

pLV-SpikeV5

Vector for lentiviral pseudotyping with SARS-CoV-2 Brazilian variant (P.1 lineage) Spike

Catalog code: plv-spike-v5

<https://www.invivogen.com/brazil-p1-spike-pseudotyping-vector>

For research use only

Version 21E07-ED

PRODUCT INFORMATION

Contents

- 20 µg of lyophilized pLV-SpikeV5 (plasmid DNA)

Storage and Stability

- Product is shipped at room temperature.
- Lyophilized DNA should be stored at -20°C.
- Resuspended DNA should be stored at -20°C and is stable for at least 1 year.

Quality control

- Plasmid construct is confirmed by restriction analysis and full-length open reading frame (ORF) sequencing.
- After purification by ion exchange chromatography, predominant supercoiled conformation is verified by electrophoresis.

PLASMID FEATURES

- **hCMV (human cytomegalovirus) enhancer & promoter** drives high expression of the SARS-CoV-2 spike gene in mammalian cells.
- **Rabbit (rbt) β-Globin intron** enhances the expression of the SARS-CoV-2 spike gene in mammalian cells.

- **Codon-optimized Spike ORF**

pLV-SpikeV5 contains the Spike coding sequence from the Brazilian (BRA.) SARS-CoV-2 variant (P.1 lineage). This variant is characterized by a number of mutations within the the Spike coding sequence (*see below*)¹. Additionally, to improve expression of the S protein in pseudovirions, the gene is codon-optimized and the last 19 amino acids, which contain an endoplasmic reticulum (ER)-retention motif (KxHxx), have been removed².

pLV-SpikeV5 includes the following sequence features:

- **S1 domain:** L18F, T20N, P26S, D138Y, R190S, D614G, H655Y
- **RBD:** K417T, E484K, N501Y
- **S1/S2 boundary:** Functional furin cleavage site
- **S2 domain:** T1072I, V1176F

Spike (S) is a structural glycoprotein expressed on the surface of SARS-CoV-2. It mediates membrane fusion and viral entry into target cells upon binding to the host receptor ACE2, and the proteolytic activity of host proteases such as furin and TMPRSS2³.

Note: For more information visit: <https://www.invivogen.com/sars2-spike>

- **Rabbit β-Globin pAn** is a strong polyadenylation (pAn) signal placed downstream of the SARS-CoV-2 spike gene. It allows efficient transcription termination and polyadenylation of the mRNA.
- **bla (Ampicillin resistance gene)** encodes the β-lactamase enzyme, which confers resistance to the antibiotic ampicillin. Therefore, ampicillin can be used to select *E. coli* transformants.
- **pMB1 ori** is a minimal *E. coli* origin of replication.

APPLICATION

pLV-SpikeV5 has been designed for pseudotyping lentiviral particles with the SARS-CoV-2 Spike protein (Brazilian variant). The basic strategy involves transfecting 293T cells with a lentiviral backbone plasmid encoding a fluorescent or luminescent reporter protein (e.g. GFP), a plasmid expressing the minimal set of lentiviral proteins necessary to assemble viral particles, and InvivoGen's pLV-SpikeV5. The transfected cells produce SARS-CoV-2 Spike-pseudotyped lentiviral particles, which can then be used to infect permissive cells.

GENERAL PROTOCOL

For a detailed protocol for producing SARS-CoV-2 Spike (S)-pseudotyped lentiviral particles, please refer to the literature⁴. In summary,

1. Co-transfect HEK293 cells with the plasmids required for lentiviral production. These include:
 - InvivoGen's pLV-SpikeV5 plasmid
 - Lentiviral backbone plasmid encoding a reporter protein (e.g. GFP or Luciferase)
 - Plasmid/s encoding the necessary virion packaging proteins
2. After ~48 hours, collect the S-pseudotyped lentiviral particles by harvesting and filtering the cell culture supernatant.
3. Determine the titre of the S-pseudotyped lentiviral particles using a permissive cell line that express the SARS-CoV-2 host receptor (e.g. InvivoGen's HEK-Blue™ hACE2 cells) in a relevant assay.

