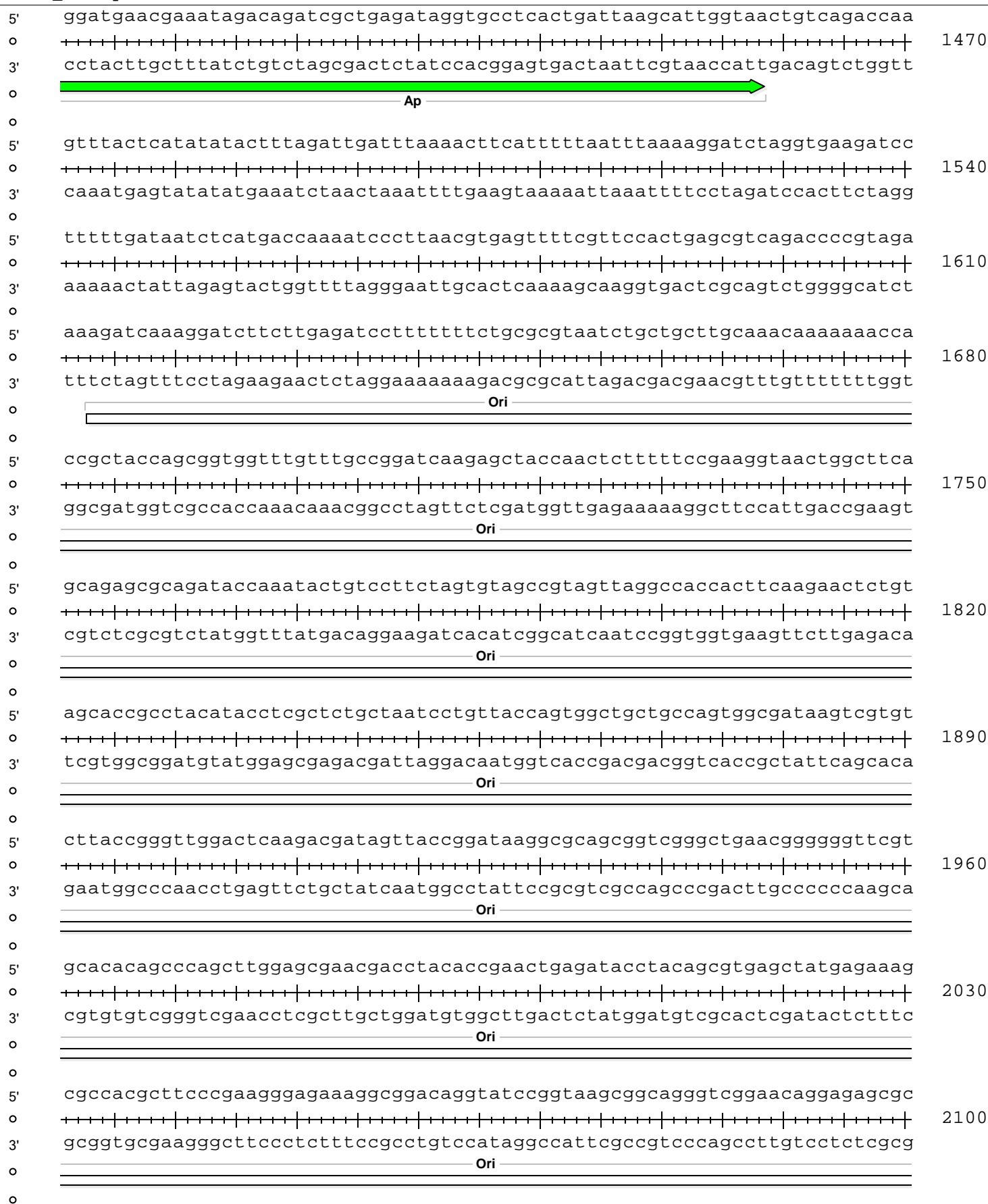


BGT66_T01a-pET32-DEST



BGT66_T01a-pET32-DEST

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 Ori

PciI

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SapI

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BstZ171

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Tth111I

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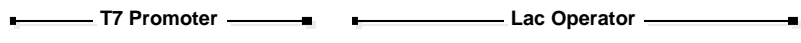
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5110
5180



o
 o
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 o
 3' caaattgaaattcttcctctatatgtatactcgcctattttaataagtgaggactgactgctgtcaaaactgt

5250



M S D K I I H L T D D S F D
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o
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 o
 3' gcctacatgagtttcgctgccccgctaggagcagctaaagaccctctcaccacgccaggcaggtttta

5320



T D V L K A D G A I L V D F W A E W C G P C K M
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o
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 o
 3' ctagcggggctaagacctactttagcgcactgcttatagtcccgtttgactggcaacgttttgacttgtag

5390



I A P I L D E I A D E Y Q G K L T V A K L N I
 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61

o
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 o
 3' ctagttttgggaccgtgacgcggctttataccgtaggcaccatagggctgagacgacgacaagtttttgc

5460



D Q N P G T A P K Y G I R G I P T L L L F K N
 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84

o
 5' gtgaagtggcggcaaccaaagtgggtgcactgtctaaaggtcagttgaaagagttcctcgacgctaacct
 o
 3' cacttcaccgccggtggtttcaccacgtgacagatttccagtcactttctcaaggagctgcgattgga

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
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BGT66_T01a-pET32-DEST

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 3' cccggccaagaccaagaccggtatacgtggtagtagtagtaagaagaccagaccacggtgccaaga

