

pLV-SpikeV4

Vector for lentiviral pseudotyping with SARS-CoV-2 Californian variant (B.1.429 lineage) Spike

Catalog code: plv-spike-v4

<https://www.invivogen.com/cal-b1429-spike-pseudotyping-vector>

For research use only

Version 21E05-ED

PRODUCT INFORMATION

Contents

- 20 µg of lyophilized pLV-SpikeV4 (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-SpikeV4 contains the Spike coding sequence from the Californian (CAL.) SARS-CoV-2 variant (B.1.429 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 a endoplasmic reticulum (ER)-retention motif (KxHxx), have been removed².

pLV-SpikeV4 includes the following sequence features:

- **S1 domain:** S13I, W152C, D614G
- **RBD:** L452R
- **S1/S2 boundary:** Functional furin cleavage site

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-SpikeV4 has been designed for pseudotyping lentiviral particles with the SARS-CoV-2 Spike protein (Californian 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-SpikeV4. 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-SpikeV4** 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. Deng, X. *et al.* 2021. Transmission, infectivity, and antibody neutralization of an emerging SARS-CoV-2 variant in California carrying a L452R spike protein mutation. medRxiv doi: 10.1101/2021.03.07.21252647.
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

InvivoGen USA (Toll-Free): 888-457-5873

InvivoGen USA (International): +1 (858) 457-5873

InvivoGen Europe: +33 (0) 5-62-71-69-39

InvivoGen Asia: +852 3622-3480

E-mail: info@invivogen.com



RELATED PRODUCTS

| Product | Description | Cat. Code |
|-------------------------------|--------------------------|-----------------|
| ChemiComp GT116 | Competent <i>E. coli</i> | gt116-11 |
| COVID-19 Product Range | | |
| HEK-Blue™ hACE2 Cells | Cell line | hkb-hace2 |
| 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:
<https://www.invivogen.com/covid-19>