PLASMID PREPARATION

- **Plasmid resuspension**
 - Quickly spin the tube containing the lyophilized plasmid to pellet the DNA.
 - To obtain a plasmid solution at 1 µg/µl, resuspend the DNA in 20 µl of sterile water.
 - Store resuspended plasmid at -20°C.
 - **Plasmid amplification and cloning**
- Plasmid amplification and cloning can be performed in *E. coli* GT116 or other commonly used laboratory *E. coli* strains, such as DH5α.

REFERENCES

1. Faria, N.R. *et al.* 2021. Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. *Science*. doi:10.1126/science.abb2644.
2. Johnson, M.C. *et al.* 2020. Optimized Pseudotyping Conditions for the SARS-COV-2 Spike Glycoprotein. *J Virol* 94.
3. Hoffmann M. *et al.*, 2020. SARS-CoV-2 cell entry depends on ACE2 and TMPRSS2 and is blocked by a clinically proven protease inhibitor. *Cell*. 181:1-16.
4. Crawford, K.H.D. *et al.* 2020. Protocol and Reagents for Pseudotyping Lentiviral Particles with SARS-CoV-2 Spike Protein for Neutralization Assays. *Viruses* 12. doi: 10.3390/v12050513.

TECHNICAL SUPPORT

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A549-hACE2-TMPRSS2 Cells	Cell Line	a549-hace2-tpsa
pUNO1-hACE2	Expression vector	puno1-hace2
pUNO1-hTMPRSS2a	Expression vector	puno1-htp2a
Anti-CoV2RBD-c1-hIgG1	Recombinant Antibody	cov2rbdc1-mab1

For a complete list of InvivoGen's COVID-19 related products visit:
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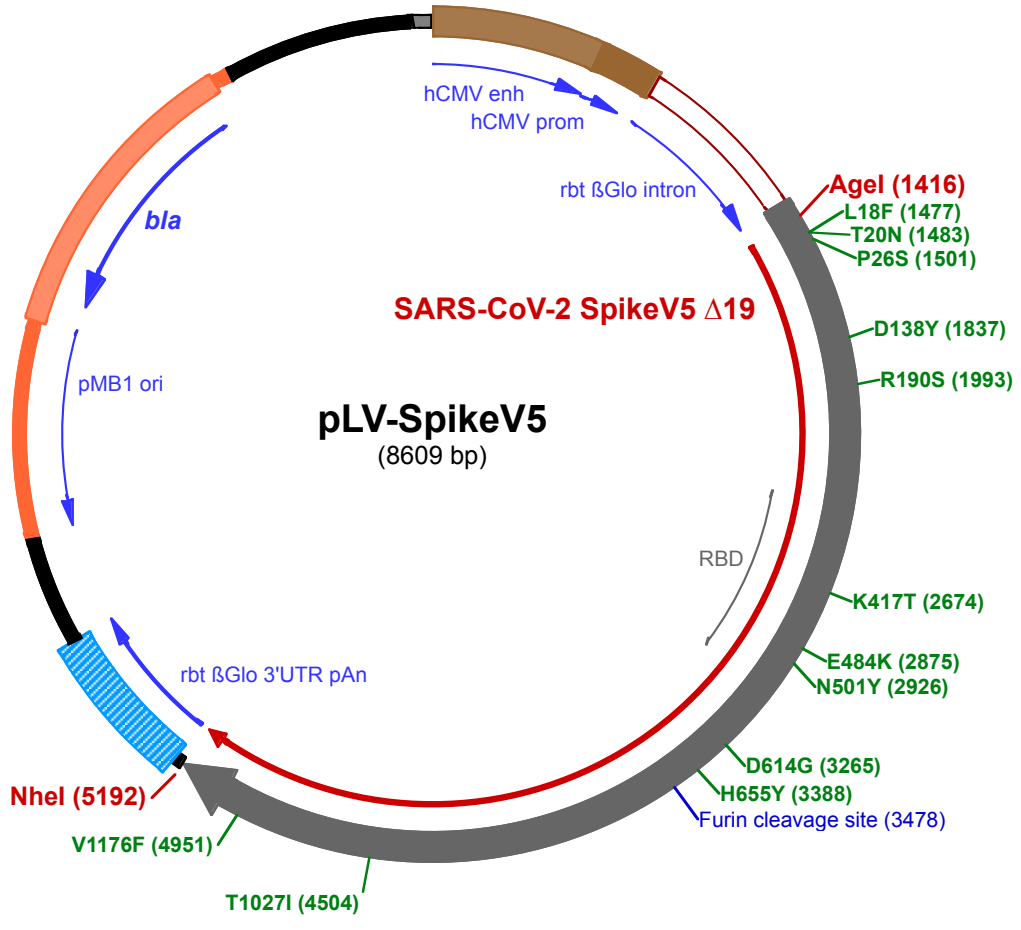
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200

