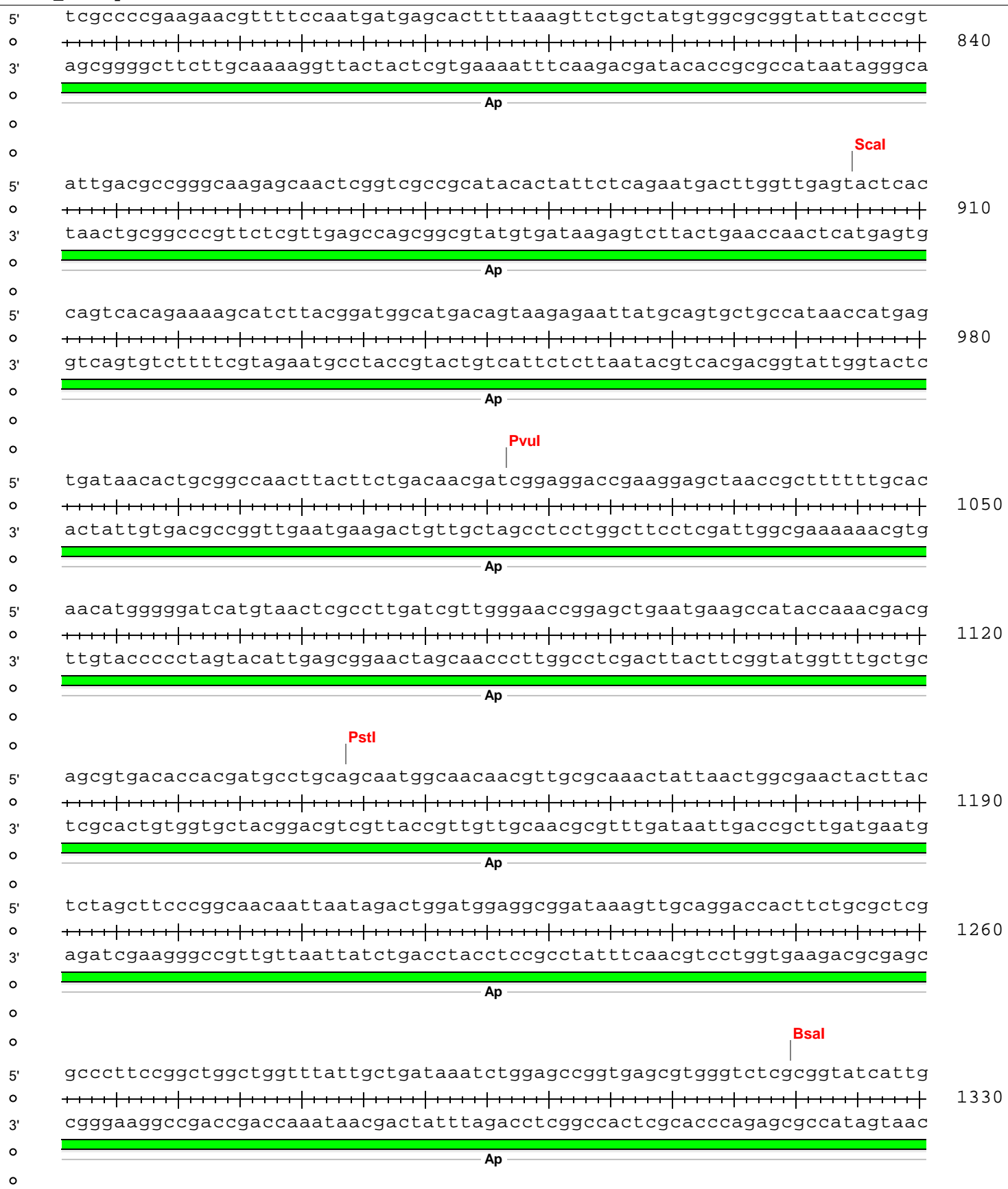


BGH02_B01a-pET32-DEST



AhdI

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o
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Ap

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o
Ori

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o
Ori

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o
Ori

o
5' gcacacagcccagcttgagcgaacgacctaaccgaaactgagatacctacagcgtgagctatgagaaag 2030
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Ori

