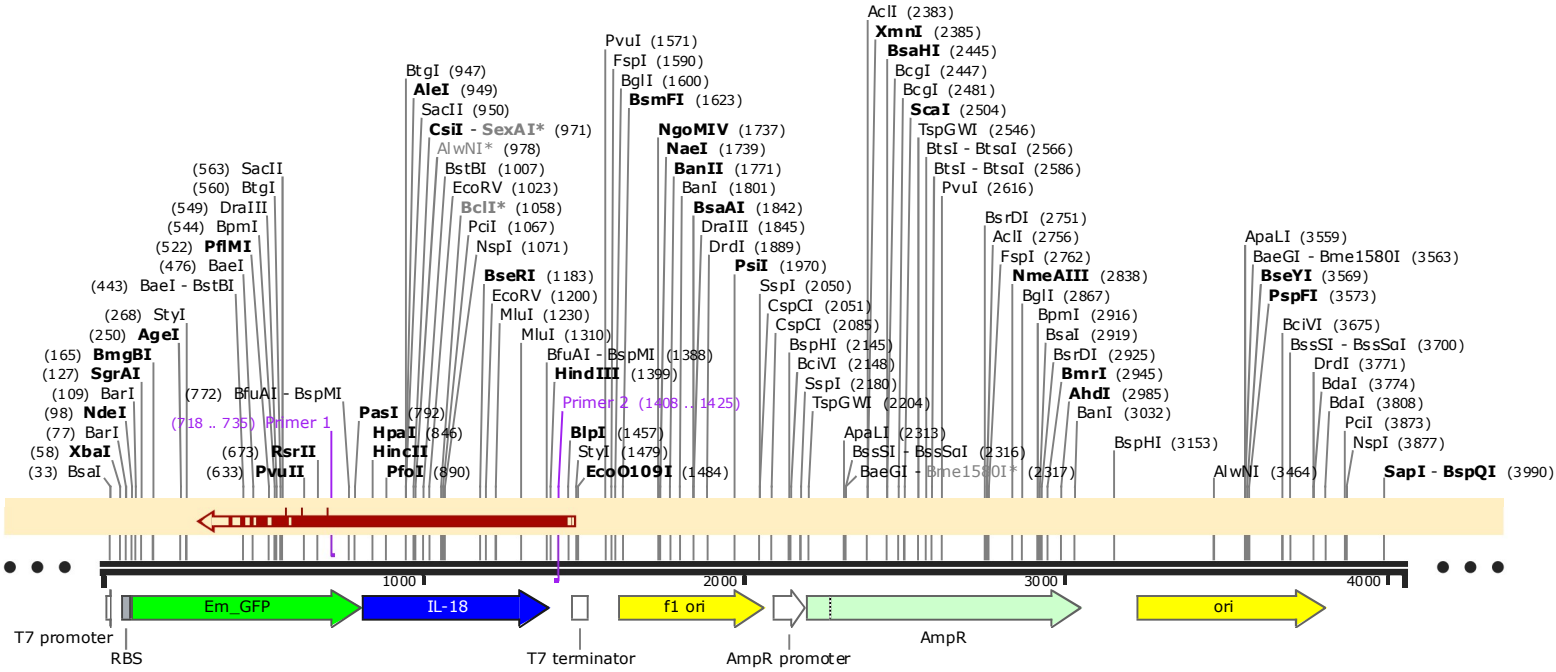
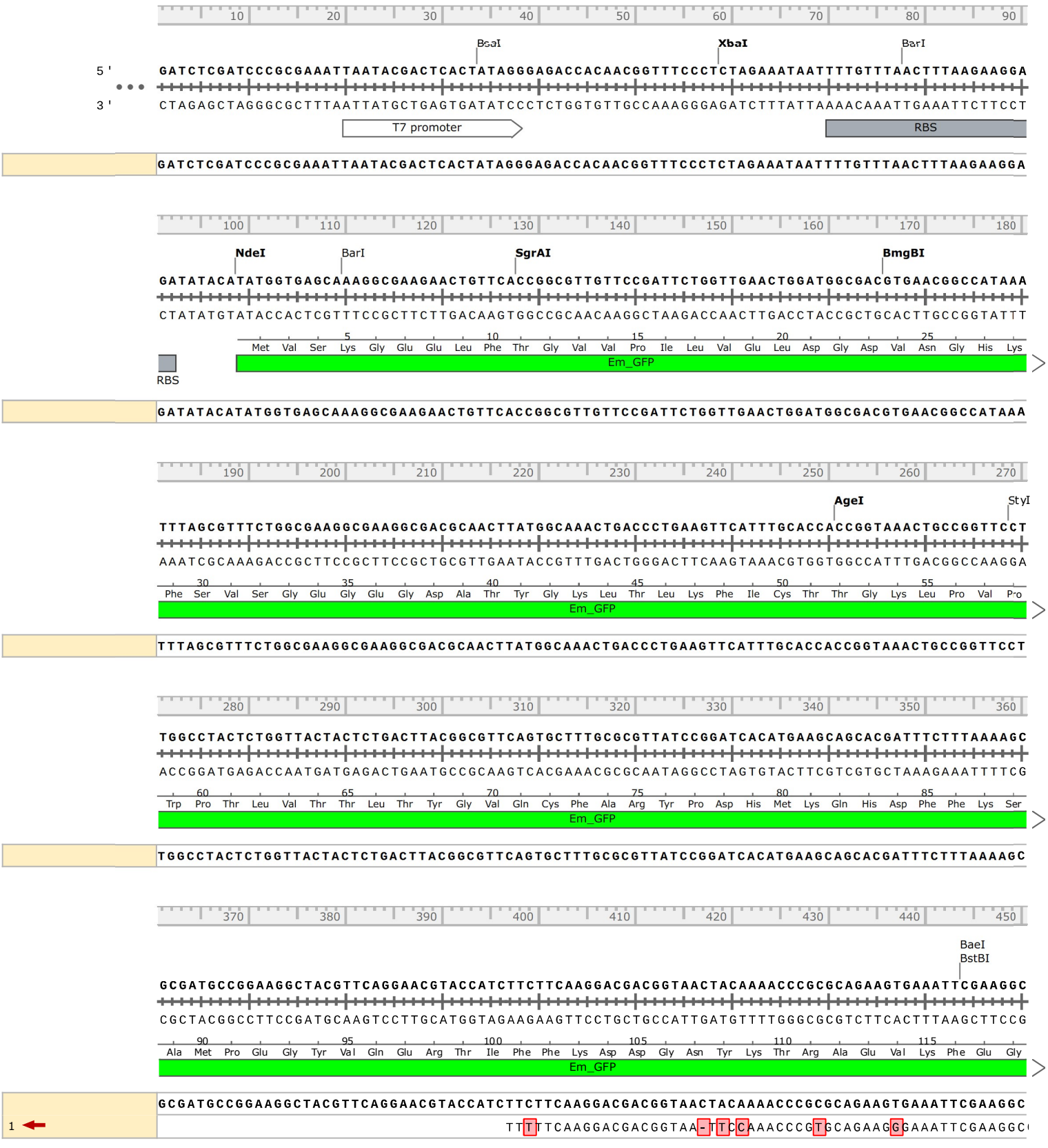
Sequence: pAE_EmGFP_IL18_(cloned_-_seq_sintese).dna (Circular / 4053 bp)
Enzymes: Unique & Dual Cutters (73 of 686 total)
Features: 9 total
Primers: 2 total