1 GAGCTTGGCCCATTGCATACGTTGTATCCATATCATAATATGTACATTTATATTGGCTCATGTCCAACATTACGCCATGTTGACATTGATTATTGACTA
101 GTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTACGGTAAATGGCCCGCTGGCTGACCGCC
201 CAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGTGGAGTATTTACGGTAA
301 ACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACA
401 TGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATA
501 GCGGTTTGACTCACGGGGATTTC AAGTCTCCACCCATTGACGTCAATGGGAGTTTGT TTTGGCACCAAATCAACGGGACTTTCCAAAATGTCGTAAC
601 AACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGGTACGGTGGGAGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGCC
701 ATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCTCCGGTGCACCGATCCTGAGAACTCAGGgtgagtttggggacccttgattg
801 ttctttcttttctgctattgtaaaattcatgttatatggagggggcaaagttttcagggtgttgttagaatgggaagatgtcccttgatcacctatgga
901 ccctcatgataattttgtttctttcactttctactctgttgacaaccattgtctcctcttattttcttttcattttctgtaacttttctgtaaaccttta
1001 gcttgcatttgtaacgaattttaattcacttttgtttatgttcagattgtaagtactttctctaatcactttttttcaaggcaatcagggtatatt
1101 atattgtacttcagcacagtttttagagaacaattgttataattaaatgataaggtagaatattttctgcatataaattctggctggcgtggaatatctt
1201 attggtagaacaactacaccctggatcatcatcctgcctttctctttatggttacaatgatatacactgtttgagatgaggataaaaactctgagtc
1301 aaccgggcccctctgtaaccatgttcatgcctttctctttctacagCTCCTGGCAACGTGCTGTTGTTGTGCTGTCTCATATTTGGCAAAGA

Agel (1416)

T20N (1483)
L18F (1477)

1401 ATTCCTCGACGGATCCACCGGTCAACATGTTTGTGTTCTTGGTGTGCTTCCACTGGTCAGTCCCAATGCGTTAATTTCCACCAACCGAACTCAACTCCC
1 M F V F L V L L P L V S S Q C V N F T N R T Q L P

P26S (1501)

1501 ATCCGCATATACAAATCCTTACCAGAGGAGTACTATCCTGACAAAGTGTTCGGTCAAGTGTCTCCACTCTACTCAGGACCTCTTTCTGCCTTTC
25 S A Y T N S F T R G V Y Y P D K V F R S S V L H S T Q D L F L P F
1601 TTTCTAACGTTACATGGTTTTCATGCAATCCATGTGTCTGGGACAAACGGCACAAACGCTTCGACAACCTGTATTGCCATTCAATGATGGGGTGTACT
59 F S N V T W F H A I H V S G T N G T K R F D N P V L P F N D G V Y
1701 TTGCTCCACAGAAATCCAACATCATTTCGAGGATGGATTTTCGGGACTACTCTGGACTCAAAGACACAGAGCCTGTGATCGTTAAACAACGCCACAAA
92 F A S T E K S N I I R G W I F G T T L D S K T Q S L L I V N N A T N

D138Y (1837)

