

## 7. ANHANG

**Abbildung A: DNA-Sequenz des plasmidkodierten 9179 bp *Sau3A*-Fragmentes aus *Pseudonocardia* sp. Stamm K1.** Gezeigt ist der nicht-kodierende DNA-Strang in 5'→3' Richtung. Die abgeleiteten Aminosäuresequenzen sind im Ein-Buchstaben-Code angegeben. Sterne symbolisieren Stopcodons. Mögliche Ribosomenbindestellen sind unterstrichen, die Startcodons durch Fettschrift hervorgehoben. Pfeile oberhalb der DNA-Sequenz kennzeichnen palindromische Sequenzen.

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1  GCGGTTCGCC AGGAAGTTCT AAGCGTGGCC TGCCAACGGA TTTTGGTCTA AGAAAGTGTG

61  GCATGTTACA TGCCACGTCG CAGTGGAGAC TCGGAGGCTG AACTATGTTC AAGATCATGT
                                     OrfY> M F K I M

121 TTGTCGTCTA CGAGCGCGAG GGTATCGATC GGGATGAGGC TCTGCGTTAT TGGCGCGAGC
    F V V Y E R E G I D R D E A L R Y W R E

181 AGCATGGTCC GCTCGCGTCC AAGGTTCCCG GCCTGCGTTA TTACGCTCAG ACGCACGCCC
    Q H G P L A S K V P G L R Y Y A Q T H A

241 TCAGCTCTGC TGACGGGGGC TCGGCCCGT ACCTCGGATC CGCTGAGATG GCGTTTCGACA
    L S S A D G G S A P Y L G S A E M A F D

301 GCCAGGGGGC TTTTGTTCGAG GCAACGGCAT CTCCCGAGTT CGATGCGGTT CTGAAGGACG
    S Q G A F V E A T A S P E F D A V L K D

361 TGGTCAACTT TGCAGATCCT GACAACGTTT CGACGGCAGT TGTCCAAGAT TACGTCTTCG
    V V N F A D P D N V P T A V V Q D Y V F

421 TCGACTGACC TCTATTTTCGG TGACTGACTG AGTTTCATCT GCATTCATAA TTGAGGTGCT
    V D *

481 TGGTTTCGTT TGCGGCGCTG GCCACACCTT TGAATGCGCG GCTCCCTCTT AGCACGTAGG

541 ACCTATTCAG CCTACCCCTC GCCGCTGAAG GAGAAATAGA ATGACCGTGA TCGCCAAGCC
                                     ThmS> M T V I A K

601 TGATCATCTA TTGCGTGACG ATGTGCAGAA GTTCATTGAT CGCCCCAAGA AACTTTTCAT
    P D H L L R D D V Q K F I D R P K K L F

661 TAATGGTCAG TGGCACGACT CGATCAAGGG TGAGACTCTC GAGGTTTATG ACCCTGCGGT
    I N G Q W H D S I K G E T L E V Y D P A

721 TGGGACGAAG ATCTGTACCG TTGCTGCGGG CGATGCGGAG GATGTCGACC GAGCTGTGGC
    V G T K I C T V A A G D A E D V D R A V

781 GGCCGCGCGC CACGCGTTCG ACGAGGGGCC GTGGTCCAAG CTAAATCCTT CGGAGCGCGG
    A A A R H A F D E G P W S K L N P S E R

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841 CAGGCTGGTT TGGCGGCTCG CGGACCTTCT CGAGGAGCAC GCGGACGAGT TCGCACAGAT  
G R L V W R L A D L L E E H A D E F A Q