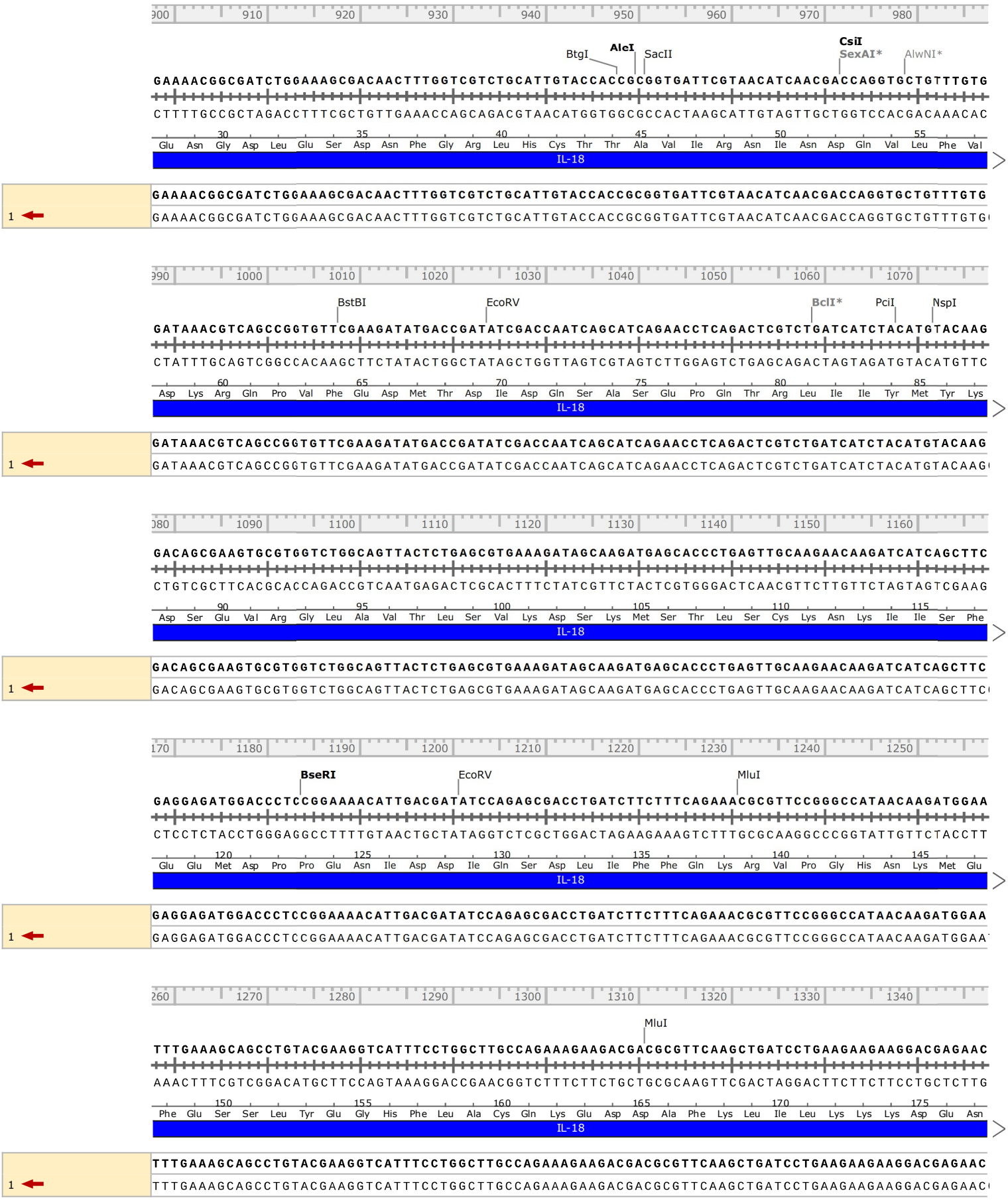
Unique Cutters **Bold**

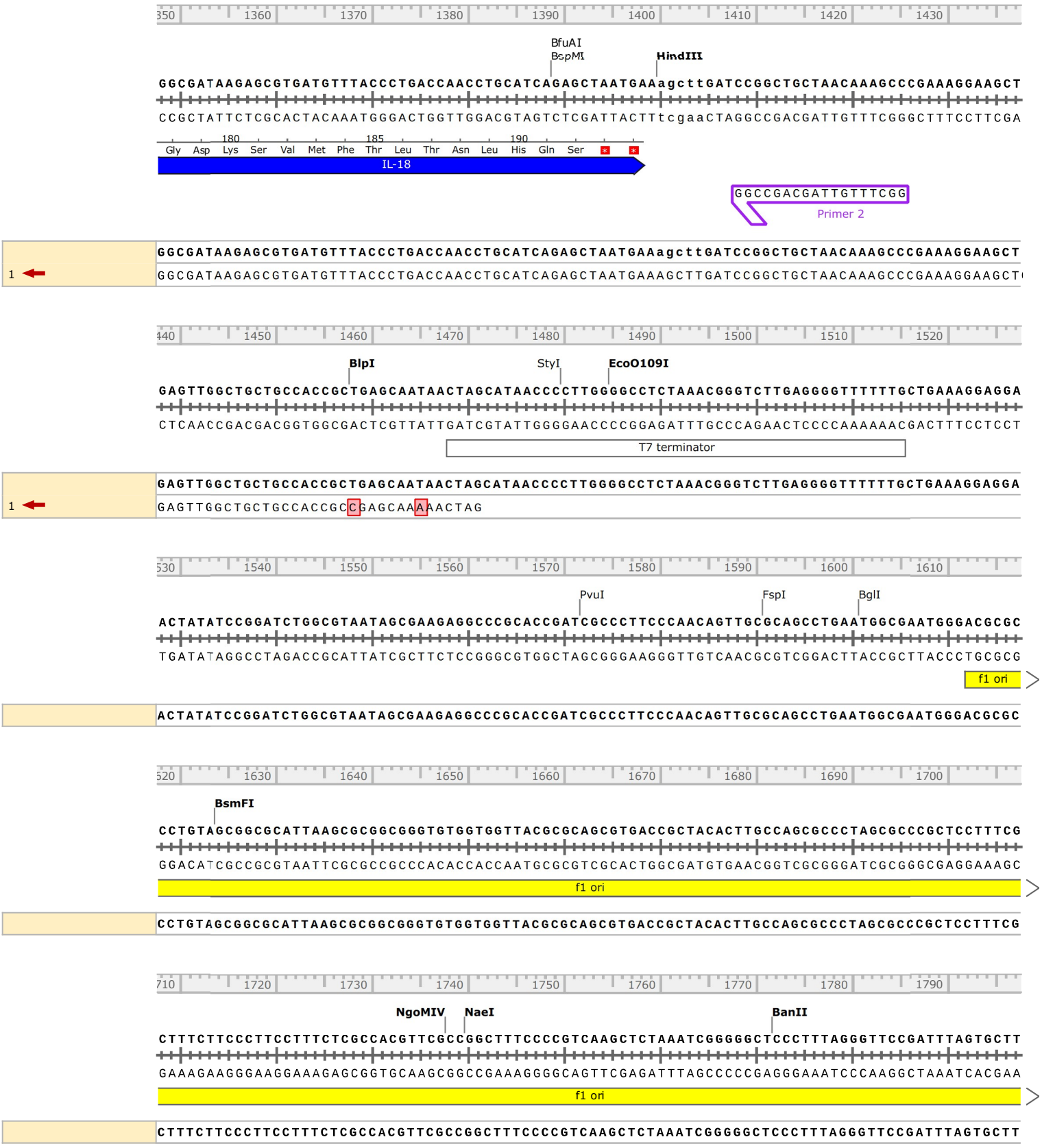


pAE_EmGFP_IL18_(cloned_-_seq_sintese)
4053 bp

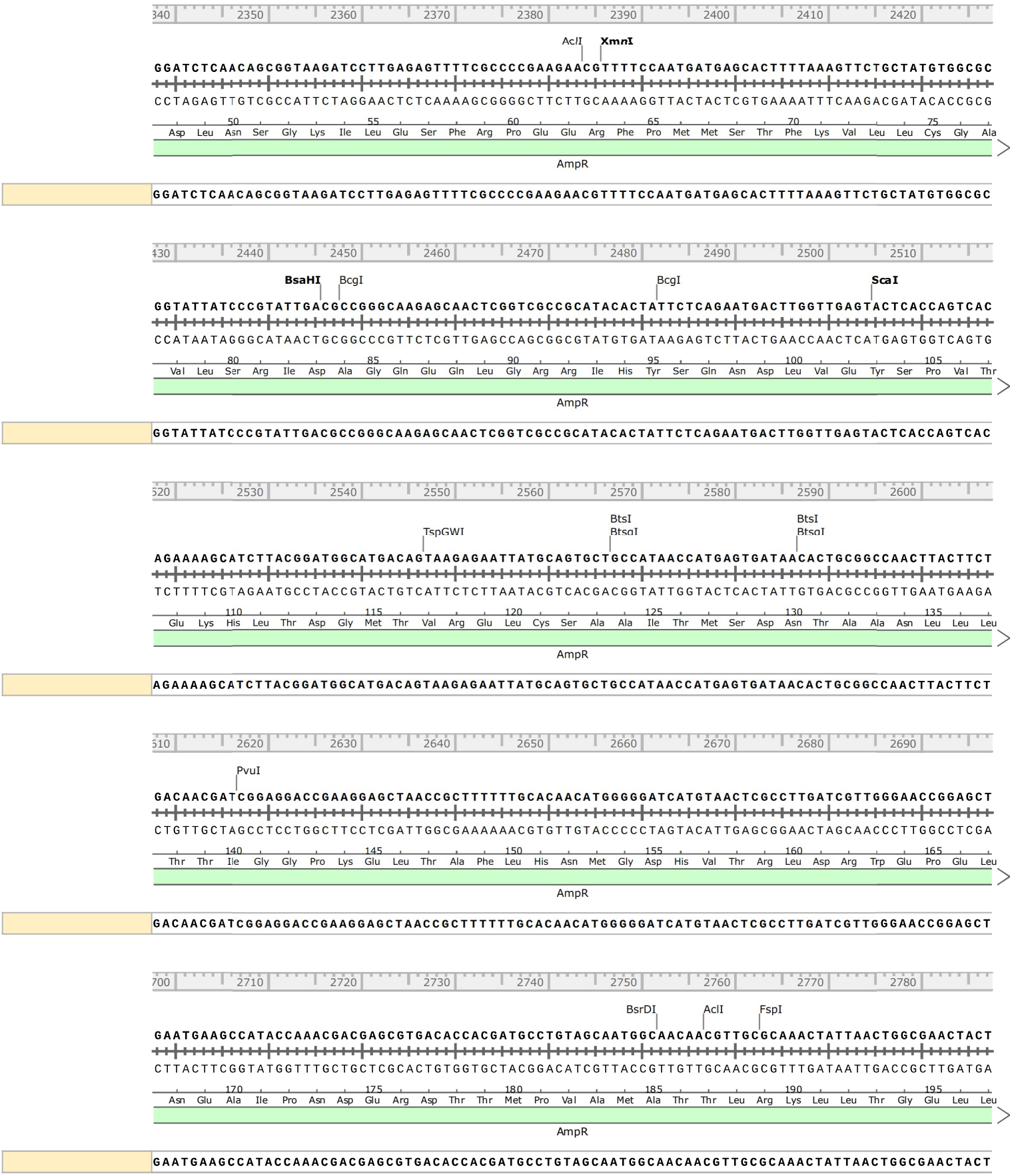

BsaI
XbaI
BarI
5 '
GATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGA
3 '
CTAGAGCTAGGGCGCTTTAATTATGCTGAGTGATATCCCTCTGGTGTTGCCAAAGGGAGATCTTTATTAAAACAAATTGAAATTCTTCCT
T7 promoter
RBS
GATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGA
NdeI
BarI
SgrAI
BmgBI
GATATACATATGGTGAGCAAAGGCGAAGAACTGTTCACCGGCGTTGTTCCGATTCTGGTTGAACTGGATGGCGACGTGAACGGCCATAAA
CTATATGTATACCACTCGTTTCCGCTTCTTGACAAGTGGCCGCAACAAGGCTAAGACCAACTTGACCTACCGCTGCACTTGCCGGTATTT
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
Em_GFP
RBS
GATATACATATGGTGAGCAAAGGCGAAGAACTGTTCACCGGCGTTGTTCCGATTCTGGTTGAACTGGATGGCGACGTGAACGGCCATAAA
AgeI
StyI
TTTAGCGTTTCTGGCGAAGGCGAAGGCGACGCAACTTATGGCAAACTGACCCTGAAGTTCATTTGCACCACCGGTAAACTGCCGGTTCCT
AAATCGCAAAGACCGCTTCCGCTTCCGCTGCGTTGAATACCGTTTGACTGGGACTTCAAGTAAACGTGGTGGCCATTTGACGGCCAAGGA
Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
Em_GFP
TTTAGCGTTTCTGGCGAAGGCGAAGGCGACGCAACTTATGGCAAACTGACCCTGAAGTTCATTTGCACCACCGGTAAACTGCCGGTTCCT
TGGCCTACTCTGGTTACTACTCTGACTTACGGCGTTCAGTGCTTTGCGCGTTATCCGGATCACATGAAGCAGCACGATTTCTTTAAAAGC
ACCGGATGAGACCAATGATGAGACTGAATGCCGCAAGTCACGAAACGCGCAATAGGCCTAGTGTACTTCGTCGTGCTAAAGAAATTTTCG
Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
Em_GFP
TGGCCTACTCTGGTTACTACTCTGACTTACGGCGTTCAGTGCTTTGCGCGTTATCCGGATCACATGAAGCAGCACGATTTCTTTAAAAGC
BaeI
BstBI
GCGATGCCGGAAGGCTACGTTCAGGAACGTACCATCTTCTTCAAGGACGACGGTAACTACAAAACCCGCGCAGAAGTGAAATTCGAAGGC
CGCTACGGCCTTCCGATGCAAGTCCTTGCATGGTAGAAGAAGTTCCTGCTGCCATTGATGTTTTGGGCGCGTCTTCACTTTAAGCTTCCG
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
Em_GFP
GCGATGCCGGAAGGCTACGTTCAGGAACGTACCATCTTCTTCAAGGACGACGGTAACTACAAAACCCGCGCAGAAGTGAAATTCGAAGGC
1
TTTTTCAAGGACGACGGTAA-TTCCAAACCCGTGCAGAAGGGAAATTCGAAGGC


460 470 480 490 500 510 520 530 540
BacI
PflMI
GATACCCTGGTGAACCGTATTGAGCTGAAAGGCATCGACTTCAAGGAAGACGGTAACATCCTGGGCCATAAGCTGGAGTACAACTACAAC
CTATGGGACCACTTGGCATAACTCGACTTTCCGTAGCTGAAGTTCCTTCTGCCATTGTAGGACCCGGTATTCGACCTCATGTTGATGTTG
120 125 130 135 140 145
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
Em_GFP
1
GATACCCTGGTGAACCGTATTGAGCTGAAAGGCATCGACTTCAAGGAAGACGGTAACATCCTGGGCCATAAGCTGGAGTACAACTACAAC