1801 CGTTGTCATCAAAGTGTGCGAATTCAGTTTTGC AATTTATCCCTTCTGGGAGTGTACTATCACAAGAATAACAAGTCTGGATGGAGAGCGAATTTCCG
125 V V I K V C E F Q F C N Y P F L G V Y Y H K N N K S W M E S E F R

R190S (1993)

1901 GTCTACAGCAGCGCAAACAACACTGCACCTTCGAGTACGTGAGTCAACCTTTCTGATGGACCTGGAAGGGAAACAGGGAAACTCAAGAACCTGAGT
159 V Y S S A N N C T F E Y V S Q P F L M D L E G K Q G N F K N L S E
2001 TTGTCTTTAAGAACATCGACGGCTATTTAAGATCTATAGTAAGCATACGCCATCAACCTGGTAAGGGATCTCCCCAGGGCTTTTCAGCCCTGGAAC
192 F V F K N I D G Y F K I Y S K H T P I N L V R D L P Q G F S A L E P
2101 TTTGGTTGACTTGCTATTGGTATCAATATCACCAGATTTTCAGACCCTTCTGGCATTGCAICGGTCTTATCTTACTCCAGGTGATTCCTCCTCGGGTGG
225 L V D L P I G I N I T R F Q T L L A L H R S Y L T P G D S S S G W
2201 ACTGCCGCGCCGCTGCCTACTATGTGCGCTATCTGCAACCAAGAAGTTCCTGCTCAAGTACAACGAAAACGGCACTATTACGGATGCTGTTGATTGTG
259 T A G A A A Y Y V G Y L Q P R T F L L K Y N E N G T I T D A V D C
2301 CCCTGGACCCTCTGTCTGAGACTAAATGCACCTCAAGAGCTTTACCGTTGAGAAGGGGATTTACCAAACAGTAATTTCCGGGTCCAACCCACCGAAAG
292 A L D P L S E T K C T L K S F T V E K G I Y Q T S N F R V Q P T E S

2401 CATTGTGCGGTTCCCAAATATACCAATCTGTGTCCCTTTGGCGAAGTGTTC AATGCTACAAGTTTGTCTGTGTACGCATGGAATAGGAAACGCATC
325 I V R F P N I T N L C P F G E V F N A T R F A S V Y A W N R K R I

2501 TCCAATTGTGTCGCTGATTACTCCGTGCTGTACAATCCGCTCTTTCTCAACCTTCAAGTGTATGGCGTTTACCTACCAAACCTAACGACCTGTGCT
359 S N C V A D Y S V L Y N S A S F S T F K C Y G V S P T K L N D L C

K417T (2674)

2601 TCACTAATGTGTATGCCGACTCTTTTGTATACGAGGCATGAAGTGAACAGATTGCACCGGGCAGACCGGCACAATTGCCGACTACAACCTACAAGCT
392 F T N V Y A D S F V I R G D E V R Q I A P G Q T G T I A D Y N Y K L

2701 TCCAGATGACTTTACCGGATGTGTTATTGCATGGAACCTCAAACAATCTGGATTTCCAAGTGGGTGGCAACTATAACTACCTGTATAGACTGTTTCAGGAAA
425 P D D F T G C V I A W N S N N L D S K V G G N Y N Y L Y R L F R K

E484K (2875)

2801 TCCAACCTGAAACCAATTCGAGCGAGATATAAGCACAGAAATCTACCAGGCTGGAAGTACGCCCTGCAACGGCGTGAAGGGTTCAACTGCTACTTCCCAT
459 S N L K P F E R D I S T E I Y Q A G S T P C N G V K G F N C Y F P

N501Y (2926)

2901 TGCAGAGTTACGGATTCCAGCCTACA TACGGGGTGGGTACCAACCCTATCGTGTCTGAGTCTTGAGTCTTCCATGCCCCAGCCAGCTG
492 L Q S Y G F Q P T Y G V G Y Q P Y R V V V L S F E L L H A P A T V C