901 CGATGCGCTT GACAATGGCA AACCGGTCAC GGACGCGCGT GCGGTAGACG TGGCGTTCTC  
I D A L D N G K P V T D A R A V D V A F

961 GATCGAATTG CTGCGCTACA TGGCTGGTTG GTCGAACAAA ATCTATGGTG AGACGATTCC  
S I E L L R Y M A G W S N K I Y G E T I

1021 GCTCACTAAC CCGGCTGACT TCCATGCATA CACGCTTCGC GAGCCGGTCG GCGTGGTCGG  
P L T N P A D F H A Y T L R E P V G V V

1081 GCAGATCGTT CCTTGGAAct TCCCCCTTAT GATGGCGGTC TGGAAGGTCG CTCCTGCCCT  
G Q I V P W N F P L M M A V W K V A P A

1141 GGCTGCAGGC TGCACCGTGA TCCTCAAGCC CGCCGAGCAG ACACCGCTGA GCGCACTTCG  
L A A G C T V I L K P A E Q T P L S A L

1201 CCTGGCCGAG CTCACCGAGG AGGCCGGCTT CCCGCCAGGT GTCTTCAACG TCATCACTGG  
R L A E L T E E A G F P P G V F N V I T

1261 CTTTGGCGAG ACTGCAGGTG CGGCGATCGC CGCCCACGAC AACATCGACA AGGTGCGGTT  
G F G E T A G A A I A A H D N I D K V A

1321 CACCGGCTCG ACCGAGGTGG GCGGTTGAT CGCCCAGGCG GCGAGCGGAA ACCTGAAGAA  
F T G S T E V G R L I A Q A A S G N L K

1381 GGTCTCTCTC GAGCTTGGCG GAAAGTCTCC CGTGATCGTG TTCGGTGATT CTGACATCGA  
K V S L E L G G K S P V I V F G D S D I

1441 GCAGGCTGTC GCTGGTGCTT CCAGCGCCAT TTTCTACAAC AACGGGCAGA CCTGCACGGC  
E Q A V A G A S S A I F Y N N G Q T C T

1501 GGGCTCTCGT CTTTATGTGC ACCGGAAGGT CTACGACAAG GTCGTGGAGG GTATCGCCAG  
A G S R L Y V H R K V Y D K V V E G I A

1561 TGAGGCGTCG GCTCTCCCGA TTGGTCACGG TCTCGACCCG GCGACCCGCA TCGGGCCGCT  
S E A S A L P I G H G L D P A T R I G P

1621 GATCTCGGCG GAGCAGCGCG ACCGTGTCAC TGGCTACATC GCACAGGGCC GTGAGGCCGG  
L I S A E Q R D R V T G Y I A Q G R E A

1681 TGCAGAGGTG ATCGTGGGCG GGGACACTGT CGGTGATGGG GGCTACTTCA TTCAGCCGAC  
G A E V I V G G D T V G D G G Y F I Q P

1741 CATCCTTACC AAGACTGATC CGAGCATGAG CGTGGTGCGC GAGGAGATCT TCGGCCAGT  
T I L T K T D P S M S V V R E E I F G P

1801 GCTGTGCGCC ATGGCCTTTG ACGAAGACAC CATTGATAGC GTCGTGCGTG AGGCGAACAA  
V L C A M A F D E D T I D S V V R E A N

1861 CTCAGTGTAT GGGTTGGCCG CGAGTATCTA CACCCGCGAC ATCAGCGTCG CCCATCGAGT  
N S V Y G L A A S I Y T R D I S V A H R

1921 CGCGAAGCGG CTCAAGGCTG GGACGATCGG TATCAATACC CACCATGTGG TCGATGTCGG  
V A K R L K A G T I G I N T H H V V D V

1981 GCTCCCATTC GGCGGATTCA AGCAGTCCGG ATATGGCCGG GACATGGGCC GCGACGCGAT  
 A L P F G G F K Q S G Y G R D M G R D A

2041 CGACCAGTAC ACCGAGGTCA AGTCGATCGG TATCGCACTC TGACCGTACT GCGCTCATCA  
 I D Q Y T E V K S I G I A L \*

2101 CGGGGGGAGC ACTCTCATTC AAGAGAAGCT TGGTACCCCG GTAAGCACGA TACCTCGGAC

2161 TCGATATCCC CGCATCGTCT GGCGCTCCAC CCACCATATG AAGGCGCCAT CAATGGGAAA

2221 GGCTTAAGAT CACG**ATG**ACT GCCCCACCGA TGAAGAGGCC GCGTCGAAGC ATTACGGCGA  
 ThmA> M T A P P M K R P R R S I T A

2281 GCCATGCCAA GATCGGCGAG CTGGGCTGGG ACCGGACATA CTACCCGCAT GAGCGCGGGA  
 S H A K I G E L G W D R T Y Y P H E R G

2341 AGTACCCAG CCGATAACAAG CTGCCGAATA AGCCAGGCCG GGATCCCATG AAGCAGATCA  
 K Y P S R Y K L P N K P G R D P M K Q I

2401 TGGGCGACTA CCTGCACATG CAGAACGAGA AGGATGATCG AGTCCACGGT GGCCTCGATG  
 M G D Y L H M Q N E K D D R V H G G L D

2461 CAGCCGTCCG CGCAGAGGTC CCCGGCAAGG CCCCCTTCG GTGGCTGGAG TTGCTCAAGC  
