





HindIII (1082)

5' cggtgaaaagaaatctgttgcttcttgcacatggtactttggaagcttgcttgctattttctgtgtagaactggcttggtggc 1120
3' gccacttttcttttagacaacgaagaacgtaccatgaaaccttcgaacgaacagtaaaagacacatcttgaccgaacaccg



synthesis 222.222.122-ECL2

T V K R N L L L L A W Y F G S L L V I F C V E L A C G
96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122
T V K R N L L L L A W Y F G S L L V I F C V E L A C G
85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111

5' gtttgggcccatgtgtattaccagaggctgagtgatgaactgaagcagcacttgaaccggactctggctgagaactacgg 1200
3' caaaccgggtacacataatggtctccgactcactacttgacttcgctggaacttggcctgagaccgactcttgatgcc



synthesis 222.222.122-ECL2

V W A H V Y Y Q R L S D E L K Q H L N R T L A E N Y G
123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149
V W A H V Y Y Q R L S D E L K Q H L N R T L A E N Y G
112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138

TstI' (1242)

TstI (1274)

BlpI (1277)

5' gcagcccgagccacgcagatcaccgcctcagtgaccgactccagcaggatttcaagtgctgtggaagcaacagctcag 1280
3' cgtcgggcctcgggtgctgtagtgccgagtcacctggctgaggtcgctcctaaagtacacaccttcggtgctgagtc



synthesis 222.222.122-ECL2

Q P G A T Q I T A S V D R L Q Q D F K C C G S N S S
150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175
Q P G A T Q I T A S V D R L Q Q D F K C C G S N S S
139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164

5' ccgactggcagcacagcagcgtacatcctgttgccggaggccgagggccgccaggtgcccgacagctgctgcaagacagtg 1360
3' ggctgaccgctgctgctgcatgtaggacaacgccctccggctcccgcggtccacgggctgctcgacgacgcttctgtcac



synthesis 222.222.122-ECL2

A D W Q H S T Y I L L R E A E G R Q V P D S C C K T V
176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202
A D W Q H S T Y I L L R E A E G R Q V P D S C C K T V
165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191

5' gtggtgcgctgcgccagcgggccaccctccaacatctataaggtggaggaggctgcctcaccaagctggagcagtt 1440
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' caccacgcgacgccggtcgcccgggtggggaggttgtagatattccacctccctccgacggagtggttcgacctcgtcaa
TSP11 extracellular loop 2
synthesis 222.222.122-ECL2
V V R C G Q R A H P S N I Y K V E G G C L T K L E Q F
203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229
V V R C G Q R A H P S N I Y K V E G G C L T K L E Q F
192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218

SbfI (1459) BbvCI (1464) BstEII (1490) PflMI (1502)
5' cctggccgaccacctgcaggtgctgaggtttctgggaatctccattggggtgacccaaatcctggccatgattctcacca 1520
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' ggaccggctggtggacgtccacgactccaaagacccttagaggttaacccactgggttaggacccggtactaagagtggt
TSP11 extr...lar loop 2 **TM 4**
synthesis 222.222.122-ECL2
L A D H L Q V L R F L G I S I G V T Q I L A M I L T
230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255
L A D H L Q V L R F L G I S I G V T Q I L A M I L T
219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244

5' ttactctgctctgggccctgtattatgatagaagggagccggggacagaccaaatgatgtccttgaagaatgacaactct 1600
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' aatgagacgagacccgggacataaatactatcttccctcggccctgtctggttactacaggaacttcttactgttgaga
TM 4 **intracellular C-terminus**
I T L L W A L Y Y D R R E P G T D Q M M S L K N D N S
256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282
I T L L W A L Y Y D R R E P G T D Q M M S L K N D N S
245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271

5' cagcacctgtcatgtccctcagtagaactgttgaaccaagcctgtcaagaatcttgaacacacatccatggcaaacag 1680
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' gtcgtggacagtagcagggagtcaccttgacaacttgggtcggacagttcttagaaacttgtgtgtaggtaccggttgtc
intracellular C-terminus
Q H L S C P S V E L L K P S L S R I F E H T S M A N S
283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309
Q H L S C P S V E L L K P S L S R I F E H T S M A N S
272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298



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5' ATCTCGGTCTATTCTTTTGTATTATAAGGGATTTTGGGGATTTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAA 2480
o +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' TAGAGCCAGATAAGAAAATAAATATTCCTAAAACCCCTAAAGCCGATAACCAATTTTTTACTCGACTAAATTGTTTT

5' ATTTAACGCGAATTAATTCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTAT 2560
o +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' TAAATTGCGCTTAATTAAGACACCTTACACACAGTCAATCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATA

SexAI (2590)
|
5' GCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCA 2640
o +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' CGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTCGT

5' TGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCAT 2720
o +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' ACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTA

5' TCTCCGCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCCTCTGCCTCTGAGCTATTCCAGAAGTA 2800
o +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' AGAGGCGGGGTACCGACTGATTAATAAATAAATACGTCTCCGGCTCCGGCGGAGACGGAGACTCGATAAGGTCTTCAT

StuI (2822) XmaI (2844) BclI (2874)
| | |
AvrII (2823) SmaI (2846)
| | |
5' GTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCAAG 2880
o +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' CACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTTTCGAGGGCCCTCGAACATATAGGTAAAAGCCTAGACTAGTTC

BsaBI (2892) EagI (2939)
| |
5' AGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTCTCCGGCCGCTTGGGTGGAGAGGCTA 2960
o +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' TCTGTCTACTCCTAGCAAAGCGTACTAACTTGTTCCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGAT

KasI (3032)
|
NarI (3033)
|
SfoI (3034)
|
PluTI (3036)
|
5' TTCGGCTATGACTGGGCACAACAGACAATCGGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTGAGCGCAGGGGCGCCCGGT 3040
o +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' AAGCCGATACTGACCCGTGTTGCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCA

5' TCTTTTGTCAAGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGA 3120
o +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' AGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTCTGCTCCGTGCGCGCCGATAGCACCGACCGGTGCT

Tth111I (3151)
|
5' CGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCAGTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG 3200
o +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' GCCCCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCC

5' CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCT 3280
o +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' GTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGA
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5' TGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTA
CTCGGATGGAAGCCGGTCTTG
3360
3' ACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAAC
5' TCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGA
ACTGTTCCGCCAGGCTCAAGGCGCGCATGCCC
3440
3' AGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTTCGGCTTGACAAGCGGTCCGAGTTCGCGCGTACGGG
5' GACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATT
3520
3' CTGCCGCTCCTAGAGCAGCACTGGGTACCCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAA

RsrII (3549)

5' CATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTG
3600
3' GTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCTGTATCGCAACCGATGGGCATAACGACTTCTCGAAC
5' GCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTT
3680
3' CGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAA
5' CTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATT
3760
3' GAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCGCTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGTCTAA

PfoI (3810)

5' TCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGC
3840
3' AGCTAAGGTGGCGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGG
5' GGGGATCTCATGCTGGAGTTCTTCGCCCACCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCAT
3920
3' CCCCTAGAGTACGACCTCAAGAAGCGGGTGGGGTTGAACAAATAACGTCAATATTACCAATGTTTATTTTCGTTATCGTA

BsmI (3955)

5' CACAAATTTACAAAATAAAGCATTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAACTCATCAATGTATCTTATCATG
4000
3' GTGTTTAAAGTGTTTATTTTCGTAATAAAGTGAACGTAAGATCAACACCAAACAGGTTTGTAGTAGTTACATAGAATAGTAC

BstZ17I (4007)

5' TCTGTATACCGTCGACCTCTAGCTAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTC
4080
3' AGACATATGGCAGCTGGAGATCGATCTCGAACCGCATTAGTACCAGTATCGACAAAGGACACACTTTAACAATAGGCGAG
5' ACAATTCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAAT
4160
3' TGTTAAGGTGTGTTGTATGCTCGGCCCTTCGTATTTACATTTTCGACCCACGGATTACTCACTCGATTGAGTGTAATTA
5' TCGGTTGCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGA
4240
3' ACGCAACGCGAGTGACGGGCGAAAGGTCAGCCCTTTGGACAGCACGGTCGACGTAATTACTTAGCCGGTTGCGCGCCCCT
5' GAGGCGGTTTTCGTATTGGGCGCTTTCGCTTCCGCTTCCGCTCACTGACTCGCTGCGCTCGGTCGTTTCGGCTGCGGCGAGCG
4320
3' CTCGGCCAAACGCATAACCCGCGAGAAGGCGAAGGAGCGAGTGACTGAGCGACGCGAGCCAGCAAGCCGACGCCGCTCGC