BGH02_B01a-pET32-DEST

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0 ++++++
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0

Bpu10I

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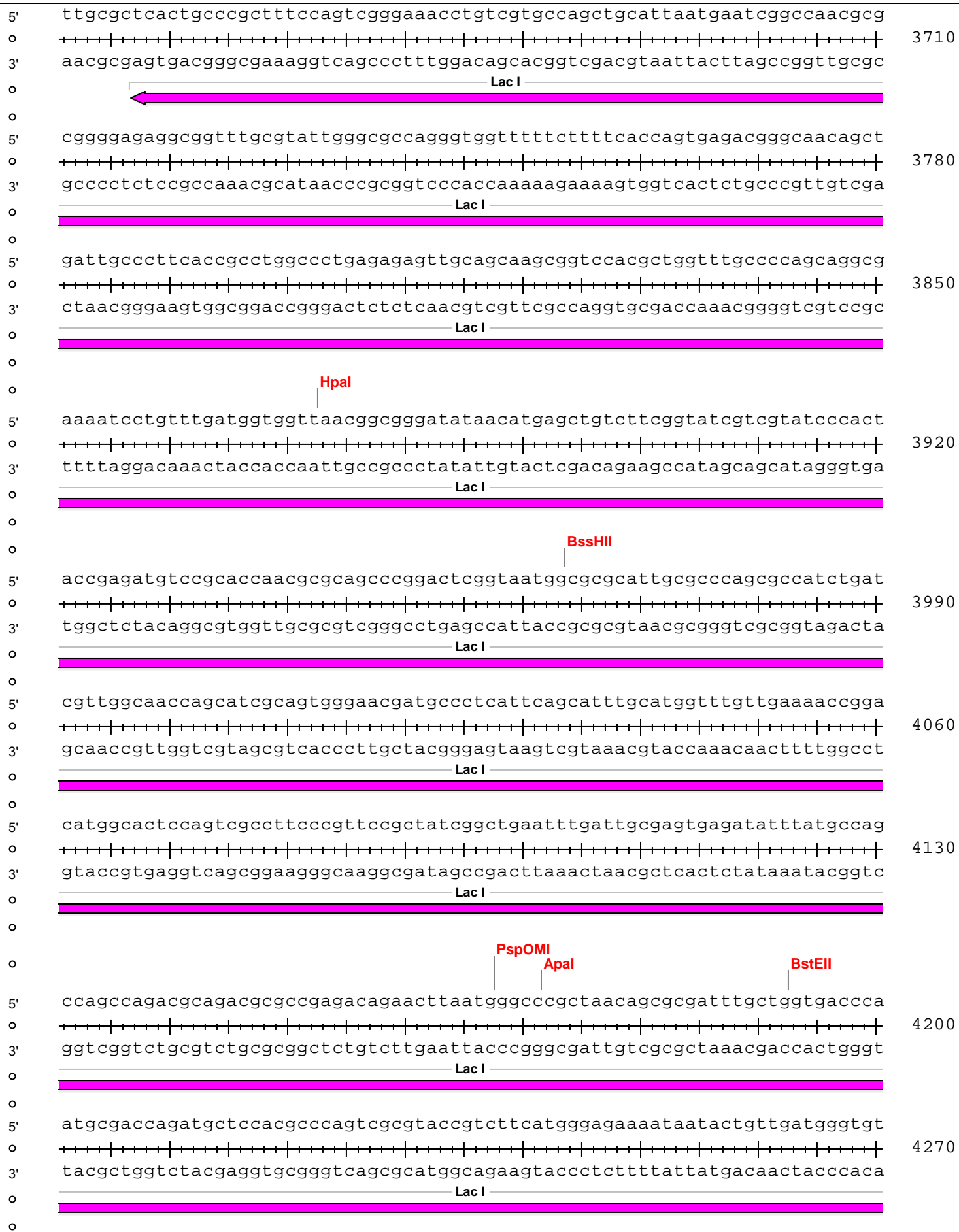
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0

PshAI

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0 ++++++
3' actatttcttctgctcagatattcacgcccgtgctatcagtacggggcggggtggccttccctcactgacc
0