 A A V R A E V P G K A P L R W L E L L K

2521 CTTACCTGCT GACCGTCATT AGCGCCGAGG CCGCTGCTAC CCGCTGCATG GGCATGCTTG  
 P Y L L T V I S A E A A A T R C M G M L

2581 TTGATGCTCT CGACGACCCT GAGCTGCAGA ACGCCTATTA CATCCAGCAG CTCGACGAGC  
 V D A L D D P E L Q N A Y Y I Q Q L D E

2641 AGCGTCACAC CGCGATGCAG ATGAACCTGT ATCGCTGGTA CATGAAGAAC ATGCCCGAGC  
 Q R H T A M Q M N L Y R W Y M K N M P E

2701 CGGTCGGCTG GAACCTCGGG CTCCAGGCCG TCGGGGGCGA CTCCATCCTG GTCGCCGCC  
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2761 AGAACCTCAC CGGAAGCTTC ATGACCGGTG ACCCCTTCCA GGCCGCGGTG GCGCTCCAGG  
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2821 TCGTCGTTGA GACAGCCTTC ACGAACACCA TCCTGGTCGC GTTCCCTGAC GTGGCAGTCC  
 V V V E T A F T N T I L V A F P D V A V

2881 GGAACCATGA CTTGCTCTG CCCACTGTCA TGAACTCCGT GCAGTCGGAC GAGGCGCGCC  
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2941 ACATCAACAA CGGCTACGCG ACACTTCTGT ACCTCCTGCA GGAGCCGGAG AACGCTCCCC  
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3001 TGCTTGAGCA GGACATCCAG CAGATGTTCT GGACCGTGCA TGCATTGTC GACGCCTTCA  
 L L E Q D I Q Q M F W T V H A F V D A F

3061 TGGGCATCCT CGTCGAGTAC GCCCCACCG ATGCGACCGA CCCGAAAGC TGGACCACGA  
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3121 AGTGGGACCG GTGGGTAAAT GACGACTATT ACCGTTCCCTA CATCGTCAAC CTCGGCAAGC  
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3181 TGGGCTTGAA GATTCCCGAC TCGATCTTCA AGCGCGCGCG CGAGCGGATC GCTGCTGACT  
 L G L K I P D S I F K R A R E R I A A D

3241 ACCACCACAA GGTCGCTGTC GGCCTCTGGG CCTCGTGGCC CTTCCTACTAC TACAAGTACG  
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3301 GCAACCTTGA GCAGAAGGAC TACGACTGGT TCGAGAGCAA GTACCCGGGC TGGAACGAGA  
 G N L E Q K D Y D W F E S K Y P G W N E

3361 AGTTCGGCGC ATTCTGGCGC GGTTACGCCG ACGTTCGCTA CCCC GGCTCG GGTCCCTTGC  
 K F G A F W R G Y A D V R Y P G S G P L

3421 AGCTGCCCCG CCTACTCGAG GGAGCCGGCC CGATCTGCTG GACCTGCCAG CTCGGATGCC  
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3481 TGGCGCCCCG GGAGCAGTGC CACCGCATTG TCGACGAGCA CACGCGGTTC TACTGCTCGC  
 L R P E E Q C H R I V D E H T R F Y C S

3541 CGGAGTGCAA GTGGATCGAC ATGACCAACC CTGGTCGCTA TGTCGGTGAC CGTGTTTGGT  
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3601 TCGACCGCTA CCACGGCTGG GAGTACTCCG AGATCGTGCG TGACCTCGGA TTCCTCCGCC  
 F D R Y H G W E Y S E I V R D L G F L R

3661 CAGACGGTAA GACGCTCACA GGGCAGCCGC ACGTCGATCC CGACCCTGCC AAGCAGTGGA  
 P D G K T L T G Q P H V D P D P A K Q W

3721 CTATCGATGA TCTCCGAGAG CTCGGCCACA TCATGCAGAG CCCGAACATC CTCACCGCGG  
 T I D D L R E L G H I M Q S P N I L T A

3781 AGCGCCTCGG CCTGCCCTAC AAGCGAGTGG AATACACCGG CACCAAGCCC GGTGACATGC  
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3841 CCCCCACCAT TCCGCCGCTC TTCGGGGTCT GAGTAAGTCC **CATG**TCTCGT CCCGGCAGGC  
 P P T I P P L F G V \* OrfX> M S R P G R  
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3901 TGCCACTCTT GATCTGGCAA CCTGCCGGGG CCTGGCATAT GACTCTCACC GAGTCATCAG  
 L P L L I W Q P A G A W H M T L T E S S