GATACC-TG-TGGAC-GTATTGAGCTGAAAG-CCTTGACTTCAAGGAAGACGGTAACATCCTGGGCCATAAGCTGGAG-ACCACTACAAC
550 560 570 580 590 600 610 620 630
BpmI
DraIII
BtgI
SacII
AGCCACAAGGTGTACATCACCGCGGATAAGCAGAAGAACGG CATCAAAGTGAACTTCAAGACCCGCCATAACATTGAAGACGGCTCAGT
TCGGTGTTCCACATGTAGTGGCGCCTATTCGTCTTCTTGCC GTAGTTTCACTTGAAGTTCTGGGCGGTATTGTAACTTCTGCCGAGTCA
150 155 160 165 170 175
Ser His Lys Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val
Em_GFP
1
AGCCACAAGGTGTACATCACCGCGGATAAGCAGAAGAACGG CATCAAAGTGAACTTCAAGACCCGCCATAACATTGAAGACGGCTCAGT
AGCCACAAGGTGTACATCACCGCGGATAAGCAGAAGAACGGGCATCAAAGTGACTTCAAGACCCGCCATAACATTGAAGACGGCTCAGT
640 650 660 670 680 690 700 710
PvuII
RsrII
TCA GCTGGCAGATCACTATCAGCAGAACACCCCTATTGGCGACGGTCCGGTTCTGCTGCCGGATAATCATTATCTGAGCACCC AGAGC
AGT CGACCGTCTAGTGATAGTCGTCTTGTGGGGATAACCGCTGCCAGGCCAAGACGACGGCCTATTAGTAATAGACTCGTGGG TCTCG
180 185 190 195 200 205
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
Em_GFP
1
TCA GCTGGCAGATCACTATCAGCAGAACACCCCTATTGGCGACGGTCCGGTTCTGCTGCCGGATAATCATTATCTGAGCACCC AGAGC
TCAAGCTGGCAGATCACTATCAGCAGAACACCCCTATTGGCGACGGTCCGGTTCTGCTGCCGGATAATCATTATCTGAGCACCCCAGAGC
720 730 740 750 760 770 780 790 800
Primer 1
GCACTGTCTAAAGATCCG
BfuAI
BspMI
PasI
GCACTGTCTAAAGATCCGAACGAAAAGCGCGATCACATGGTTCTGCTGGAATTTGTGACCGCAGCAGGTATTACCCTGGGTATGGACGAA
CGTGACAGATTTCTAGGCTTGCTTTTCGCGCTAGTGTACCAAGACGACCTTAAACACTGGCGTCGTCCATAATGGGACCCATACCTGCTT
210 215 220 225 230 235
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
Em_GFP
1
GCACTGTCTAAAGATCCGAACGAAAAGCGCGATCACATGGTTCTGCTGGAATTTGTGACCGCAGCAGGTATTACCCTGGGTATGGACGAA
GCACTGTCTAAAGATCCGAACGAAAAGCGCGATCACATGGTTCTGCTGGAATTTGTGACCGCAGCAGGTATTACCCTGGGTATGGACGAA
810 820 830 840 850 860 870 880 890
HpaI
HincII
PfoI
CTGTACAAGATGGCAGCGATGAGCGAAGATTCTTGCGTTAACTTCAAGGAGATGATGTTCATCGACAACACCCTGTACTTCATCCCGGAA
GACATGTTCTACCGTCGCTACTCGCTTCTAAGAACGCAATTGAAGTTCCTCTACTACAAGTAGCTGTTGTGGGACATGAAGTAGGGCCTT
240 1 5 10 15 20 25
Leu Tyr Lys Met Ala Ala Met Ser Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met Phe Ile Asp Asn Thr Leu Tyr Phe Ile Pro Glu
Em_GFP
IL-18
1
CTGTACAAGATGGCAGCGATGAGCGAAGATTCTTGCGTTAACTTCAAGGAGATGATGTTCATCGACAACACCCTGTACTTCATCCCGGAA
CTGTACAAGATGGCAGCGATGAGCGAAGATTCTTGCGTTAACTTCAAGGAGATGATGTTCATCGACAACACCCTGTACTTCATCCCGGAA