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0 ++++++
3' caacttccgagagttcccgtagccagctctagggccacggattactcactcgattgaatgtaattaaacgc
0

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BGH02_B01a-pET32-DEST

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 0
 3' cacttcaccgcccgttggtttcacccacgtgacagatttccagtcaactttctcaaggagctgcgattgga
 0
 0
 0
 Trx Tag

5530

G E V A A T K V G A L S K G Q L K E F L D A N L
 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108

MscI

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 0
 3' ccggccaagaccaagaccggtatacgtggtagtagtagtaagaagaccagaccacggtgcgccaaga
 0
 0
 0
 -T...g His6-tag Thrombin

5600

A G S G S G H M H H H H H S S G L V P R G S
 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131

BstBI

BglII

Acc65I

KpnI

5' ggtatgaaagaaaccgctgctgctaaattcgaacgccagcacatggacagcccagatctgggtaccgacg
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 3' ccatactttcttggcgacgacgatttaagcttgcggtcgtgtacctgtcgggtctagacctatggctgc
 0
 0
 0
 En...e

5670

G M K E T A A A K F E R Q H M D S P D L G T D
 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154

NcoI

5' acgacgacaaggccatggcgatATCAACAAGTTTGTACAAAAAAGCAGGCTctgaaaacttgtactttca
 0
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 0
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 0
 Enterokinase attB1 TEV site

5740

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D D D K A M A I S T S L Y K K A G S E N L Y F Q
 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178

5' aggcCAAGGTAATGACACTTCGGAAGTCATGCTACTGGATACCGGTTGGGAATTTTCTCAATCAGGGACT
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 3' tccgGTTCCATTACTGTGAAGCCTTCAGTACGATGACCTATGGCCAACCCTTAAAAGAGTTAGTCCCTGA
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 0
 0
 BGH02_B01a BGH02_B01a-pDONR221

5810

G Q G N D T S E V M L L D T G W E F S Q S G T
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5' GAAAAGTGGATGCCAGCCACGGTTCCTGGTACGGTTCATCAGGACCTGATCAGTCATGAATTA

5880

... BGH02_B01a ...

... BGH02_B01a-pDONR221 ...

E K W M P A T V P G T V H Q D L I S H E L L P

5' ATCCATTTTATGGGATGAATGAAAAGAAAATTCAATGGGTGGAGAATGAGGACTGGGAATATA

5950

... BGH02_B01a ...

... BGH02_B01a-pDONR221 ...

N P F Y G M N E K K I Q W V E N E D W E Y R T S

MfeI

5' CTTTATAGTCTCCGAAGAGCAATTGAATCGTGACGGAATCCAACCTATTTTTGAAGGTC

6020

... BGH02_B01a ...

... BGH02_B01a-pDONR221 ...

F I V S E E Q L N R D G I Q L I F E G L D T Y

5' GCAGACGTATATCTCAACGGCTCATTACTGCTGAAGGCTGATAATATGTTTGTGGTTATA

6090

... BGH02_B01a ...

... BGH02_B01a-pDONR221 ...

A D V Y L N G S L L L K A D N M F V G Y T L P

5' TAAAATCTGTGTTGCGGAAGGCGAGAATCACTTATATATTTATTTCCATTCACCTATTC

6160

... BGH02_B01a ...

... BGH02_B01a-pDONR221 ...

V K S V L R K G E N H L Y I Y F H S P I R Q T L

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5' GCCACAATATGCTTCCAATGGCTTCAATTATCCGGCGGATAACGATCATCACGAGAAACATCTTAGTG
 0 ++++++
 3' CGGTGTTATACGAAGGTTACCGAAGTTAATAGGCCGCCTATTGCTAGTAGTGCTCTTTGTAGAATCACAC

6230

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P Q Y A S N G F N Y P A D N D H H E K H L S V
 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341

5' TTCAGCCGTAAGGCTCCGTATAGTTACGGTTGGGACTGGGGCATCCGAATGGTGACAAGTGGTGTCTGGC
 0 ++++++
 3' AAGTCGGCATTCCGAGGCATATCAATGCCAACCTGACCCCGTAGGCTTACCACTGTTCCACCACAGACCG