3961 ATGAGTGGTC GCAGGTTCCG AAGGTGGCGA GCAG**ATGGGA** ACCTTCAACG TAAGGTTCGA  
 D E W S Q V R K V A S R W E P S T \*  
 ThmD> M G T F N V R F

4021 GCCGATTGGC GAAGAGATCG AGTGCGGCGA GGACGAGACA ATTCTCGATG CAGCGTTTCCG  
 E P I G E E I E C G E D E T I L D A A F

4081 ATCTGGTTTG AACCTTGTGC ACGGTTGCCG CGAGGGGCGC TGCTCGGCGT GCAAGGCATT  
 R S G L N L V H G C R E G R C S A C K A

4141 CGTCCTCGAT GAAGGATGGA TATATCTAAA GAAGTATTCA AGCTTCGCCC TTTCCGACCA  
 F V L D E G W I Y L K K Y S S F A L S D

4201 AGAGGAAGAG GGTGGATATA CACTTCTGTG CCGGGCAGTC CCAGAGTCAG ATGTTACGAT  
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4261 TGAGCTGCTC AACTACGATC CTGACCACTA TCGGCTAGAG CATGCAATTA CCGATGGAGT  
 I E L L N Y D P D H Y R L E H A I T D G

4321 TGGCCAAGTG GTCGAGGTGG AGGCGTTGAC GCACGATATT AGACGCTTGG AACTCCAGAT  
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4381 CGAGTCACCT CAGGGCTTCG GATTTCTTCC TGGTCAGTTC GTCGACATCT GGATCCCCGG  
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4441 GACAGAGCAG CGACGGTCGT TCTCGATGGC AAACCTTCCT AGCGACGGGC GCCTCGAGTT  
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4501 CATCATCAAG CAGTATCCGG GCGGCCGATT CGGGGCGCTG CTCGACGACG GCCTGGCGGT  
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4561 GGGTGATCCA GTGAAGTTCA CCGGGCCTTA TGGTACATGC TATCTCCGTG ATACCGGGCG  
 V G D P V K F T G P Y G T C Y L R D T G

4621 GAGTCGTTTCG GCGCTACTCA TCGCCGGCGG TTCGGGTATG GCGCCGATTC TTTCTCTGCT  
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4681 GCGTCAGATG TCAGACGACG GTCAGGGGCG CACCGTTTCG GTGTTCTACG GTGGACGTAC  
 L R Q M S D D G Q G R T V S V F Y G G R

4741 GAGACGCGAT CTCTTCTATA CCGAGCTCGT ACAGTCCCTC GGAAAGCGAA TCGAGCAGTT  
 T R R D L F Y T E L V Q S L G K R I E Q

4801 CGAGTTCATC CAGGTAGTCT CGGATGAACC TGATAGTGAC GGTGACGATG TCGGATACGG  
 F E F I Q V V S D E P D S D G D D V R Y

4861 ATTCGTACAT GATGCCGTTG ATCAATGGAT AGAGACTTCC GGGTTCGCT TGGACGCGTG  
 G F V H D A V D Q W I E T S G F R L D A

4921 TGACGTCTAT ATGGCAGGTC CACCACCGAT GGTGATGCG GTGAACGATG TTCTGACGCT  
 C D V Y M A G P P P M V D A V N D V L T

4981 CAGACATCAG GTGGAGCAGA ACCGAATCTT CGTAGACAAG TTCACCTCGA CCGGCCCCGA  
 L R H Q V E Q N R I F V D K F T S T G P

5041 GGA~~CT~~CTGCC GATTCGGATT CTGTATCGTC GCTTTAAGAT TTGTTCTCCA GAGAGGAGAT  
 E D S A D S D S V S S L \*

5101 CTGCGCA**ATG** AGTGCATCAG CTGCCGAGCG GCGCGAGCTG CGAGAGCTTG AGCGGTCACA  
 ThmB> M S A S A A E R R E L R E L E R S

5161 GCACTGGTTC ATCCCGGAGC GGAAACGTTT GTCGCTCTAT GAGGACGTCA CTATCGACGT  
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5221 CCAGCCGAGC GTCCACCGGC ACACCAGGTT TGGCTATCCT ATCGCATTCC CAAACGGGCG  
 V Q P S V H R H T R F G Y P I A F P N G