Pcil (4386)

o
5' GTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAGG 4400
o
3' CATAGTCGAGTGAGTTTCGCCATTATGCCAATAGGTGTCTTAGTCCCTATTGCGTCCTTTCTTGTACACTCGTTTTTC
o
5' CCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACA 4480
o
3' GGTCGTTTTTCGGTCTTGGCATTTTTCCGGCGCAACGACCGCAAAAAGGTATCCGAGGCGGGGGACTGCTCGTAGTGT
o
5' AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCTC 4560
o
3' TTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAG
o
5' GTGCGCTCTCCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA 4640
o
3' CACGCGAGAGGACAAGGCTGGGACGGCGAATGGCTATGGACAGGCGAAAGAGGGAAGCCCTTCGCACCGCGAAAGAGT
o
5' ATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGC 4720
o
3' TACGAGTGCAGCATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTGACCCGACACACGTGCTTGGGGGGCAAGTCG
o
5' CCGACCGCTGCGCCTTATCCGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC 4800
o
3' GGCTGGCGACGCGGAATAGCCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCTCGG
o
5' ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACAC 4880
o
3' TGACCATTGTCCATAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACCACCGGATTGATGCCGATGTG
o
5' TAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCA 4960
o
3' ATCTTCCTGTCAAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGT
o
5' AACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGAT 5040
o
3' TTGTTTGGTGGCGACCATCGCCACCAAAAAACAACGTTTCGTCTAATGCGCGTCTTTTTTTCCTAGAGTCTTTCTA
o
5' CCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAA 5120
o
3' GGAAACTAGAAAAGATGCCCCAGACTGCGAGTACCTTGCTTTTGAGTGAATTCCTAAAACCGTACTCTAATAGTTT
o
5' AAGGATCTTACCTAGATCCTTTAAATTA AAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTG 5200
o
3' TTCTTAGAAGTGATCTAGGAAAATTTAATTTTTACTTCAAATTTAGTTAGATTTTATATATACTCATTTGAACCAGAC
o

Ahdl (5279)

o
5' ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCC 5280
o
3' TGTC AATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGG
o
5' GTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC 5360
o
3' CAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGG
o
5' GGCTCCAGATTTATCAGCAATAAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCCTCCA 5440
o
3' CCGAGGTCTAAATAGTCGTTATTTGGTCCGTCGGCCTTCCGGCTCGCGTCTTACCAGGACGTTGAAATAGGCGGAGGT
o


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5'   TCCAGTCTATTAATTGTTGCCGGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCACAACGTTGTTGCCATTGCT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3'   AGGTCAGATAATTAACAACGGCCCTTCGATCTCATTCATCAAGCGGTCAAT'TATCAAACGCGT'TGCAACAACGGTAACGA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
5'   ACAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGT'TCCAACGATCAAGGCGAGTTACATG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3'   TGTCCGTAGCACCACAGTGCAGCAGCAAACCATAACCGAAGTAAGTCGAGGCCAAGGGT'TGCTAGTTCGGCTCAATGTAC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

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PvuI (5649)

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5'   ATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCCTCCGATCGTTTGTGAGAAGTAAGTTGGCCGCAGTGTTAT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3'   TAGGGGTACAACACGTTTTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACCGCGTCACAATA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

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SalI (5759)

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5'   CACTCATGGTTATGGCAGCACTGCATAAATTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTAC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3'   GTGAGTACCAATACCGTCGTGACGTATTAAGAGAATGACAGTACGGTAGGCAT'TCTACGAAAAGACACTGACCACTCATG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

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Bcgl (5784)

Bcgl' (5818)

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5'   TCAACCAAGTCATTCTGAGAATAGTGTATGCGGGGACCGAGTTGCTCTTGCCCCGGCGTCAATACGGGATAATACCGCGCC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3'   AGTTGGTTCAGTAAGACTCTTATCACATACGCCGCTGGCTCAACGAGAACGGGCGCAGTTATGCCCTATTATGGCGCGG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

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5'   ACATAGCAGAACTTTAAAAAGTGTCTCATCATTTGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3'   TGTATCGTCTTGAAATTTTACGAGTAGTAACCTTTTGAAGAAGCCCCGCTTTTGAGAGTTCCTAGAATGGCGACAAC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

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5'   GATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3'   CTAGGTCAAGCTACATTGGGTGAGCAGTGGGTGACTAGAAGTCGTAGAAAATGAAAGTGGTCGAAAGACCCACTCGT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

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5'   AAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCTTTTTTCA
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3'   TTTTGTCTTCCGTTTACGGCGTTTTTCCCTTATTCCTCGTGTGCCTTTACAACCTTATGAGTATGAGAAGGAAAAAGT
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

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Sspl (6083)

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5'   ATATTATTGAAGCATTATATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3'   TATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAACTTACATAAATCTTTTTATTTGTTTATC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

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SgrDI (6200)

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5'   GGGTTCGCGCACATTTCCCGAAAAAGTGCCACCTGACGTCGACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3'   CCAAGGCGCGTGTAAGGGCTTTTACGGTGGACTGCAGCTGCCTAGCCCTCTAGAGGGCTAGGGGATACCAGCTGAG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

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5'   TCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGC
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3'   AGTCATGTTAGACGAGACTACGGCGTATCAATTCGGTCATAGACGAGGGACGAACACACAACCTCCAGCGACTCATCAG
  +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

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