3001 TGGCCCCAAGAAAAGCACAATCTGGTGAAGAACAATGCGTGAACCTTAACTTTAACGGACTCACAGGAACCGGCGTATTGACGGAGAGTAACAAGAA
525 G P K K S T N L V K N K C V N F N F N G L T G T G V L T E S N K K

3101 TTCCTGCCATTCCAGCAGTTGCGTGCAGATATTGCCGACACTACCGACTGTCCGAGATCCCAGACATTGGAGATTCTTGATATCACACCCTGTAGTT
559 F L P F Q Q F G R D I A D T T D A V R D P Q T L E I L D I T P C S

D614G (3265)

3201 TCGGCGGAGTGAGCGTGATTACGCCGGAACCAATACCAGCAATCAGTTGCCGCTCTGTATCAGGCGTGAATTGCACCGAGGTACCTGTCGCCATCCA
592 F G G V S V I T P G T N T S N Q V A V L Y Q G V N C T E V P V A I H

H655Y (3388)

3301 CGTGACCAACTACACCACATGGCGAGTATTCCACCGGCTCCACGCTTTTCAGACACGTGCTGGATGTCTGATCGGTGCAGAA TACGTTAATAAT
625 A D Q L T P T W R V Y S T G S N V F Q T R A G C L I G A E Y V N N

Furin cleavage site (3478)

3401 AGCTACGAGTGTGATATCCCATCGGTGCTGGAATATGCGCCTTTATCAAACCTCAAACCACTCTCCTAGGCGGGCAGTAGTGATACCCAAAGTA
659 S Y E C D I P I G A G I C A S Y Q T Q T N S P R R A R S V A S Q S

3501 TCATTGCCTACACAATGAGCCTCGGTGCTGAGAATTCTGTCGCCTACAGCAACAACCTCATTGCTATCCCTACTAACTTCAACATCAGTGTGACAACCTGA
692 I I A Y T M S L G A E N S V A Y S N N S I A I P T N F T I S V T T E

3601 AATTCTGCCCGTATCTATGACCAAAAAGCGTTGACTGCACCATGTACATCTGTGGCATTCTACCGAATGTAGCAATCTCCTCCTGCAATACGGATCA
725 I L P V S M T K T S V D C T M Y I C G D S T E C S N L L L Q Y G S

3701 TTCTGCACTCAGTGAATCGTGCCTCACAGGATTCAGTGTGAGCAGGACAAGAATACGCAGGAAGTGTTCGCCAGGTGAAGCAAATCTACAAAATC
759 F C T Q L N R A L T G I A V E Q D K N T Q E V F A Q V K Q I Y K T

3801 CACCCATAAAGACTTTGGCGGATTCAATTTCTCACAGATCTGCCGATCCCTCAAACCCTCAAGCGTAGCTTATCGAGGATCTGCTCTCAACAA
792 P P I K D F G G F N F S Q I L P D P S K P S K R S F I E D L L F N K

3901 GGTAAACCCTCGCAGATGCCGTTTTCATCAAGCAGTATGGCGATTGTCTGGGAGACATCGCGCTCGGGACCTGATCTGTGCACAGAAGTTCATGGACTG
825 V T L A D A G F I K Q Y G D C L G D I A A R D L I C A Q K F N G L

4001 ACCGTGCTGCCTCCCTTGCTGACCGACGAGATGATAGCCCAATACACTAGCGCCTGCTGGCCGGCACCATCACTTCTGGGTGGACATTCGGAGCTGGCG
859 T V L P P L L T D E M I A Q Y T S A L L A G T I T S G W T F G A G

4101 CTGCCCTCAGATTCTTTTTGCTATGCAGATGGCCTACCGCTTAAACGGCATCGGTGTGACACAAAACGTTTCTGTATGAAAACAGAAACTCATCGCCAA
892 A A L Q I P F A M Q M A Y R F N G I G V T Q N V L Y E N Q K L I A N