TECHNICAL SUPPORT

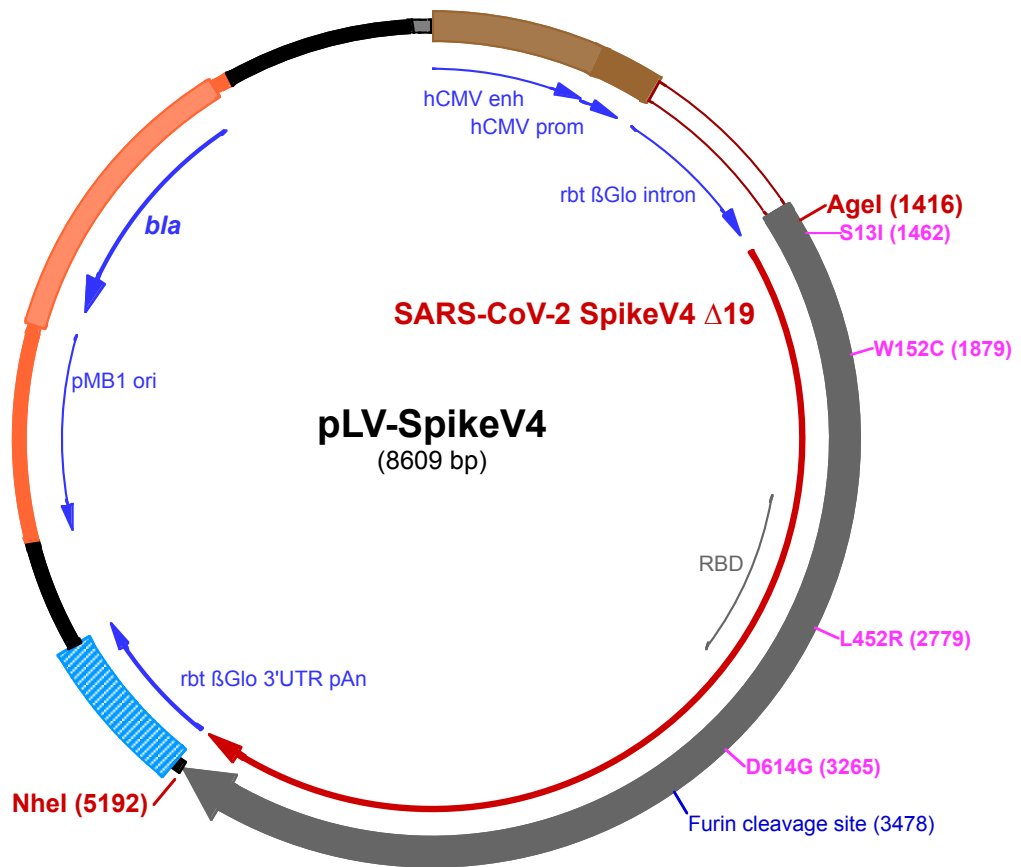
InvivoGen USA (Toll-Free): 888-457-5873

InvivoGen USA (International): +1 (858) 457-5873

InvivoGen Europe: +33 (0) 5-62-71-69-39

InvivoGen Hong Kong: +852 3622-3480

E-mail: info@invivogen.com



200

1 GAGCTTGGCCATTGCATACGTTGTATCCATATCATAATATGTACATTTATATTGGCTCATGTCCAACATTACGCCATGTTGACATTGATTATTGACTA
101 GTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTACGGTAAATGGCCCGCTGGCTGACCGCC
201 CAACGACCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAA
301 ACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACA
401 TGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATA
501 GCGGTTTGACTCACGGGGATTTC AAGTCTCCACCCATTGACGTCAATGGGAGTTTGT TTTGGCACCAAATCAACGGGACTTTCCAAAATGTCGTAAC
601 AACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGGTACGGTGGGAGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGCC
701 ATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGGTGCACCGATCCTGAGAACTCAGGgtgagtttggggacccttgattg
801 ttctttctttttcgtattgtaaaattcatgttatatggagggggcaaagttttcagggtgttgttagaatgggaagatgtcccttgatcacctatgga
901 ccctcatgataattttgtttctttcactttctactctgttgacaaccattgtctcctcttattttcttttcattttctgtaactttttcgtaaacttta
1001 gcttgcatttgtaacgaattttaattcacttttgtttatgttcagattgtaagtactttctctaatcactttttttcaaggcaatcagggtatatt
1101 atattgtacttcagcacagttttagagaacaattgttataattaaatgataaggtagaatattttctgcatataaattctggctggcgtggaatatctt
1201 attggtagaacaactacaccctggtcatcatcctgcctttctctttatggttacaatgatatacactgtttgagatgaggataaaaactctgagtcca
1301 aaccgggcccctctgtaaccatgttcatgcctttctctttctacagCTCCTGGCAACGTGCTGTTGTTGTGCTGTCTCATATTTGGCAAAGA

Agel (1416)

S131 (1462)

1401 ATTCTCGACGGATCCACCGTCAACATGTTTGTGTTCTTGGTGTGCTTCCACTGGTCAGTATCAATGCCTTAATCTCACACCCGAACCTCAACTCCC
1 M F V F L V L L P L V S I Q C V N L T T R T Q L P
1501 ACCCGCATATACAAATTCCTTACCAGAGGAGTGTACTATCCTGACAAAGTTCGTCAGTGTCTCCACTCTACTCAGGACCTCTTTCTGCCTTTC
25▶ P 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 TTTTCTAACGTTACATGGTTTCATGCAATCCATGTGTCTGGGACAAACGGCACAAACGCTTCGACAAACCTGTATTGCCATTCAATGATGGGGTGTACT
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 TTGCCTCCACAGAGAAATCCAACATCATTGAGGATGGATTTTCGGGACTACTCTGGACTCAAAGACACAGAGCCTGTGATGCTTAACAACGCCACAAA
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

W152C (1879)