5281 TCCGTCATTC TGGGATGACT CCACTGCGAT CCAGTCCAGC GACTGGTATG CATTTCGTGA  
 R P S F W D D S T A I Q S S D W Y A F R

5341 TCCGGGCGGC CTCTGGGAGC GCACCTTCTT CCAGACGGGC TCAACTCATG AGCGCGAGAT  
 D P G G L W E R T F F Q T G S T H E R E

5401 CGAGAATGAT CTCCAGGTGG CGCGGGACAA TAATCTGTTC GATGCGGTAA GCAAGGAGTG  
 I E N D L Q V A R D N N L F D A V S K E

5461 GGTGACTTC TTGTCTGCTC AGCTTCTGCC GATCAGCCTT ACCGAGTACG GTCTGGTTGC  
 W V D F L S A Q L L P I S L T E Y G L V

5521 CCCGCAGTCG GCGGCACTCC GGCCTGCCCT GGGTGATGCC ATCGCGAACT GCCTCGGCTA  
 A P Q S A A L R P A L G D A I A N C L G

5581 CAGCGCCGGT TACAACTTC GGCAGGCTCA GCGCCTTGTT CTCTACGGGG GAGAACTGGA  
 Y S A G Y K L R Q A Q A L V L Y G G E L

5641 GCGGGAGATC CCCGATTTT CGACCGCCGA CGGGAAGCGC CGTTTCTTGG AGGATCCGGA  
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5701 ATGGCAGCCG ACACGTCGCT ATCTTGAGCG GCTGGCGTCG ATCACGGACT GGGCGGAGAC  
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5761 CATCGTCGCC GCCAACATCT GCTTCGAGCC GCTCATTGGA TCTTTGCTGC GCCGCGAGGT  
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5821 GCTGATCCGA CTCGCCGAT CCTACGGCGA CGCCACCACA CCGACCCTCG GCCAGGTTGC  
 V L I R L A G S Y G D A T T P T L G Q V

5881 CCAAGCCGAG TGGGGGTGGG TGCCTGACTG GTCCGTCGCT CTCGTTTCGCT TCATTCTGAA  
 A Q A E W G W V R D W S V A L V R F I L

5941 TGACACTACC TATTCCGAGG CCAACACCCA GAAGGTCCAG GAGTGGCTGG AGGACTGGGG  
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6001 AACGATGGCT CGCGAGGCGA TCGATGCGCT GGAACCCGTT TTCAGCTCAA TCGACCCCGC  
 G T M A R E A I D A L E P V F S S I D P

6061 TTA~~CT~~CCGAA ACCCGTCAGC GTCTTAACCA AGATCATGCC GACCTGCTTC AGGAATGCGG  
 A Y S E T R Q R L N Q D H A D L L Q E C

6121 TCTCAAGTCG AGCGAGGTGA CGGTCTG**ATG** ACGGATGCCA CGGCTACGTC GCGGGCTGAG  
 G L K S S E V T V \*  
 ThmC> M T D A T A T S A A E

6181 AATGGGAGCG GCGACGCCGC TTATGACTAT GTGGGGCTGG TTATGCAGCG CACTCCGGAA  
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6241 GGCGAAGCGG TCGGCCGGGT GTGCTCGCAG ACTCCTGGTG TCGAGGTCAT CACGAACACA  
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6301 ACGTTTCTTG ATGTCAGGGC CAAGGATCGG CTGATCGTCA ACTTCGACGC GGTGCGCGAA  
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6361 GAGCTCGGCA GCGACATGGA CGGTTACGTT CTTCAGGAAC ACATGACCAC TCACTATGGC  
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6421 CGGATGGCAA TGACCGATGA CTCATTCATC CTGGTCGCCG ATCCCCTCGA GCTGATCGAG  
 R M A M T D D S F I L V A D P L E L I E