4201 CCAGTTCAACAGTGTATCGGTAAAGATACAGGATAGCCTGTCATCCACTGCCAGCGCATTGGGAAAAGTTGCAGGATGTAGTGAACAGAAATGCCAGCA
925 Q F N S A I G K I Q D S L S S T A S A L G K L Q D V V N Q N A Q A

4301 CTAAACACCTGGTGAACAGCTCTCTTCAAATTTGGTGCCATTTCTAGCGTGTGAATGACATACTGAGCCGGTTGGACAAGTGGAGGCTGAAGTGC
959 L N T L V K Q L S S N F G A I S S V L N D I L S R L D K V E A E V

4401 AGATTGATAGGCTGATAACTGGCGCCCTCAGTCTCTCAGACCTATGTGACCAGCAGCTCATCCGGCTGCTGAAATTCGCGCATCCGTAACCTGGC
992 Q I D R L I T G R L Q S L Q T Y V T Q Q L I R A A E I R A S A N L A

T1027I (4504)

4501 AGCAATIAAAAATGTCGAGTGTGTGCTGGGTGACTCTAAGAGAGTGGACTTTTGCGGGAAGGGGATCACCTGATGTCTTCTCAGTCTGCACCCCAT
1025 A I K M S E C V L G Q S K R V D F C G K G Y H L M S F P Q S A P H

4601 GGTGTGGTCTTCTGCACGTGACTTATGTCCCAGCTCAGGAAAAGAACTTCACTACAGCCAGCCATCTGCCAGATGGGAAAGCCACTTTCCCAGGG
1059 G V V F L H V T Y V P A Q E K N F T T A P A I C H D G K A H F P R

4701 AAGGCGTATTCTGTCCAATGGTACTCATTGGTTCGCTCACTCAGAGAAATTTCTACGAGCCCAAGATTATAACCACTGACAATACATTTGTATCCGGCAA
1092 E G V F V S N G T H W F V T Q R N F Y E P Q I I T T D N T F V S G N

4801 TTGTGATGTGGTTATCGGGATTGTGAATAACTGTTACGATCCCTTGACGAGCAGAGCTGGACTCCTCAAGGAGGAGCTTGACAAAATTTAAGAAAT
1125 C D V V I G I V N N T V Y D P L Q P E L D S F K E E L D K Y F K N

V1176F (4951)

4901 CACACATCACCTGACGTGACCTCGGAGATATTTGAGAATCAATGCTTCC TITGTCATATTGAGAAGGAGATAGACAGGCTGAATGAGGTTGCCAAGA
1159 H T S P D V D L G D I S G I N A S F V N I Q K E I D R L N E V A K

5001 ACCTCAACGAGTCTCTGATCGATCTGCAGGAGTTGGGCAAGTACGAACAGTATATCAAATGGCCATGGTACATTTGGCTTGGGTTATTGCTGGGCTGAT
1192 N L N E S L I D L Q E L G K Y E Q Y I K W P W Y I W L G F I A G L I

NheI (5192)

5101 AGCTATCGTCATGGTACAAATATGTTGTGTTGCATGACATCCTGCTGTAGTTGTCTGAAGGCTGCTGCTCATGCGGACGCTGTTGTAAAGCTAGCCT
1225 A I V M V T I M L C C M T S C C S C L K G C C S C G S C C

5201 CGAGGGATCCGTCGAGGAATCACTCCTCAGGTCAGGCTGCCTATCAGAAGGTGGTGGTGGTGGCCATGCCCTGGCTCACAATACCACTGAGAT
5301 CTTTTTCCCTGCAAAAATATGGGGACATCATGAAGCCCTTGTAGCATCTGACTTCTGGCTAATAAAGGAAATTTATTTTCATTGCAATAGTGTGTT