1801 CGTTGTCATCAAAGTGTGCGAATTCAGTTTTGCAATGATCCCTTCCCTGGGAGTGTACTATACAAGAATAACAAGTCCATGGAGAGCGAATTTCCGG
125▶ V V I K V C E F Q F C N D P F L G V Y Y H K N N K S C M E S E F R
1901 GTCTACAGCAGCGCAAACACTGCACCTTCGAGTACGTGAGTCAACCTTTCTGATGGACCTGGAAGGAAACAGGGAACCTCAAGAACCTGAGAGAGT
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 R E
2001 TTGTCTTTAAGAACATCGACGGCTATTTAAGATCTATAGTAAGCATACGCCTATCAACCTGGTAAGGGATCTTCCCCAGGGCTTTTCAGCCCTGGAACC
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 TTTGGTTGACTTGCTATTGGTATCAATATCACCAGATTTAGACCCTTCTGGCATTGCAICGGTCTTATCTTACTCCAGGTGATTCCTCCTCCGGGTGG
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 ACTGCCGCGCCGCTGCCTACTATGTGCGGTATCTGCAACCAAGAAGTTCCTGCTCAAGTACAACGAAAACGGCACTATTACGGATGCTGTTGATTGTG
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 CCCTGGACCCTGTCTGAGACTAAATGCACCTCAAGAGCTTTACCGTTGAGAAGGGGATTTACCAAACAGTAATTTCCGGGTCCAACCCACCGAAAG
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 CATTGTGCGGTTCCCAAATATACCAATCTGTGTCCTTTGGCGAAGTGTCAATGCTACAAGTTTGTCTGTGTACGCATGGAATAGGAAACGCATC
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 TCCAATTGTGTCGCTGATTACTCCGTGCTGTACAATCCGCCTCTTTCTCAACCTTCAAGTGTATGGCGTTTACCTACCAAACCTAACGACCTGTGCT
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

2601 TCACTAATGTGTATGCCGACTCTTTTGTGATACGAGGCGATGAAGTGAAGCAGATTGCACCAGGGCAGACCGGCAAATTTGCCGACTACAACCTACAAGCT
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 K I A D Y N Y K L

L452R (2779)

2701 TCCAGATGACTTTACCGGATGTGTTATTGCATGGAACCTCAAACAATCTGGATTCCAAGTGGGTGGCAAATAAATACTCGCTATAGACTGTTTCAGGAAA
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 R Y R L F R K

2801 TCCAACCTGAAACCATTCGAGCGAGATATAAGCACAGAATCTACCAGGCTGGAAGTACGCCCTGCAACGGCTGGAAGGGTTCAACTGCTACTTCCCAT
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 E G F N C Y F P

2901 TGCAGAGTTACGGATTCCAGCCTACAAACGGGGTGGGTTACCAACCCTATCGTGTCTAGTCTGAGTTTTGAGCTCCTCCATGCCCCAGCCACAGTCTG
492▶ L Q S Y G F Q P T N 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 TGGCCCCAAGAAAAGCACCAATCTGGTGAAGAACAATGCGTGAACTTAACTTTAACGGACTCACAGGAACCGGCGTATTGACGGAGAGTAACAAGAAG
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 TTCCTGCCATTCCAGCAGTTCGGTCGCGATATTGCCGACACTACCGACGCTGTCCGAGATCCCAGACATTGGAGATTCTTGATATCACACCCTGTAGTT
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

3201 TCGGCGGAGTGAGCGTGATTACGCCCGGAACCAATACCAGCAATCAGGTTGCCGCTGTATCAGGGGTGAATTGCACCGAGGTACCTGTCGCCATCCA
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

3301 CGCTGACCAACTTACACCACATGGCGAGTATATTCCACCGGCTCCAACGCTTTTCAGACAGGTGCTGGATGCTGATCGGTGCGAAGACGTTAATAAT
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 H V N N