6300

BGH02_B01a

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F S R K A P Y S Y G W D W G I R M V T S G V W
 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364

5' GCCCCGTTACTCTTCGTTTTTACGACATAGCTACCATATCCGACTACTATGTCAGACAATTATCGCTGAC
 0 ++++++
 3' CGGGCCAATGAGAAGCAAAAATGCTGTATCGATGGTATAGGCTGATGATACAGTCTGTTAATAGCGACTG

6370

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R P V T L R F Y D I A T I S D Y Y V R Q L S L T
 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388

5' AGATGAAAACGCTCGTCTGTCTAATGAGCTGATTGTAACCAGATCGTTCCTCAGAAAATTCCGGCTGAA
 0 ++++++
 3' TCTACTTTTGGCAGCAGACAGATTACTCGACTAACATTTGGTCTAGCAAGGAGTCTTTTAAGCCGACTT

6440

BGH02_B01a

BGH02_B01a-pDONR221

D E N A R L S N E L I V N Q I V P Q K I P A E
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5' GTAAGGGTCAATGTATCGTTGAATGGAACCTACCGTTACAGAAGTAAAACAGCAGGTGACACTGCAACCCG
 0 ++++++
 3' CATTCCAGTTACATAGCAACTTACCTTGATGGCAATGTCTTCATTTTGTCTCCACTGTGACGTTGGGC

6510

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V R V N V S L N G T T V T E V K Q Q V T L Q P
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Psrl

BspMI
AarI

Psrl'

XmaI
SmaI

BGH02_B01a-pET32-DEST

5' GGATAAATCATATCACTCTTCTGCTGAAGTGACGAACCCTGTACGATGGATGCCAAATGGTTGGGGAAC
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 3' CCTATTTAGTATAGTGAGAAGGACGACTTCACTGCTTGGGACATGCTACCTACGGTTTACCAACCCCTTG

6580

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G I N H I T L P A E V T N P V R W M P N G W G T
 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458

5' TCCGACTCTGTATGATTTCTCGGCTCAGATAGCTTGTGGAGATCGGATTGTTGCGGAACAATCTCATCGG
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 3' AGGCTGAGACATACTAAAGAGCCGAGTCTATCGAACACCTCTAGCCTAACCAACGCCTTGTAGAGTAGCC

6650

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P T L Y D F S A Q I A C G D R I V A E Q S H R
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5' ATTGGTTTACGAACGATTCGTGTGGTAAATGAAAAAGATAAGGACGGAGAATCTTTTTATTTTGAAGTCA
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 3' TAACCAAATGCTTGCTAAGCACACCATTACTTTTTCTATTCTGCCTCTTAGAAAAATAAACTTCAGT

6720

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I G L R T I R V V N E K D K D G E S F Y F E V
 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504

Bsu36I

5' ATGGCATAACCGATGTTTGCCAAAGGAGCTAATTATATTCCTCAGGATGCACTGCTGCCTAATGTTACTAC
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 3' TACCGTATGGCTACAAACGGTTTCTCGATTAATATAAGGAGTCCTACGTGACGACGGATTACAATGATG

6790

BGH02_B01a

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N G I P M F A K G A N Y I P Q D A L L P N V T T
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5' GGAACGCTATCAGACTTTGTTCCGTGACATGAAGGAGGCCAATATGAATATGGTTCGTATATGGGGTGGT
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 3' CCTTGCGATAGTCTGAAACAAGGCACTGTACTTCTCCGTTTACTTATAACCAAGCATATACCCACCA

6860

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5' GGGACATATGAGAATAATCTTTTCTATGACCTTGCCGATGAGAACGGGATACTTGTCTGGCAGGATTTTA
 0 ++++++
 3' CCCTGTATACTCTTATTAGAAAAGATACTGGAACGGCTACTCTTGCCCTATGAACAGACCGTCCTAAAAT

6930

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5' TGTTTGCCTGTACCCCTTATCCATCCGATCCTACTTTCCTGAAACGGGTAGAGGCGGAGGCTGTTTACAA
 0 ++++++
 3' ACAAACGCACATGGGGAATAGGTAGGCTAGGATGAAAGGACTTTGCCCATCTCCGCCTCCGACAAATGTT