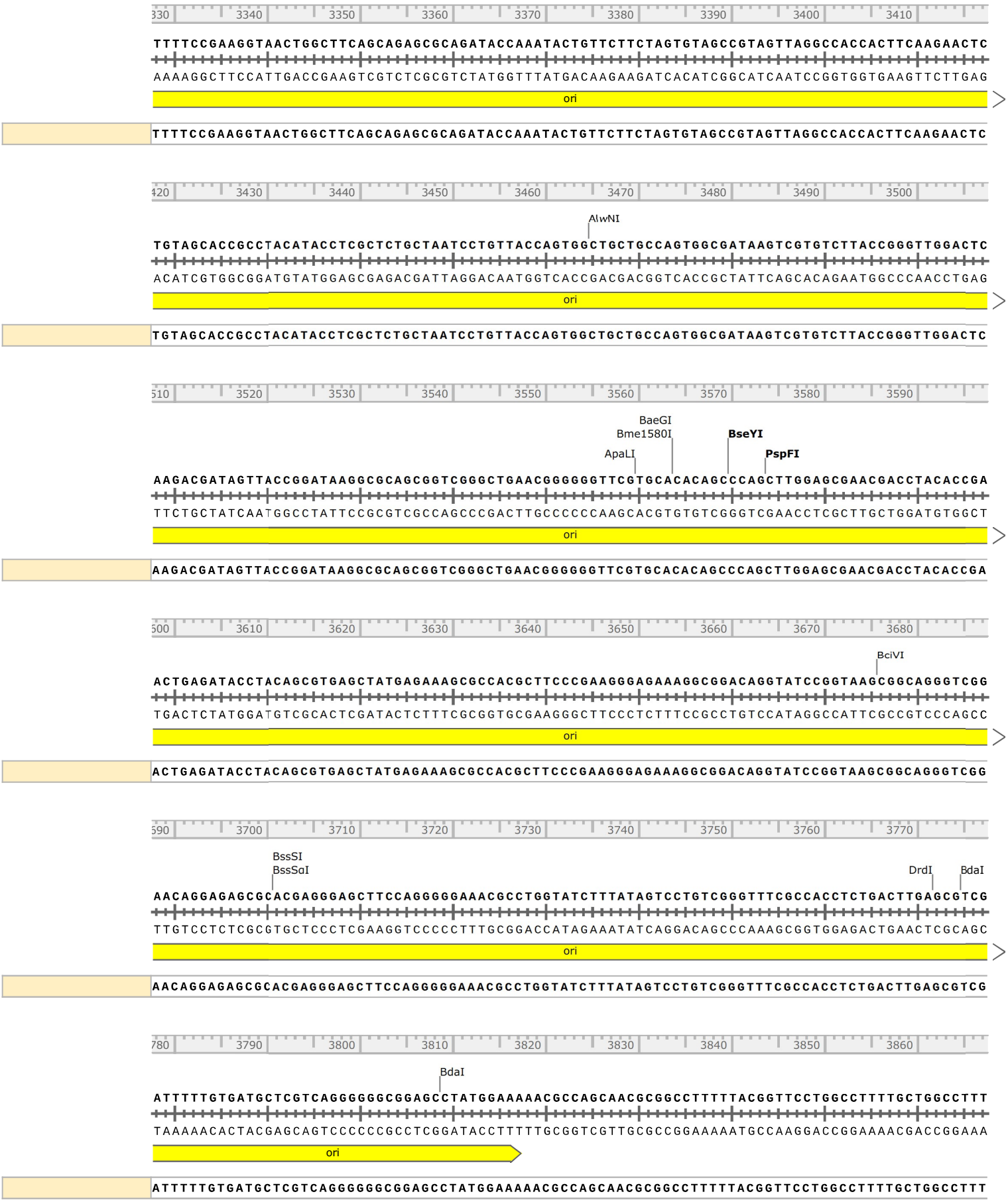

BtgI
AleI
SacII
CsiI
SexAI*
AlwNI*
BstBI
EcoRV
BclI*
PciI
NspI
BseRI
EcoRV
MluI
MluI
IL-18

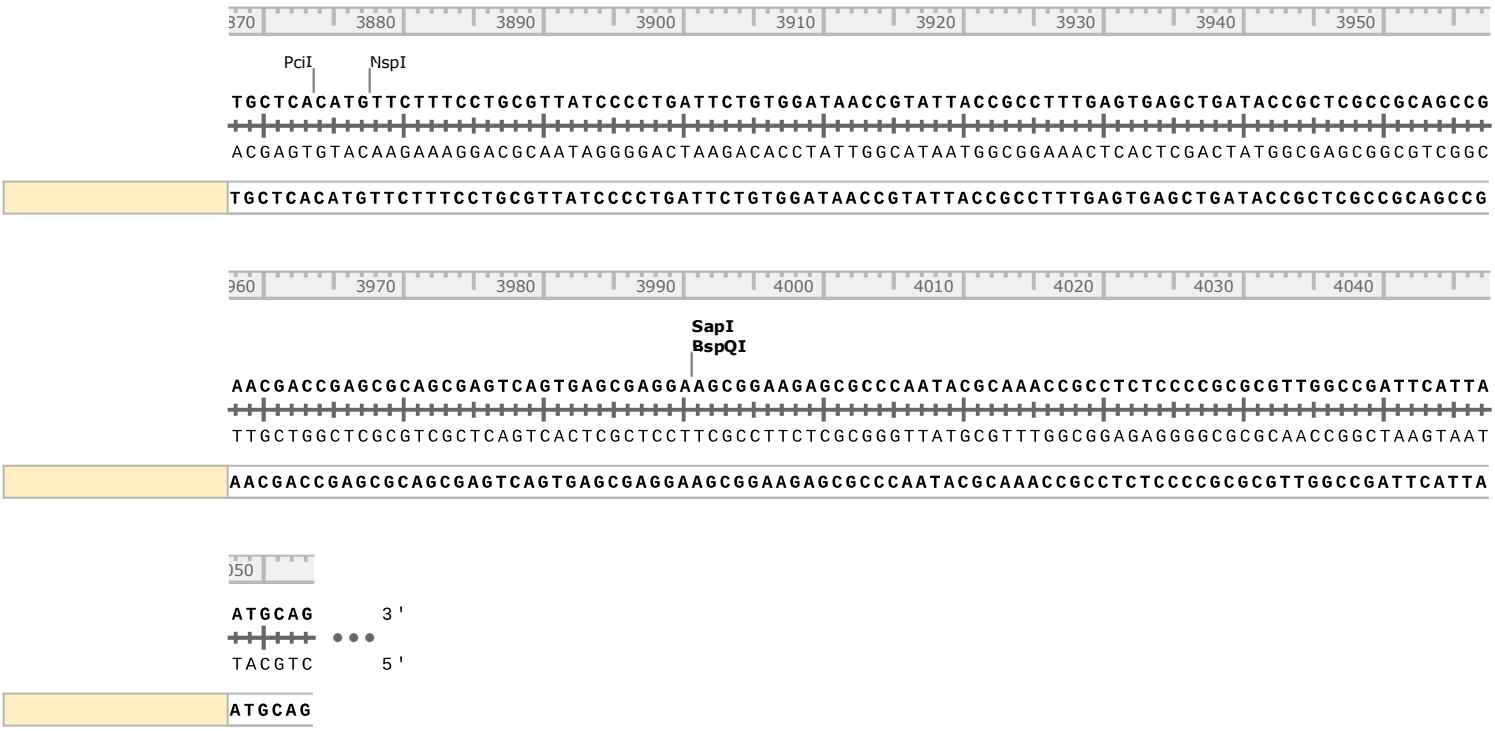

BfuAI
BspMI
HindIII
IL-18
Primer 2
BlpI
StyI
EcoO109I
T7 terminator
PvuI
FspI
BglI
f1 ori
BsmFI
f1 ori
NgoMIV
NaeI
BanII
f1 ori


1800 1810 1820 1830 1840 1850 1860 1870 1880
BanI
BsaAI
DraIII
TACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGT
ATGCCGTGGAGCTGGGGTTTTTTGAACTAATCCCACTACCAAGTGCATCACCCGGTAGCGGGACTATCTGCCAAAAAGCGGGAAACTGCA
f1 ori
TACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGT
1890 1900 1910 1920 1930 1940 1950 1960 1970
DrdI
PsiI
TGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGA
ACCTCAGGTGCAAGAAATTATCACCTGAGAACAAGGTTTGACCTTGTTGTGAGTTGGGATAGAGCCAGATAAGAAAACTAAATATTCCCT
f1 ori
TGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGA
1980 1990 2000 2010 2020 2030 2040 2050 2060
SspI
CspCI
TTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT
AAAACGGCTAAAGCCGGATAACCAATTTTTTACTCGACTAAATTGTTTTTAAATTGCGCTTAAAATTGTTTTATAATTGCGAATGTTAAA
f1 ori
TTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT
2070 2080 2090 2100 2110 2120 2130 2140 2150
CspCI
BspHI
BciVI
AGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATA
TCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTAT
AmpR promoter
AGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATA
2160 2170 2180 2190 2200 2210 2220 2230 2240
SspI
TspGWI
ACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATT
TGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCATACTCATAAGTTGTAAAGGCACAGCGGGAATAAGGGAAAAAACGCCGTAA
1 5 10 15
Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala Phe
AmpR promoter
signal sequence
AmpR
ACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATT
2250 2260 2270 2280 2290 2300 2310 2320 2330
BssSI
BssSαI
BaeGI
Bme1580I*
ApaLI
TTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACT
AACGGAAGGACAAAAACGAGTGGGTCTTTGCGACCACTTTCATTTTCTACGACTTCTAGTCAACCCACGTGCTCACCCAATGTAGCTTGA
20 25 30 35 40 45
Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu
signal sequence
AmpR
TTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACT


AclI
XmnI
AmpR
BsaHI
BcgI
BcgI
ScaI
AmpR
TspGWI
BtsI
BtsaI
BtsI
BtsaI
AmpR
PvuI
AmpR
BsrDI
AclI
FspI
AmpR


NmeAIII
BglI
BpmI
BsaI
BsrDI
BmrI
AhdI
BanI
BspHI
AmpR
ori


3330 3340 3350 3360 3370 3380 3390 3400 3410
TTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTC
AAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAAGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAG
ori
TTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTC
3420 3430 3440 3450 3460 3470 3480 3490 3500
AlwNI
TGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTC
ACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAG
ori
TGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTC
3510 3520 3530 3540 3550 3560 3570 3580 3590
BaeGI
Bme1580I
ApaLI
BseYI
PspFI
AAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGA
TTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCT
ori
AAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGA
3600 3610 3620 3630 3640 3650 3660 3670 3680
BciVI
ACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGG
TGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCC
ori
ACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGG
3690 3700 3710 3720 3730 3740 3750 3760 3770
BssSI
BssSαI
DrdI
BdaI
AACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCG
TTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGC
ori
AACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCG
3780 3790 3800 3810 3820 3830 3840 3850 3860
BdaI
ATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTT
TAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAA
ori
ATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTT

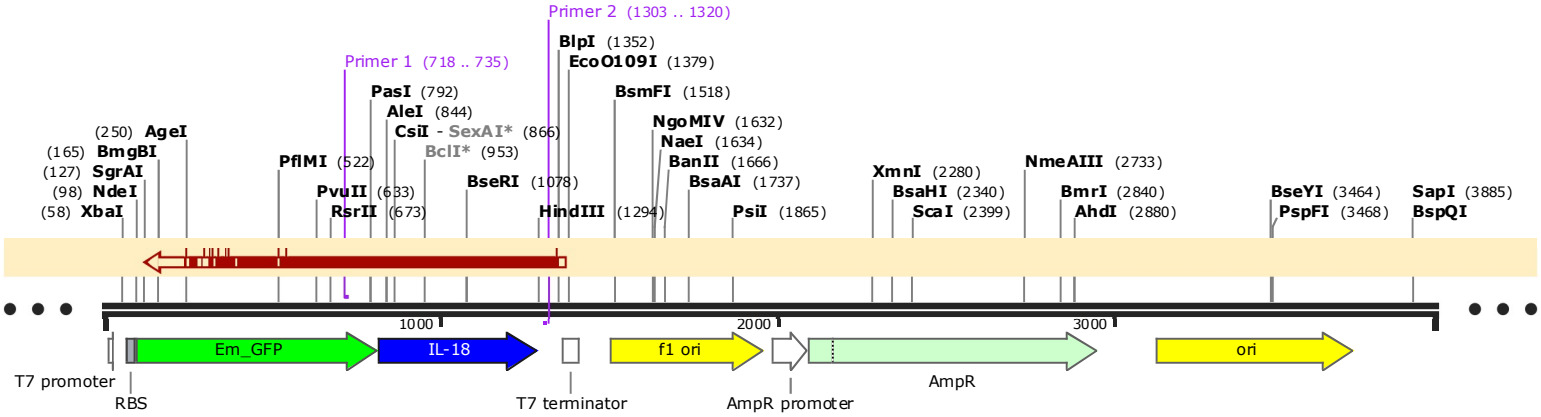


Original Sequence: pAE_EmGFP_IL18_(cloned_-_seq_sintese).dna
1 .. 4053

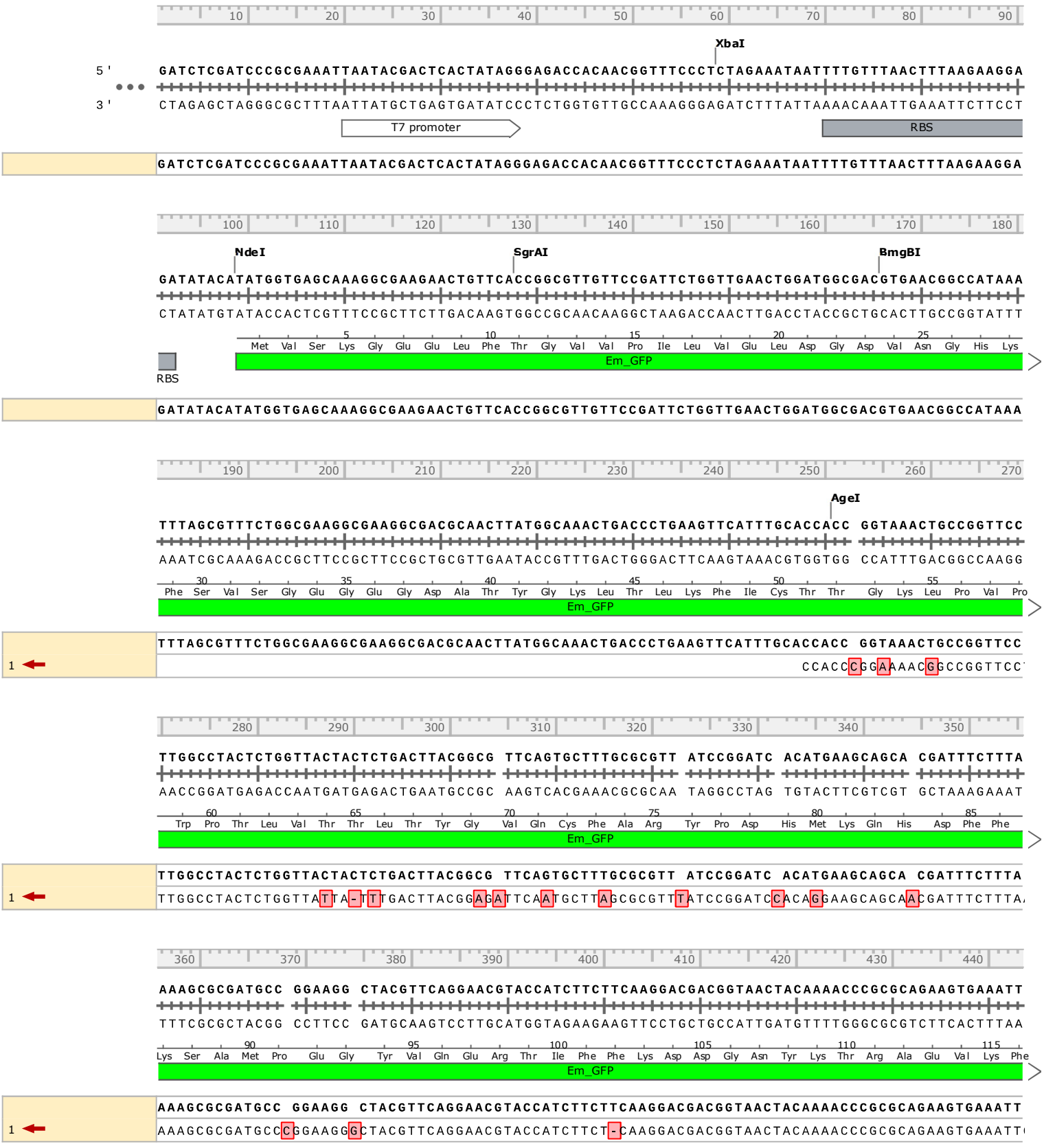
5-pAE-proll-18-EmGFP-SS-466-Seq-pAE-R_G05
1174 bases / 10 Apr 2024
14 .. 1085 (13 mismatches, 9 gaps)

Sequence: pAE_EmGFP_IL18_ativa_(cloned_-_seq_sintese).dna (Circular / 3948 bp)
Enzymes: Unique Cutters (33 of 686 total)
Features: 9 total
Primers: 2 total