6481 CTGATCAACT CTGGGTCGTA GGAAGAGATC ATCAAGGTGA TCTCGCCCCT CGGGTGAGTG  
 L I N S G S \*

6541 ATTCTGTGTT TCACTCCTTG AT**ATG**TGGGA AGCCCTATCT GGGTGGTGTG TCGCTCCCCC  
 OrfQ> M W E A L S G W C V A P



7801 CCGTCGCTGC GATGCACGCG GCGAGGGATG TTGTCGGGGC AACATCGGCT CATCGGCGAG  
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7861 CATCTGCACT GTCGCATGTC GCAGACAGGC TTGAGCAGCG TTCAGAGGAG GCCGCTCAGG  
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7921 TCATCGTGCT CGAGAGCGGT AAGCCCATCA AGTGGGCCAG GGTGGAGGTA GCGCGAGCAG  
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7981 CCTCCACGTT CCGATGGGCG GCAGAGGAGG CGCGGCGTTG GTCGGGAACC CTGCAGCGAT  
A S T F R W A A E E A R R W S G T L Q R

8041 TGGATAACCGA CGCCGGCGGA GCTGGACGGC TTGCGCTTGT TCGGCGGTTT CCACGAGGTT  
L D T D A G G A G R L A L V R R F P R G

8101 CTCTGCTCGC AATTACGCCG TTCAACTTTC CACTTAATCT CGTCGCGCAC AAAGTGGCGC  
S L L A I T P F N F P L N L V A H K V A

8161 CGGCGATCGC GGTCGGAGTG CCGGTTATCA TCAAACCTGC CCCGTCGACT CCGCTCTCAT  
P A I A V G V P V I I K P A P S T P L S

8221 CGTTGTTCTT GGGTCAGCTC CTCGCTGAAA CGGATCTGCA CCAGGGCAGC TGGTCTGTGC  
S L F L G Q L L A E T D L H Q G S W S V

8281 TGCCGTTTCC AAATAGTCAG ATGGAGCACC TTATTCTTGA TCCGAGGCTT CCTATTATCT  
L P V P N S Q M E H L I L D P R L P I I

8341 CTTTCACAGG GTCGGGGCCG GTGGGCTGGG ATATTAAGAG CTTTGTCCCT CGTAAGCATG  
S F T G S G P V G W D I K S L V P R K H

8401 TGACGCTTGA GCTTGGCGGG AATGCGGCGG CCGTTGTATG TTCCGACTGG TCGAGTGAGC  
V T L E L G G N A A A V V C S D W S S E

8461 AAGATCTGGA GTGGGCAGCT CAGCGGATCG CTCTCTTTGC GAACTATCAG GCGGGCCAGT  
Q D L E W A A Q R I A L F A N Y Q A G Q

8521 CGTGTATCTC GGTGCAGCGA GTCTATGTGC CACGTGAGCT GTACGAGGTG TTTACCGTGC  
S C I S V Q R V Y V P R E L Y E V F T V

8581 TGCTTTTCGCG GCATATTGGC GCACTTAGGC AGGGGAATCC GAATGACGAC GCAACTGATG  
L L S R H I G A L R Q G N P N D D A T D

8641 TCGGTCCTGT CATTAAATGAG GCATCAGCCA TCAGGATCGA GCAGTGGATC GATGACGCAG  
V G P V I N E A S A I R I E Q W I D D A

8701 TCCATGCTGG GGC GAAGATT CTGGTCGGGG GCCGCCGAA CGGGACAAGT CTTGAGCCGA  
V H A G A K I L V G G R R N G T S L E P

8761 CGCTTTTGGC TGACGTTCCG CTCGCCGCAC GGATTCTTCG TGACGAGGCA TTCGGCCCCG  
T L L A D V P L A A R I L R D E A F G P

8821 TGGTAAGTAT TACGCCTTTC GACAGTCTAG ACTCGGCGTT TGCTGCCGTT AATGATTCTG  
V V S I T P F D S L D S A F A A V N D S

8881 ACTTCGGTCT GCAGACAGGT GTCTTTACGC GTGATATTCG GACTGCATTC CGCGCGCATC  
D F G L Q T G V F T R D I R T A F R A H

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8941 GCGACCTTGA GGTGGGTGGG GTCATTATTG GAGATGTTCC GAGCTACCGT GCGGACCAGA  
R D L E V G G V I I G D V P S Y R A D Q

9001 TGCCGTATGG TGGAATGAAG GATTCTGGTA TAGGCAGAGA AGGCGTCCGC TCAGCTATGG  
M P Y G G M K D S G I G R E G V R S A M

9061 ACGACTTCAC GGTGGAGAAG GTTCTCGTGC TTGCCGGGGT CGCGCTGTGA AAAGCGTTGC  
D D F T V E K V L V L A G V A L \*

9121 TCTGTGCCCT TTGATTCTT ACTGACCTCC CCGGTGCCGG CCGGTGCCCA ACAGTGATC