3401 AGCTACGAGTGTGATATCCCCATCGGTGCTGGAATATGCGCCTTTATCAAACCTCAAACCAACTCTCCTAGCGGGCACGTAGTGTAGCATCCCAAAGTA
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 TCATTGCCTACACAATGAGCCTCGGTGCTGAGAATTCTGTCGCTACAGCAACAATCCATTGCTATCCCTACTAACTTACAATCAGTGTGACAACTGA
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 AATTCTGCCGTATCTATGACCAAAAACAGCGTTGACTGCACCATGTACATCTGTGGCGATTCTACCGAATGTAGCAATCTCCTCCTGCAATACGGATCA
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 TTCTGCACTCAGTGAATCGTGCCTCACAGGTATTGAGTGTAGCAGGACAAGAATACCGAGGAAGTGTTCGCCAGGTGAAGCAATCTACAAAACCTC
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 CACCCATAAAAAGACTTTGGCGGATTCAATTTCTCACAGATCCTGCCGATCCCTCAAACCCCTCAAAGCGTAGCTTTATCGAGGATCTGCTCTTCAACAA
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 GGTAAACCTCGCAGATGCCGTTTCATCAAGCAGTATGGCGATTGTCTGGGAGACATCGCCGCTCGGGACCTGATCTGTGCACAGAAGTTCAATGGACTG
825▶ V T L A D A G F I K Q Y G D C L G N D I A A R D L I C K F N G L

4001 ACCGTGCTGCCTCCCTTGTGACCGACGAGATGATAGCCCAATACACTAGCGCCTGCTGGCCGGCACCATCACTTCTGGGTGGACATTGGAGCTGGCG
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 CTGCCCTTCAAGTTCCTTTTGTATGACAGTGGCTACCGCTTAAACGGCATCGGTGTGACACAAAACGTTCTGTATGAAAACAGAACTCATCGCCAA
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 CCAGTTCAACAGTGTATCGGTAAGATACAGGATAGCTGTATCCACTGCCAGCGCATTGGGAAAGTTGCAGGATGTAGTGAACCAGAATGCCAGGCA
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 A Q A

4301 CTTAACACCTGGTGAACAGCTCTCTCAAATTTTGGTGCCATTTTAGCGTGTGAATGACATACTGAGCCGTTGGACAAGGTGGAGGCTGAAGTGC
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 AGATTGATAGGCTGATAACTGGGCGCCTTCACTCTCTTACAGCCTATGTGACCAGCAGCTCATCCGCGTGTGAAATTCGCGCATCCGCTAACCTGGC
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

4501 AGCAACCAAAATGTCGAGTGTGTGCTGGGTGACTAAGAGAGTGGACTTTTTCGGGAAAGGGTATCACCTGATGTCTTTTCTCAGTCTGCACCCCAT
1025▶ A T 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 GGTGTGGTCTTTTGCACGTGACTTATGTCACAGTCAAGAAAAGAACTTCACTACAGCCCGACCATCTGCCACGATGGGAAAGCCACTTTCCAGGG
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 R

4701 AAGGCGTATTCTGTCCTCAATGGTACTATTGGTTCGCTCACTCAGAGAAATTTCTACGAGCCCAAGATTATAACCACTGACAATACATTTGTATCCGGCAA
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 TTGTGATGTGGTTATCGGGATTGTGAATAAATACTGTTTACGATCCTTTGCAGCCAGAGCTGGACTCCTTCAAGGAGGAGCTTGACAAATATTTAAGAAT
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

4901 CACACATCACCTGACGTGACCTCGGAGATATTTTCAAGAAATCAATGCTTCCGTTGGTCAATATTTCAGAAAGGAGATAGACAGGCTGAATGAGGTTGCCAAGA
1159▶ H T S P D V D L G D I S G I N A S V V N I Q K E I D R L N E V A K