MscI

His6-tag Thrombin

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

5600

5' ggtatgaaagaaaccgctgctgctaaattcgaacgccagcacatggacagcccagatctgggtaccgacg
 3' ccatactttcttggcgacgacgatttaagcttgcggctcgtgtacctgctcgggtctagaccatggctgc

BstBI BglII Acc65I KpnI

En...e

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

5670

5' acgacgacaaggccatggcgatATCAACAAGTTTGTACAAAAAAGCAGGCTctgaaaacttgtactttca
 3' tgctgctgttccggtaccgctaTAGTTGTTCAAACATGTTTTTTCGTCCGAgacttttgaacatgaaagt

NcoI

Enterokinase attB1 TEV site

BGT66_T01a-pDONR221

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

5740

5' aggcTATAAAGCACCAACAGTTTTTCTCAAATGAAGCATCATTATTAATCAATTAATAAATATAGCC
 3' tccgATATTTTCGTGGTTGTCAAAAAGAGTTTTACTTCGTAGTAATAATTTAGTTAATTTTTATATCGG

AjuI' AjuI

T... →

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BGT66_T01a-pDONR221

5810

G Y K A P T V F S Q N E A S L L N Q L K N I A
 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201

5' AATAGAGAAGATTATGTGGTAACTTGGTGGGATTATGGTTATCCTGTGCGTTATTATAGTGATGTGAAAA
 3' TTATCTCTTCTAATACACCATTGAACCACCCTAATACCAATAGGACACGCAATAATATCACTACACTTTT

BGT66_T01a

BGT66_T01a-pDONR221

N R E D Y V V T W W D Y G Y P V R Y Y S D V K
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5880

BGT66_T01a-pET32-DEST

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5' CTTTAGTAGATGGTGGAAAGCATTAGGTAAGGATAATTTTTCCCTTCTTTTGCTTTAAGCAAAGATGA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' GAAATCATCTACCACCTTTCGTAAATCCATTCCTATTAATAAGGGAAGAAAACGAAATTCGTTTCTACT

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5950

BGT66_T01a

BGT66_T01a-pDONR221

T L V D G G K H L G K D N F F P S F A L S K D E
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5' ACAAGCTGCAGCTAATATGGCAAGACTTAGTGTAGAATATACAGAAAAAGCTTTTATGCTCCGCAAAAT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' TGTTTCGACGTCGATTATACCGTTCTGAATCACATCTTATATGTCTTTTTTCGAAAATACGAGGCGTTTTA

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6020

BGT66_T01a

BGT66_T01a-pDONR221

Q A A A N M A R L S V E Y T E K S F Y A P Q N
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5' GATATTTTAAAAACAGACATTTTACAAGCCATGATGAAAGATTATAATCAAAGCAATGTGGATTTGTTTC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' CTATAAAATTTTGTCTGTAATAATGTTTCGGTACTACTTTCTAATATTAGTTTTCGTTACACCTAAACAAAG

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6090

BGT66_T01a

BGT66_T01a-pDONR221

D I L K T D I L Q A M M K D Y N Q S N V D L F
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```

5' TAGCTTCATTATCAAAACCTGATTTTAAAATCGATACACCAAAAACCTCGTGATTTTATCTTTATATGCC
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3' ATCGAAGTAATAGTTTTGGACTAAAATTTAGCTATGTGGTTTTTGAGCACTATAAATAGAAATATACGG

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6160

BGT66_T01a

BGT66_T01a-pDONR221

L A S L S K P D F K I D T P K T R D I Y L Y M P
 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318

Bael'

```

5' CGCTAGAATGTCTTTGATTTTTTCTACGGTGGCTAGTTTTTCTTTTATTAATTTAGATACAGGATTTTG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' GCGATCTTACAGAAACTAAAAAAGATGCCACCGATCAAAAAGAAAATAATTAATCTATGTCCTCAAAAC

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6230

BGT66_T01a

BGT66_T01a-pDONR221

A R M S L I F S T V A S F S F I N L D T G V L
 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341

BGT66_T01a-pET32-DEST

Bael

5' GATAAACCTTTTACCTTTAGCACAGCTTATCCACTTGATGTTAAAAATGGAGAAATTTATCTTAGCAACG
 3' CTATTTGGAAAATGGAAATCGTGTCTGAATAGGTGAACTACAATTTTACCTCTTTAAATAGAATCGTTGC

6300

BGT66_T01a

BGT66_T01a-pDONR221

D K P F T F S T A Y P L D V K N G E I Y L S N
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5' GAGTGGTTTTAAGCGATGATTTTAGAAGTTTTAAAATAGGTGATAATGTGGTTTCTGTAAATAGTATCGT
 3' CTCACCAAATTCGCTACTAAAATCTTCAAATTTTATCCACTATTACACCAAAGACATTTATCATAGCA

6370

BGT66_T01a

BGT66_T01a-pDONR221

G V V L S D D F R S F K I G D N V V S V N S I V
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MfeI

5' AGAGATTAATTCTATTAACAAGGTGAATACAAAATCACTCCAATTGATGATAAGGCTCAGTTTTATATT
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6440

BGT66_T01a

BGT66_T01a-pDONR221

E I N S I K Q G E Y K I T P I D D K A Q F Y I
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5' TTTTATTTAAAGGATAGTGCTATTCCTTACGCACAATTTATTTAATGGATAAAACCATGTTTAAATAGTG
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6510

BGT66_T01a

BGT66_T01a-pDONR221

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6580

BGT66_T01a

BGT66_T01a-pDONR221

A Y V Q M F F L G N Y D K N L F D L V I N S R D
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