5401 GGAATTTTTTGTGTCTCTCACTCGGAAGGACATATGGGAGGGCAAATCATTAAAAACATCAGAATGAGTATTTGGTTTGTAGGTTGGCAACATATGCCCA

5501 TATGCTGGCTGCCATGAACAAAGGTTGGCTATAAAGAGGTCACTAGTATATGAAACAGCCCTGCTGTCCATTCTTATTCCATAGAAAAGCCTTGACT

5601 TGAGGTTAGATTTTTTTATATTTTTGTGTTATTTTTTCTTAAACATCCATAAAATTTTCTTACATGTTTTACTAGCCAGATTTTTCTCTCTCT

5701 C**CTGACTACTCCAGTCATAGCTGTCCCTCTTCTTTAT**GGAGATCCCTCGACGGATCGGCCGAATTCGTAATCATGTCATAGCTGTTTCCTGTGTGAA
5801 ATTGTTATCCGCTCACAATTCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT
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6001 TCCGCTTCTCGCTCACTGACTCGCTCGCTCGGTCGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCAG
6101 GGGATAACGCAGGA**AGAAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCC**
6201 **TGACGAGCATCACA**AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATAACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGC
6301 **TCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTT**
6401 **CGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC**
6501 **GGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTCTTGAAAGTGGTGGCT**
6601 **AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA**AAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAA
6701 **CCACCGCTGGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA**
6801 **CGCTCAGTGGAACGAAA**ACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTACCTAGATCCTTTTAAATTAATAAATGAAGTTTTAAA
6901 **TCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTATCCATAG**
7001 **TTGCTGACTCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCAAGTCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCC**
266 **A Q S G T T Y I V V I R S P K G D P G L A A I I G R S G R E G A G**
7101 **AGATTTATCAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGGAA**
233 **S K D A I F W G A P L A S R L L P G A V K D A E M W D I L Q Q R S**
7201 **GCTAGAGTAAGTAGTTCCGCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACAGCTCGTCTTTGGTATGGCTTCATTCA**
199 **A L T L L E G T L L K R L T T A M A V P M T T D R E D N P I A E N L**
7301 **GCTCCGGTCCCAACGATCAAGCGAGTTACATGATCCCCATGTTGCAAAAAAGCGTTAGCTCCTTCGGTCCCTCCGATGTTGTCAGAAAGTAAGTT**
166 **E P E W R D L R T V H D G M N H L F A T L E K P G G I T T L L L N**
7401 **GGCCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTTACTGTATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAAGTACTCAACC**
133 **A A T N D S M T I A A S C L E R V T M G B D T L H K E T V P S Y E V**
7501 **AAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTAAAAGTGCTCA**
99 **L D N Q S Y H I R R G L Q E Q G A D I R S L V A G C L L V K F T S M**
7601 **TCATTGGAAAACGTTCTTCGGGGCGAAA**ACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGC
66 **M P F R E E P R F S E L I K G S N L D L E I Y G V R A G L Q D E A**
7701 **ATCTTTTACTTTACCCAGCGTTTCTGGGTGAGCAAACAGGAAGGCCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATA**
33 **D K V K V L T E P H A F V P L C F A A F F P I L A V R F H Q I S M**
7801 **CTTCTCTTTTCAATATTATTGAAGCATTTATCAGGGTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACAAATAGGGGTTT**
7901 **CGCGCACATTTCCCGAAAAGTGCCACCTAAATGTAAGCGTTAATATTTTGTAAAATTCGCGTTAAATTTTGTAAATCAGCTCATTTTTTAACCAA**
8001 **TAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAGAAGC**
8101 **TGGACTCAAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTGGGGTCGAGGTGCCGTAA**
8201 **AGCACTAAATCGAACCTAAAGGGAGCCCGGATTTAGAGCTTGACGGGAAAAGCCGGCGAACGTTGGCGAGAAAGGAAGGAAAGCAAGGAGGCG**
8301 **GGCGTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGGTAACCACACCCCGCCGCGCTAATGCGCCGTACAGGGCGCGTCCCATTCGCCATTCA**
8401 **GGTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTTCGCTATTACGCCAGCTGGCGAAAAGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAAC**
8501 **GCCAGGTTTTCCAGTCACGACGTTGTA**AAACGACGGCCAGTGAGCGCGGTAATACGACTCACTATAGGGCAATTGGAGCTCCACCGGGTGGCGGC
8601 CGCTCTAGA