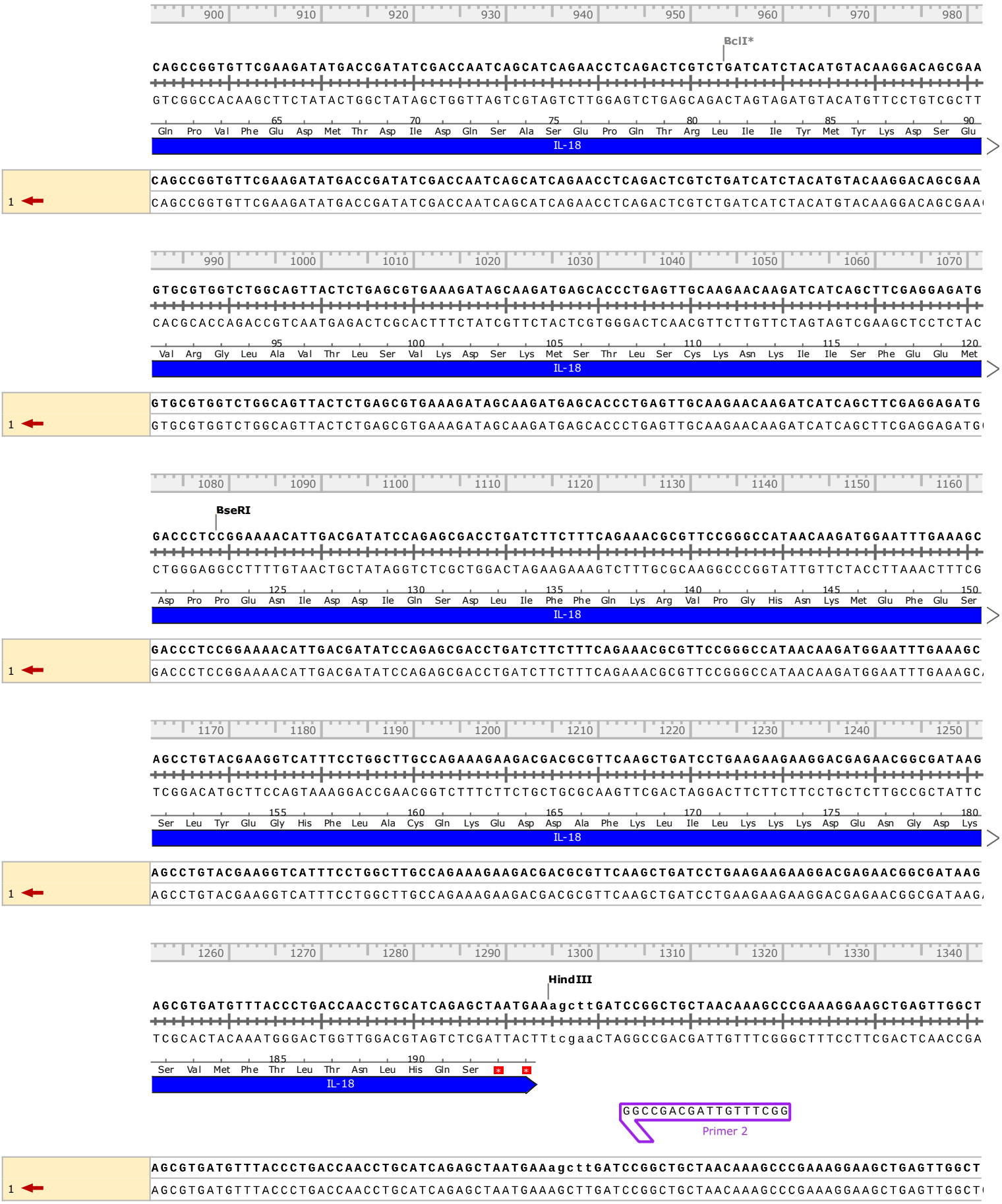
Unique Cutters **Bold**



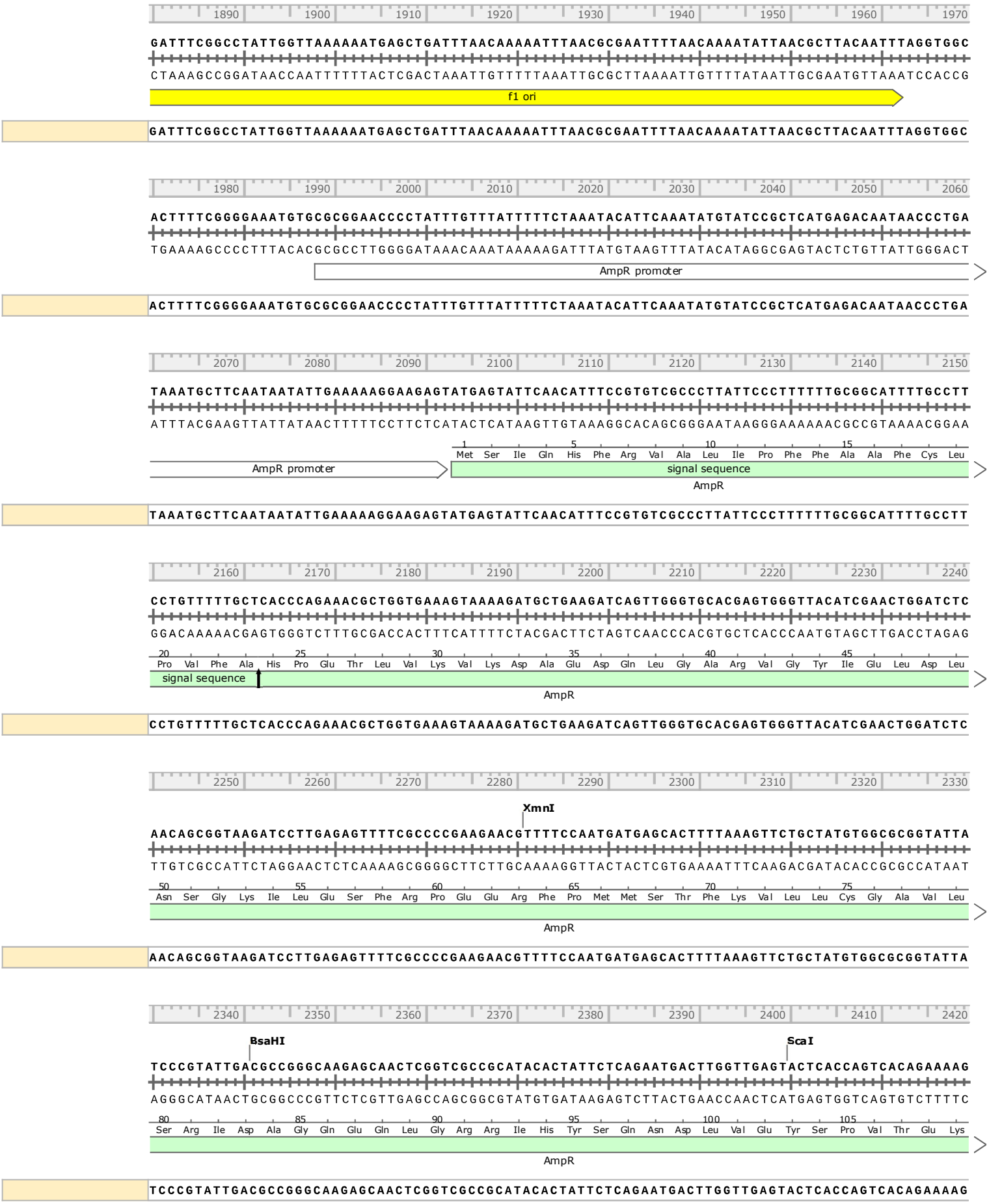
pAE_EmGFP_IL18_ativa_(cloned_-_seq_sintese)
3948 bp

