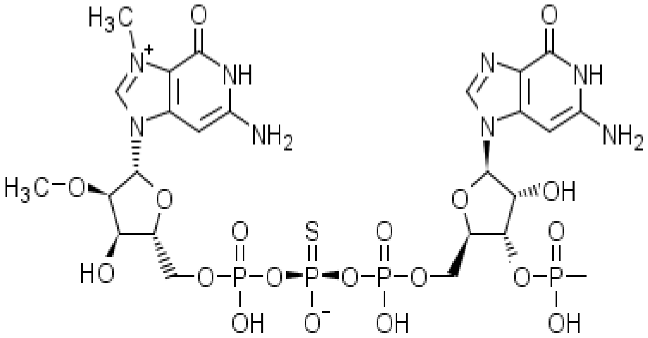
Table of features

Element	Description	Position
5´cap	A specific capping structure at the 5´-end for improved RNA stability and translational efficiency.	1-2
5’-UTR (hAg-Kozak)	5´-UTR sequence derived from the human alpha-globin RNA with an optimized “Kozak sequence”.	3-53
sec	The secretory signal peptide “sec” derived from the sequence encoding the human MHC Class I complex alpha chain “HLA-I, Cw*” is used as a fusion-protein tag to improve antigen processing and presentation.	54-131
GS	Sequences that code for short GS-rich linker peptides generally consisting of the amino acids glycine and serine (usually GGSGGGGSGG).	132-161, 702-731 and 927-968
NY-ESO-1	Codon-optimized sequences encoding the target protein NY-ESO-1	162-701
P2P16	Sequence coding for tetanus toxoid-derived helper epitopes to break immunological tolerance.	732-926
MITD	MITD corresponds to the transmembrane and cytoplasmic domain of the MHC class I molecule and is used as a fusion-protein tag to improve antigen processing and presentation.	969-1139
3’-UTR (FI element)	The 3´-UTR is a combination of two sequence elements derived from the AES mRNA (called F) and the mitochondrial encoded 12S ribosomal RNA (called I) to confer RNA stability and highest total protein expression.	1140-1456
Poly(A)	A poly(A)-tail measuring 110 nucleotides in length, consisting of a stretch of 30 adenosine residues, followed by a 10-nucleotide linker sequence and another 70 adenosine residues.	1457-1566

Abbreviations: AES = amino terminal enhancer of split; GS = glycine and serine; HLA = human leukocyte antigen, MHC = major histocompatibility complex; MITD = MHC class I transmembrane domain; UTR = untranslated region.

5'- capping structure = G^1G^2: m^7Guo^+2'*O*Me-5'-p-(*R*)p^S-p-5'-G

X^1G^2-:



1-2 : cap m^7Guo^+2'*O*Me-5'-p-*(R)*p^S-p-5'-G; *3-53* : 5'UTR; **54-131** : sec; **132-161** : $G_2SG_4SG_2$ linker; 162-701 : NY-ESO1 antigen; **702-731** : $G_2SG_4SG_2$ linker; **732-926** : P2P16 tetanus toxoid-derived helper epitopes; **927-968** : $GS_2G_4SPG_3S_2$ linker; **969-1139** : MITD; *1140-1456* : FI element (3' UTR); **1457-1566** : A30L70 polyA tail.

Sequence / Séquence / Secuencia

GG*GGCGAACU* *AGUAUUCUUC* *UGGUCCCCAC* *AGACUCAGAG* *AGAACCCGCC* 50
*ACC***AUGAGAG** **UGAUGGCCCC** **CAGAACCCUG** **AUCCUGCUGC** **UGUCUGGCGC** 100
CCUGGCCCUG **ACAGAGACAU** **GGGCCGGAAG** **CGGCGGCUCU** **GGAGGAGGCG** 150
GCUCCGGAGG CAUGCAGGCC GAGGGCAGAG GAACAGGCGG CAGCACAGGC 200
GACGCAGAUG GACCAGGCGG CCCUGGAAUC CCUGAUGGCC CAGGCGGCAA 250
UGCUGGGGGA CCAGGAGAAG CUGGCGCCAC AGGCGGGAGA GGACCUAGAG 300
GAGCUGGAGC CGCUAGAGCU UCUGGACCUG GGGGAGGCGC CCCUAGAGGA 350
CCACAUGGAG GCGCUGCCAG CGGCCUGAAU GGCUGCUGCA GAUGCGGCGC 400
CAGAGGCCCU GAGAGCCGGC UGCUGGAAUU CUACCUGGCC AUGCCCUUCG 450
CCACCCCCAU GGAAGCCGAG CUGGCCAGAA GAUCCCUGGC UCAGGACGCU 500
CCUCCUCUGC CUGUGCCCGG CGUGCUGCUG AAAGAAUUCA CCGUGUCCGG 550
CAACAUCCUG ACCAUCAGAC UGACAGCCGC CGAUCACAGA CAGCUCCAGC 600
UGAGCAUCAG CUCUUGCCUG CAGCAGCUGA GCCUGCUGAU GUGGAUCACC 650
CAGUGCUUUC UGCCCGUGUU CCUGGCCCAG CCACCCAGCG GACAGAGAAG 700
C**GGAGGAUCC GGUGGUGGCG GCAGCGGCGG CAAGAAGCAG UACAUCAAGG** 750
CCAACAGCAA GUUCAUCGGC AUCACCGAGC UGAAGAAGCU GGGAGGGGGC 800
AAACGGGGAG GCGGCAAAAA GAUGACCAAC AGCGUGGACG ACGCCCUGAU 850
CAACAGCACC AAGAUCUACA GCUACUUCCC CAGCGUGAUC AGCAAAGUGA 900
ACCAGGGCGC UCAGGGCAAG AAACUG**GGCU CUAGCGGAGG GGGAGGCUCU** 950
CCUGGCGGGG **GAUCUAGCAU** **CGUGGGAAUU** **GUGGCAGGAC** **UGGCAGUGCU** 1000
GGCCGUGGUG **GUGAUCGGAG** **CCGUGGUGGC** **UACCGUGAUG** **UGCAGACGGA** 1050
AGUCCAGCGG **AGGCAAGGGC** **GGCAGCUACA** **GCCAGGCCGC** **CAGCUCUGAU** 1100
AGCGCCCAGG **GCAGCGACGU** **GUCACUGACA** **GCCUAGUAA***C* *UCGAGCUGGU* 1150
ACUGCAUGCA *CGCAAUGCUA* *GCUGCCCCUU* *UCCCGUCCUG* *GGUACCCCGA* 1200
GUCUCCCCCG *ACCUCGGGUC* *CCAGGUAUGC* *UCCCACCUCC* *ACCUGCCCCA* 1250
CUCACCACCU *CUGCUAGUUC* *CAGACACCUC* *CCAAGCACGC* *AGCAAUGCAG* 1300
CUCAAAACGC *UUAGCCUAGC* *CACACCCCCA* *CGGGAAACAG* *CAGUGAUUAA* 1350

CCUUUAGCAA UAAACGAAAG UUUAACUAAG CUAUACUAAC CCCAGGGUUG 1400
GUCAAUUUCG UGCCAGCCAC ACCGAGACCU GGUCCAGAGU CGCUAGCCGC 1450
*GUCGCU***AAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGCAU AUGACUAAAA** 1500
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1550
AAAAAAAAAA AAAAAA 1566