5001 ACCTCAACGAGTCTGATCGATCTGCAGGAGTTGGCAAGTACGAACAGTATATCAAATGGCCATGGTACATTTGGCTTGGGTTTATTGCTGGGCTGAT
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 AGCTATCGTCATGGTGACAATTATGTTGTGTTGCATGACATCCTGCTGTAGTTGTCTGAAGGGCTGCTGCTCATGCGGACGCTGTTGCTAAAGCTAGCCT
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 CGAGGGATCCGTCGAGGAATTCACTCCTCAGGTGCAGGCTGCCTATCAGAAGTGGTGGCTGGTGGCCAATGCCCTGGCTCACAATACCACTGAGAT

5301 CTTTTTCCCTCTGCCAAAATATGTTGGGACATCATGAAGCCCTTGGAGCATCTGACTTCTGGCTAATAAGGAAATTTATTTTTCATTGCAATAGTGTGTT

5401 GGAATTTTTTGTCTCTCACTCGGAAGGACATATGGGAGGGCAAATCATTTAAAACATCAGAATGAGTATTTGGTTAGAGTTTGGCAACATATGCCCA

5501 TATGCTGGCTGCCATGAACAAAGGTTGGCTATAAAGAGGTCATCAGTATATGAACAGCCCTGCTGTCCATTCTTATTCCATAGAAAAGCCTTGAAT

5601 TGAGGTTAGATTTTTTTATATTTTGTGTTATTTTTTCTTTAACATCCCTAAAATTTTCTTACATGTTTTACTAGCCAGATTTTTCTCTCTCT

5701 CCTGACTACTCCAGTCATAGCTGTCCCTTCTCTTATGGAGATCCCTCGACGGATCGGCCGAATTCGTAATCATGTCATAGCTGTTTCTGTGTGAA

5801 ATTGTTATCCGCTCACAATTCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGTAACTCACATTAATTGCGTT

5901 GCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCAACCGCGGGGAGAGGCGGTTTTCGTTATTGGGCGCTCT

6001 TCCGCTTCTCGCTCACTGACTCGTGCCTCGGTCGTTCCGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAG

6101 GGGATAACGCAGGAAGAAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCC

6201 TGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGC
6301 TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTT
6401 CGGTGTAGGTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC
6501 GGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT
6601 AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAA
6701 CCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA
6801 CGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTAAATTAATAAATGAAGTTTTAAA
6901 TCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCCATAG
287 • W H K I L S A G I E A I Q R N R E D M T
7001 TTGCTGACTCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCAAGTGTGCAATGATACCGCGAGACCCAGCTCACC GGCTCC
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 AGATTTATCAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAA
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 GCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCACAACGTTTGGCATTGCTACAGGCATCGTGGTGTACGCTCGTCTGTTGGTATGGCTTCATTCA
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 GCTCCGGTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGTTAGTCTCTCGGTCTCCGATCGTTGTCAGAAAGTAAGTT
166 E P E W R D L R T V H D B M N H L F A T L E K P G G I T T L L L N
7401 GGCCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACC
133 A A T N D S M T I A A S C L E R V T M G D T L H K E T V P S Y E V
7501 AAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCA
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 TCATTGAAAACGTTCTTCGGGGCGAAAACCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGACCCCAACTGATCTTCAGC
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 ATCTTTTACTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGAAAAAAGGAATAAGGGCGACACGGAAATGTTGAATACTCATA
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 CTCTTCTTTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGATTTAGAAAAATAAACAAATAGGGGTTT
7901 CGCGCACATTTCCCGAAAAGTGCCACCTAAATGTAAGCGTTAATATTTTGTAAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAA
8001 TAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAGAACG
8101 TGGACTCCAACGTCAAAGGGCGAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAA
8201 AGCACTAAATCGAACCCTAAAGGGAGCCCGGATTTAGAGCTTGACGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGAAGAAAGCGAAAGGAGCG
8301 GGCCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCGTTAATGCGCCGCTACAGGGCGCGTCCCATTCGCCATTCA
8401 GGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAAC
8501 GCCAGGGTTTTCCAGTCACGACGTTGTAACACGACGGCCAGTGAGCGCGCGTAATACGACTCACTATAGGGCGAATTGGAGCTCCACCGCGGTGGCGCG
8601 CGCTCTAGA