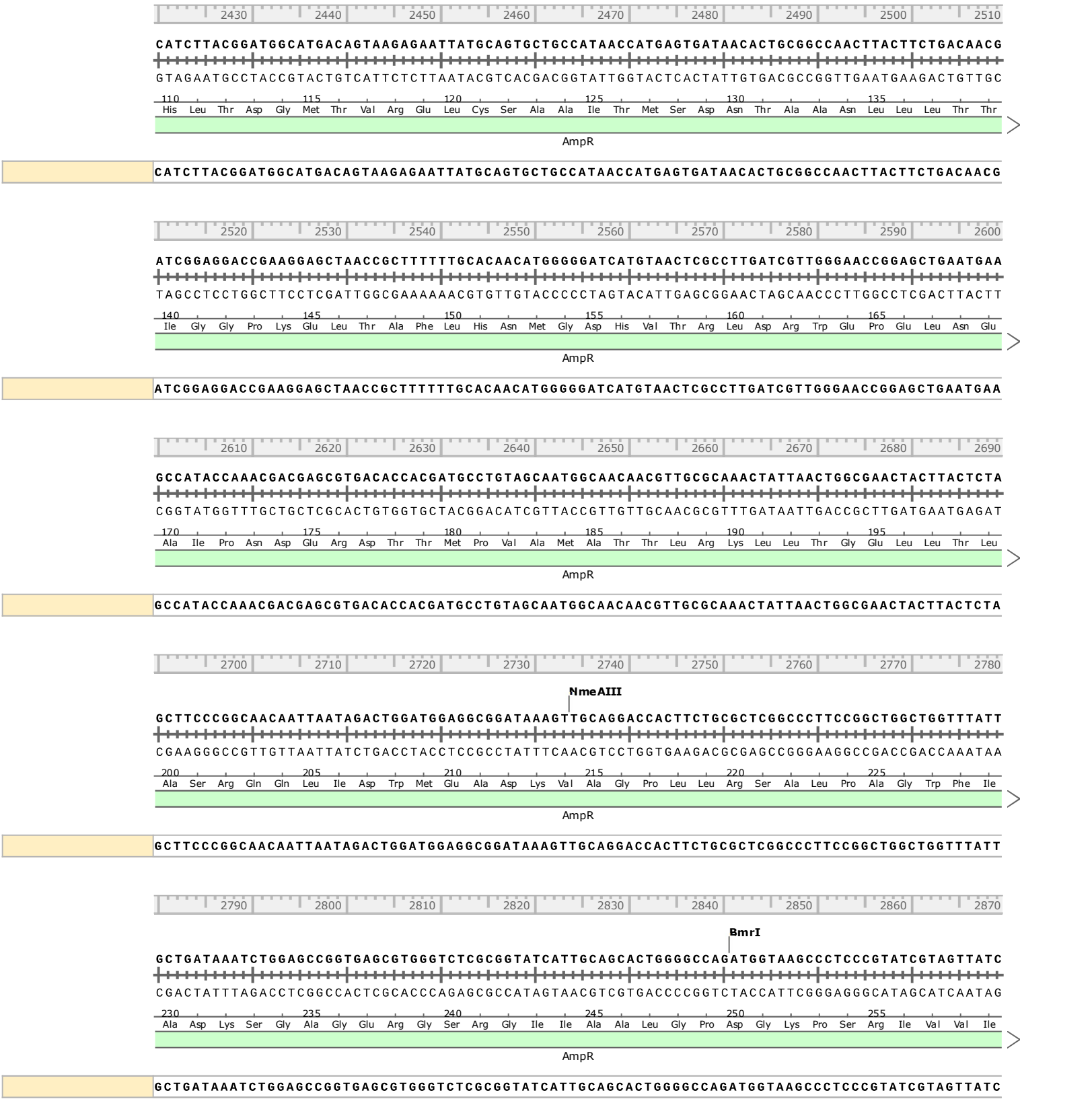

XbaI
5 '
GATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGA
3 '
CTAGAGCTAGGGCGCTTTAATTATGCTGAGTGATATCCCTCTGGTGTTGCCAAAGGGAGATCTTTATTAAAACAAATTGAAATTCTTCCT
T7 promoter
RBS
NdeI
SgrAI
BmgBI
GATATACATATGGTGAGCAAAGGCGAAGAACTGTTCACCGGCGTTGTTCCGATTCTGGTTGAACTGGATGGCGACGTGAACGGCCATAAA
CTATATGTATACCACTCGTTTCCGCTTCTTGACAAGTGGCCGCAACAAGGCTAAGACCAACTTGACCTACCGCTGCACTTGCCGGTATTT
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
RBS
Em_GFP
AgeI
TTTAGCGTTTCTGGCGAAGGCGAAGGCGACGCAACTTATGGCAAACTGACCCTGAAGTTCATTTGCACCACC GGTAAACTGCCGGTTCC
AAATCGCAAAGACCGCTTCCGCTTCCGCTGCGTTGAATACCGTTTGACTGGGACTTCAAGTAAACGTGGTGG CCATTTGACGGCCAAGG
Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
Em_GFP
TTTAGCGTTTCTGGCGAAGGCGAAGGCGACGCAACTTATGGCAAACTGACCCTGAAGTTCATTTGCACCACC GGTAAACTGCCGGTTCC
1
CCACCCGGAAAACGGCCGGTTCC
TTGGCCTACTCTGGTTACTACTCTGACTTACGGCG TTCAGTGCTTTGCGCGTT ATCCGGATC ACATGAAGCAGCA CGATTTCTTTA
AACCGGATGAGACCAATGATGAGACTGAATGCCGC AAGTCACGAAACGCGCAA TAGGCCTAG TGTACTTCGTCGT GCTAAAGAAAT
Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
Em_GFP
TTGGCCTACTCTGGTTACTACTCTGACTTACGGCG TTCAGTGCTTTGCGCGTT ATCCGGATC ACATGAAGCAGCA CGATTTCTTTA
1
TTGGCCTACTCTGGTTATTA-TTTGACTTACGGAGATTCAATGCTTAGCGCGTTTATCCGGATCCACAGGAAGCAGCAACGATTTCTTTA
AAAGCGCGATGCC GGAAGG CTACGTTCAGGAACGTACCATCTTCTTCAAGGACGACGGTAACTACAAAACCCGCGCAGAAGTGAAATT
TTTCGCGCTACGG CCTTCC GATGCAAGTCCTTGCATGGTAGAAGAAGTTCCTGCTGCCATTGATGTTTTGGGCGCGTCTTCACTTTAA
Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
Em_GFP
AAAGCGCGATGCC GGAAGG CTACGTTCAGGAACGTACCATCTTCTTCAAGGACGACGGTAACTACAAAACCCGCGCAGAAGTGAAATT
1
AAAGCGCGATGCCCGGAAGGGCTACGTTCAGGAACGTACCATCTTCT-CAAGGACGACGGTAACTACAAAACCCGCGCAGAAGTGAAATT


PflMI
Em_GFP
PvuII
RsrII
Primer 1
GCACTGTCTAAAGATCCG
PasI
AleI
CsiI
SexAI*
IL-18

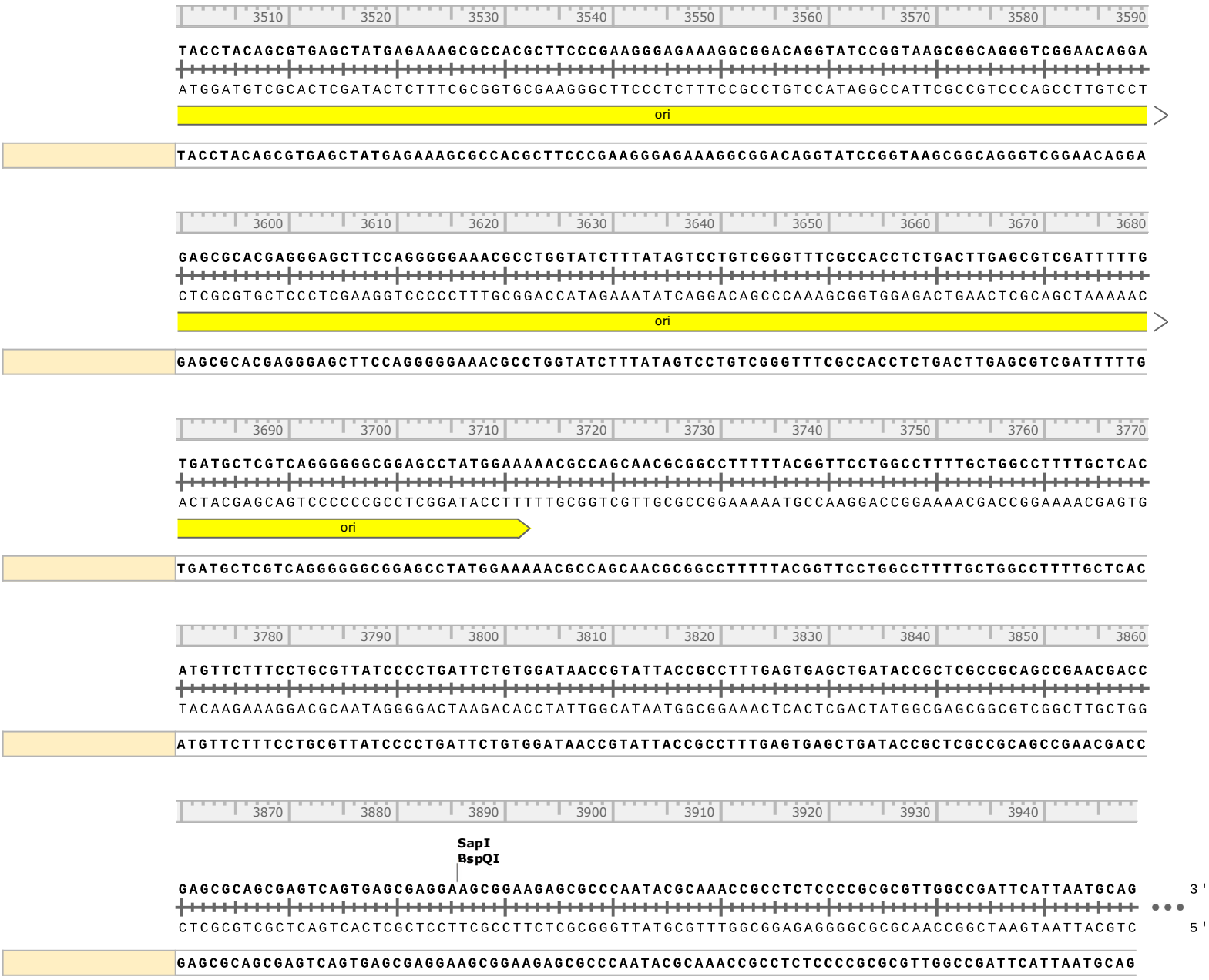

900 910 920 930 940 950 960 970 980
BclI*
CAGCCGGTGTTCGAAGATATGACCGATATCGACCAATCAGCATCAGAACCTCAGACTCGTCTGATCATCTACATGTACAAGGACAGCGAA
GTCGGCCACAAGCTTCTATACTGGCTATAGCTGGTTAGTCGTAGTCTTGGAGTCTGAGCAGACTAGTAGATGTACATGTTCCTGTCGCTT
65 70 75 80 85 90
Gln Pro Val Phe Glu Asp Met Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile Tyr Met Tyr Lys Asp Ser Glu
IL-18
1
CAGCCGGTGTTCGAAGATATGACCGATATCGACCAATCAGCATCAGAACCTCAGACTCGTCTGATCATCTACATGTACAAGGACAGCGAA
CAGCCGGTGTTCGAAGATATGACCGATATCGACCAATCAGCATCAGAACCTCAGACTCGTCTGATCATCTACATGTACAAGGACAGCGAA
990 1000 1010 1020 1030 1040 1050 1060 1070
GTGCGTGGTCTGGCAGTTACTCTGAGCGTGAAAGATAGCAAGATGAGCACCCTGAGTTGCAAGAACAAGATCATCAGCTTCGAGGAGATG
CACGCACCAGACCGTCAATGAGACTCGCACTTTCTATCGTTCTACTCGTGGGACTCAACGTTCTTGTTCTAGTAGTCGAAGCTCCTCTAC
95 100 105 110 115 120
Val Arg Gly Leu Ala Val Thr Leu Ser Val Lys Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile Ser Phe Glu Glu Met
IL-18
1
GTGCGTGGTCTGGCAGTTACTCTGAGCGTGAAAGATAGCAAGATGAGCACCCTGAGTTGCAAGAACAAGATCATCAGCTTCGAGGAGATG
GTGCGTGGTCTGGCAGTTACTCTGAGCGTGAAAGATAGCAAGATGAGCACCCTGAGTTGCAAGAACAAGATCATCAGCTTCGAGGAGATG
1080 1090 1100 1110 1120 1130 1140 1150 1160
BseRI
GACCCTCCGGAAAACATTGACGATATCCAGAGCGACCTGATCTTCTTTCAGAAACGCGTTCCGGGCCATAACAAGATGGAATTTGAAAGC
CTGGGAGGCCTTTTGTAACTGCTATAGGTCTCGCTGGACTAGAAGAAAGTCTTTGCGCAAGGCCCGGTATTGTTCTACCTTAAACTTTCG
125 130 135 140 145 150
Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu Phe Glu Ser
IL-18
1
GACCCTCCGGAAAACATTGACGATATCCAGAGCGACCTGATCTTCTTTCAGAAACGCGTTCCGGGCCATAACAAGATGGAATTTGAAAGC
GACCCTCCGGAAAACATTGACGATATCCAGAGCGACCTGATCTTCTTTCAGAAACGCGTTCCGGGCCATAACAAGATGGAATTTGAAAGC
1170 1180 1190 1200 1210 1220 1230 1240 1250
AGCCTGTACGAAGGTCATTTCCTGGCTTGCCAGAAAGAAGACGACGCGTTCAAGCTGATCCTGAAGAAGAAGGACGAGAACGGCGATAAG
TCGGACATGCTTCCAGTAAAGGACCGAACGGTCTTTCTTCTGCTGCGCAAGTTCGACTAGGACTTCTTCTTCCTGCTCTTGCCGCTATTC
155 160 165 170 175 180
Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys
IL-18
1
AGCCTGTACGAAGGTCATTTCCTGGCTTGCCAGAAAGAAGACGACGCGTTCAAGCTGATCCTGAAGAAGAAGGACGAGAACGGCGATAAG
AGCCTGTACGAAGGTCATTTCCTGGCTTGCCAGAAAGAAGACGACGCGTTCAAGCTGATCCTGAAGAAGAAGGACGAGAACGGCGATAAG
1260 1270 1280 1290 1300 1310 1320 1330 1340
HindIII
AGCGTGATGTTTACCCTGACCAACCTGCATCAGAGCTAATGAAagcttGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCT
TCGCACTACAAATGGGACTGGTTGGACGTAGTCTCGATTACTTtcgaaCTAGGCCGACGATTGTTTCGGGCTTTCCTTCGACTCAACCGA
185 190
Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
IL-18
GGCCGACGATTGTTTCGG
Primer 2
1
AGCGTGATGTTTACCCTGACCAACCTGCATCAGAGCTAATGAAagcttGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCT
AGCGTGATGTTTACCCTGACCAACCTGCATCAGAGCTAATGAAAGCTTGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCT


1350 1360 1370 1380 1390 1400 1410 1420 1430
BlpI
EcoO109I
GCTGCCACC GCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAACTATAT
CGACGGTGG CGACTCGTTATTGATCGTATTGGGGAACCCCGGAGATTTGCCCAGAACTCCCCAAAAAACGACTTTCCTCCTTGATATA
T7 terminator
GCTGCCACC GCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAACTATAT
1
GCTGCCACCCCGCTG
1440 1450 1460 1470 1480 1490 1500 1510 1520
BsmFI
CCGGATCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGGACGCGCCCTGTAG
GGCCTAGACCGCATTATCGCTTCTCCGGGCGTGGCTAGCGGGAAGGGTTGTCAACGCGTCGGACTTACCGCTTACCCTGCGCGGGACATC
f1 ori
CCGGATCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGGACGCGCCCTGTAG
1530 1540 1550 1560 1570 1580 1590 1600 1610
CGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTT
GCCGCGTAATTCGCGCCGCCCACACCACCAATGCGCGTCGCACTGGCGATGTGAACGGTCGCGGGATCGCGGGCGAGGAAAGCGAAAGAA
f1 ori
CGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTT
1620 1630 1640 1650 1660 1670 1680 1690 1700
NgoMIV
NaeI
BanII
CCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCA
GGGAAGGAAAGAGCGGTGCAAGCGGCCGAAAGGGGCAGTTCGAGATTTAGCCCCGAGGGAAATCCCAAGGCTAAATCACGAAATGCCGT
f1 ori
CCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCA
1710 1720 1730 1740 1750 1760 1770 1780 1790
BsaAI
CCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTC
GGAGCTGGGGTTTTTTGAACTAATCCCACTACCAAGTGCATCACCCGGTAGCGGGACTATCTGCCAAAAAGCGGGAAACTGCAACCTCAG
f1 ori
CCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTC
1800 1810 1820 1830 1840 1850 1860 1870 1880
PsiI
CACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCC
GTGCAAGAAATTATCACCTGAGAACAAGGTTTGACCTTGTTGTGAGTTGGGATAGAGCCAGATAAGAAAACTAAATATTCCCTAAAACGG
f1 ori
CACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCC


1890 1900 1910 1920 1930 1940 1950 1960 1970
GATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTAGGTGGC
CTAAAGCCGGATAACCAATTTTTTACTCGACTAAATTGTTTTTAAATTGCGCTTAAAATTGTTTTATAATTGCGAATGTTAAATCCACCG
f1 ori
GATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTAGGTGGC
1980 1990 2000 2010 2020 2030 2040 2050 2060
ACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGA
TGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACT
AmpR promoter
ACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGA
2070 2080 2090 2100 2110 2120 2130 2140 2150
TAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTT
ATTTACGAAGTTATTATAACTTTTTCCTTCTCATACTCATAAGTTGTAAAGGCACAGCGGGAATAAGGGAAAAAACGCCGTAAAACGGAA
1 5 10 15
Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala Phe Cys Leu
AmpR promoter
signal sequence
AmpR
TAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTT
2160 2170 2180 2190 2200 2210 2220 2230 2240
CCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTC
GGACAAAAACGAGTGGGTCTTTGCGACCACTTTCATTTTCTACGACTTCTAGTCAACCCACGTGCTCACCCAATGTAGCTTGACCTAGAG
20 25 30 35 40 45
Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu
signal sequence
AmpR
CCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTC
2250 2260 2270 2280 2290 2300 2310 2320 2330
XmnI
AACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTA
TTGTCGCCATTCTAGGAACTCTCAAAAGCGGGGCTTCTTGCAAAAGGTTACTACTCGTGAAAATTTCAAGACGATACACCGCGCCATAAT
50 55 60 65 70 75
Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu
AmpR
AACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTA
2340 2350 2360 2370 2380 2390 2400 2410 2420
BsaHI
ScaI
TCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAG
AGGGCATAACTGCGGCCCGTTCTCGTTGAGCCAGCGGCGTATGTGATAAGAGTCTTACTGAACCAACTCATGAGTGGTCAGTGTCTTTTC
80 85 90 95 100 105
Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys
AmpR
TCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAG


2430 2440 2450 2460 2470 2480 2490 2500 2510
CATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACG
GTAGAATGCCTACCGTACTGTCATTCTCTTAATACGTCACGACGGTATTGGTACTCACTATTGTGACGCCGGTTGAATGAAGACTGTTGC
110 115 120 125 130 135
His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr
AmpR
CATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACG
2520 2530 2540 2550 2560 2570 2580 2590 2600
ATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAA
TAGCCTCCTGGCTTCCTCGATTGGCGAAAAAACGTGTTGTACCCCCTAGTACATTGAGCGGAACTAGCAACCCTTGGCCTCGACTTACTT
140 145 150 155 160 165
Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
AmpR
ATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAA
2610 2620 2630 2640 2650 2660 2670 2680 2690
GCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTA
CGGTATGGTTTGCTGCTCGCACTGTGGTGCTACGGACATCGTTACCGTTGTTGCAACGCGTTTGATAATTGACCGCTTGATGAATGAGAT
170 175 180 185 190 195
Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
AmpR
GCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTA
2700 2710 2720 2730 2740 2750 2760 2770 2780
NmeAIII
GCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATT
CGAAGGGCCGTTGTTAATTATCTGACCTACCTCCGCCTATTTCAACGTCCTGGTGAAGACGCGAGCCGGGAAGGCCGACCGACCAAATAA
200 205 210 215 220 225
Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile
AmpR
GCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATT
2790 2800 2810 2820 2830 2840 2850 2860 2870
BmrI
GCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATC
CGACTATTTAGACCTCGGCCACTCGCACCCAGAGCGCCATAGTAACGTCGTGACCCCGGTCTACCATTCGGGAGGGCATAGCATCAATAG
230 235 240 245 250 255
Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile
AmpR
GCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATC


2880 2890 2900 2910 2920 2930 2940 2950 2960
AhdI
TACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCA
ATGTGCTGCCCCTCAGTCCGTTGATACCTACTTGCTTTATCTGTCTAGCGACTCTATCCACGGAGTGACTAATTCGTAACCATTGACAGT
260 265 270 275 280 285
Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp *
AmpR
TACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCA
2970 2980 2990 3000 3010 3020 3030 3040 3050
GACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTC
CTGGTTCAAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAG
GACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTC
3060 3070 3080 3090 3100 3110 3120 3130 3140
ATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTT
TACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAA
ori
ATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTT
3150 3160 3170 3180 3190 3200 3210 3220 3230
CTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCG
GACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGC
ori
CTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCG
3240 3250 3260 3270 3280 3290 3300 3310 3320
AAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCA
TTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAAGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGT
ori
AAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCA
3330 3340 3350 3360 3370 3380 3390 3400 3410
CCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGA
GGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCT
ori
CCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGA
3420 3430 3440 3450 3460 3470 3480 3490 3500
BseYI PspFI
TAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGA
ATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCT
ori
TAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGA



Original Sequence: pAE_EmGFP_IL18_ativa_(cloned_-_seq_sintese).dna
1 .. 3948

7-pAE-Il-18-EmGFP-SS-468-Seq-pAE-R_A04
1263 bases / 12 Apr 2024
27 .. 1142 (9 mismatches, 12 gaps)