7000

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M F A C T P Y P S D P T F L K R V E A E A V Y N
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5' TATTCGTCTGCTTCGGAATCATGCCTCTTTGGCGATGTGGTGTGGTAATAATGAAATACTGGAAGCTCTG
 0 ++++++
 3' ATAAGCAGCAGAAGCCTTAGTACGGAGAAACCGCTACACCACACCATTATTACTTTATGACCTTCGAGAC

7070

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I R R L R N H A S L A M W C G N N E I L E A L
 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621

Nsil

5' AAATATTGGGGTTTTGAGAAGAAGTTTACTCCGGAGGTTTATCAAGGATTAATGCATGGTTATGATAAAC
 0 ++++++
 3' TTTATAACCCCAAAACTCTTCTTCAAATGAGGCCTCCAAATAGTTCCTAATTACGTACCAATACTATTTG

7140

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K Y W G F E K K F T P E V Y Q G L M H G Y D K
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5' TGTTCCGTGAGCTGTTGCCTTCAACGGTTAAAGAATTTGATTCCGATCGTTTTTATGTGCACAGTTCCGC
 0 ++++++
 3' ACAAGGCACTCGACAACGGAAGTTGCCAATTTCTTAAACTAAGCCTAGCAAAAATACACGTGTCAAGCGG

7210

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L F R E L L P S T V K E F D S D R F Y V H S S P
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BGH02_B01a-pET32-DEST

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7280

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7350

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5' TTCCGGAGATGAAAACCTATTGCTGCTTTTGCTGCTCCTGAAGATTATCAGATTGAGTCTGAAGTGATGAA
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 3' AAGGCCTCTACTTTTGATAACGACGAAAACGACGAGGACTTCTAATAGTCTAACTCAGACTTCACTACTT

7420

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F P E M K T I A A F A A P E D Y Q I E S E V M N
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BsmI

5' TGCGCATCAGAAGAGTAGTATTGGTAATTCGTTGATCCGTACTIONTATATGGAACGTGATTATATCATTCCC
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 3' ACGCGTAGTCTTCTCATCATAACCATTAAGCAACTAGGCATGAATATACCTTGCACTAATATAGTAAGGG

7490

BGH02_B01a

BGH02_B01a-pDONR221

A H Q K S S I G N S L I R T Y M E R D Y I I P
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5' GAAAGTTTCGAGGATTTTGTTGATGTCGGATTAGTCTTGCAAGGACAGGGGATGCGGCATGGACTGGAAG
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 3' CTTTCAAAGCTCCTAAAACACATACAGCCTAATCAGAACGTTTCTGTCCCCTACGCCGTACCTGACCTTC

7560

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E S F E D F V Y V G L V L Q G Q G M R H G L E
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BGH02_B01a-pET32-DEST

5' CTCACAGACGCAATCGTCCTTATTGTATGGGGACATTGTATTGGCAGTTGAACGACAGTTGGCCGGTAGT
 ++++++
 3' GAGTGTCTGCGTTAGCAGGAATAACATAACCCCTGTAACATAACCGTCAACTTGCTGTCAACCGGCCATCA

7630

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BGH02_B01a-pDONR221

A H R R N R P Y C M G T L Y W Q L N D S W P V V
 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808

5' ATCCTGGTCAAGTATTGATTATTATGGTAATTGGAAGGCATTACATTATCAGGCAAAGCGTGCTTTTGCA
 ++++++
 3' TAGGACCAGTTTCATAACTAATAATACCATTAACCTTCCGTAATGTAATAGTCCGTTTCGCACGAAAACGT

7700

BGH02_B01a

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S W S S I D Y Y G N W K A L H Y Q A K R A F A
 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831

5' CCGGTCTTGATCAATCCTATACAGCAGAAATGACAGTTTGAGTGTCTATCTGATCTCAGACCGGCTTGATA
 ++++++
 3' GGCCAGAACTAGTTAGGATATGTCGTCTTACTGTCAAACCTCACAGATAGACTAGAGTCTGGCCGAACTAT

7770

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P V L I N P I Q Q N D S L S V Y L I S D R L D
 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854

5' CAATGGAGCAAATGACATTGGAAATGAAAAGTCGTGGATTTTGATGGAAAAACGCTGGGTAAGAAGATACA
 ++++++
 3' GTTACCTCGTTTACTGTAACCTTTACTTTCAGCACCTAAAACCTTTTTGCGACCCATTCTTCTATGT

7840

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T M E Q M T L E M K V V D F D G K T L G K K I Q
 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878

5' AGTACATTCGTTGGAAGTTCCGGCAAATACTTCAAAATGTGTTTATCGTGCAAAACTGGATGGCTGGCTG
 ++++++
 3' TCATGTAAGCAACCTTCAAGCCGTTTATGAAGTTTTACACAAATAGCACGTTTGTGACCTACCGACCGAC

7910

BGH02_B01a

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V H S L E V P A N T S K C V Y R A K L D G W L
 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901

BGH02_B01a-pET32-DEST

5' ACTCCCGAAGACTGCCGACGTAGCTTCTTGAAATTGATACTCAAAGATAAATCGGGACATCAGGTGGCTG
 3' TGAGGGCTTCTGACGGCTGCATCGAAGAACTTTAACTATGAGTTTCTATTTAGCCCTGTAGTCCACCGAC

7980

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T P E D C R R S F L K L I L K D K S G H Q V A
 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924

Bael

5' AGAGCGTCCATTTTTTCAGAAAGACGAAAGATTTGCAACTTCTCCGACATCAGTATCCTATCAAATGAA
 3' TCTCGCAGGTAAAAAAGTCTTTCTGCTTCTAAACGTTGAAGGAGGCTGTAGTCATAGGATAGTTTACTT

8050

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E S V H F F R K T K D L Q L P P T S V S Y Q M K
 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948

Bael'

5' GCAGACGGATGGTAAATGTGAATTGACTCTCTTTTCATCAATGTTGGCAAAGATATTTTTATTGAGACT
 3' CGTCTGCCTACCATTTACTTAACTGAGAGAAAAGTAGTTACAACCGTTTTCTATAAAAATAACTCTGA

8120

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Q T D G K C E L T L F S S M L A K D I F I E T
 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971

5' CCATTGCAAGGAGCCCGTTACAGTGACAACCTTCTTTGATCTCTTACCCGGAGAACGTAAGAAAGTAATTA
 3' GGTAACGTTCTCGGGCAATGTCACTGTTGAAGAACTAGAGAATGGGCCTCTTGCATTCTTTCATTAAT

8190

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P L Q G A R Y S D N F F D L L P G E R K K V I
 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994

5' TCACTTCTCCCCGATAAAGAAGGGAGAAGAATTACCTGTCAATATCAAGCATATTCGAGAAACCTATAA
 3' AGTGAAGAGGGCCTATTTCTTCCCTCTTCTTAATGGACAGTTATAGTTTCGTATAAGCTCTTTGGATATT

8260

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I T S P R I K K G E E L P V N I K H I R E T Y K
 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018

0
5' ATAGGACCCAGCTTTCTTGACAAAGTGGTTGATatcggatccgaattcgagctccgtcgacaagcttgc 8330
0
3' TATCCTGGGTTCGAAAGAACATGTTTCACCAACTAtagcctaggcttaagctcgaggcagctgttcgaacg

BamHI EcoRI EcoICRI SacI Sall HindIII



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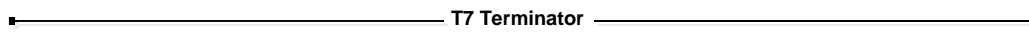


NotI EagI PspXI XhoI

5' ggccgcactcgagcaccaccaccaccactgagatccggctgctaacaaagcccgaaaggaagctgag 8400
0
3' ccggcgtgagctcgtggtggtggtggtgactctaggccgacgattgtttcgggctttccttcgactc

BipI

5' ttggctgctgccaccgctgagcaataactagcataacccttggggcctctaaacgggtcttgaggggtt 8470
0
3' aaccgacgacggtggcgactcgttattgatcgtattggggaaccccgagatttgcccagaactcccaa



5' ttttgctgaaaggaggaactatatccggat 8500
0
3' aaaacgactttcctccttgatataggccta

— T... —