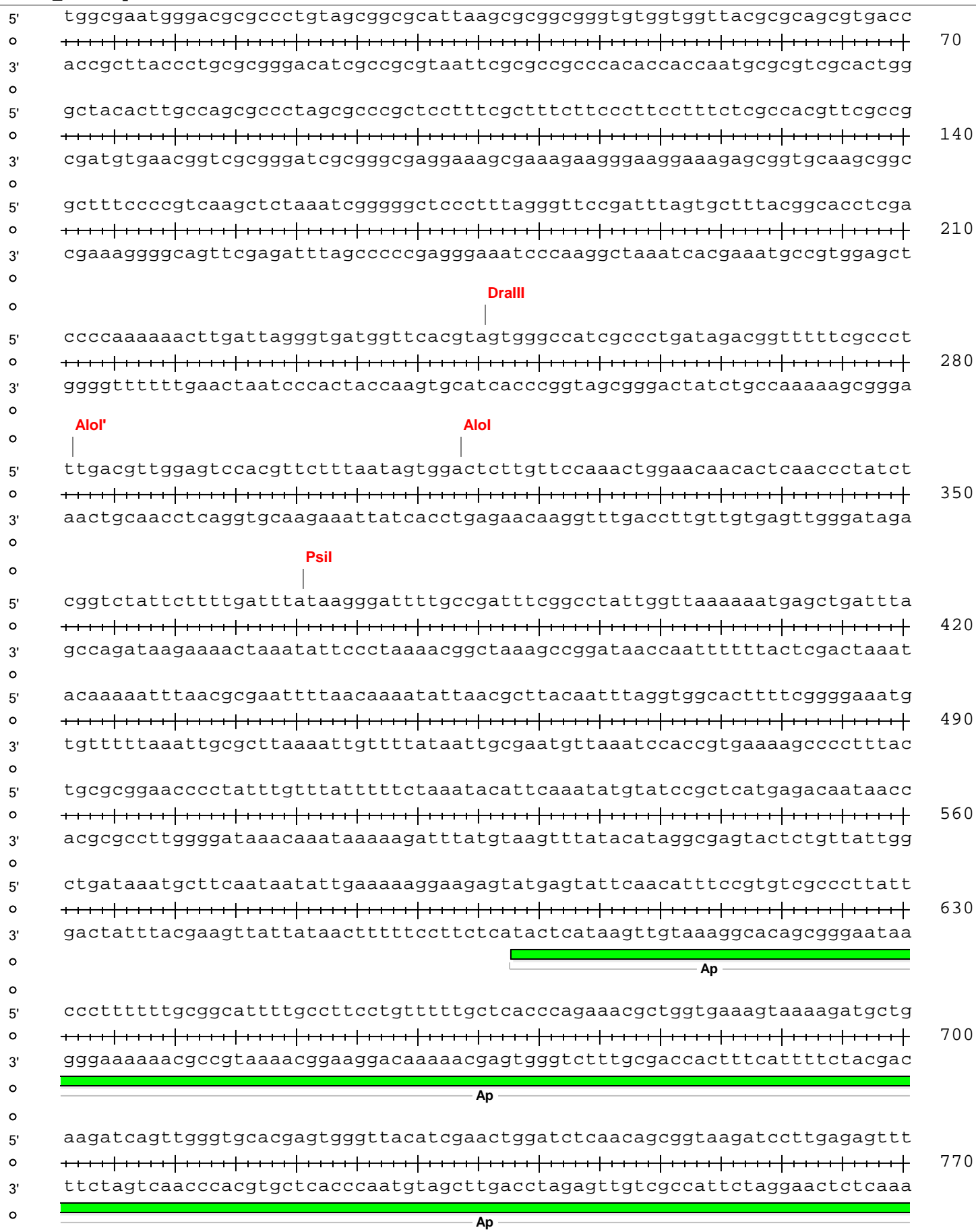
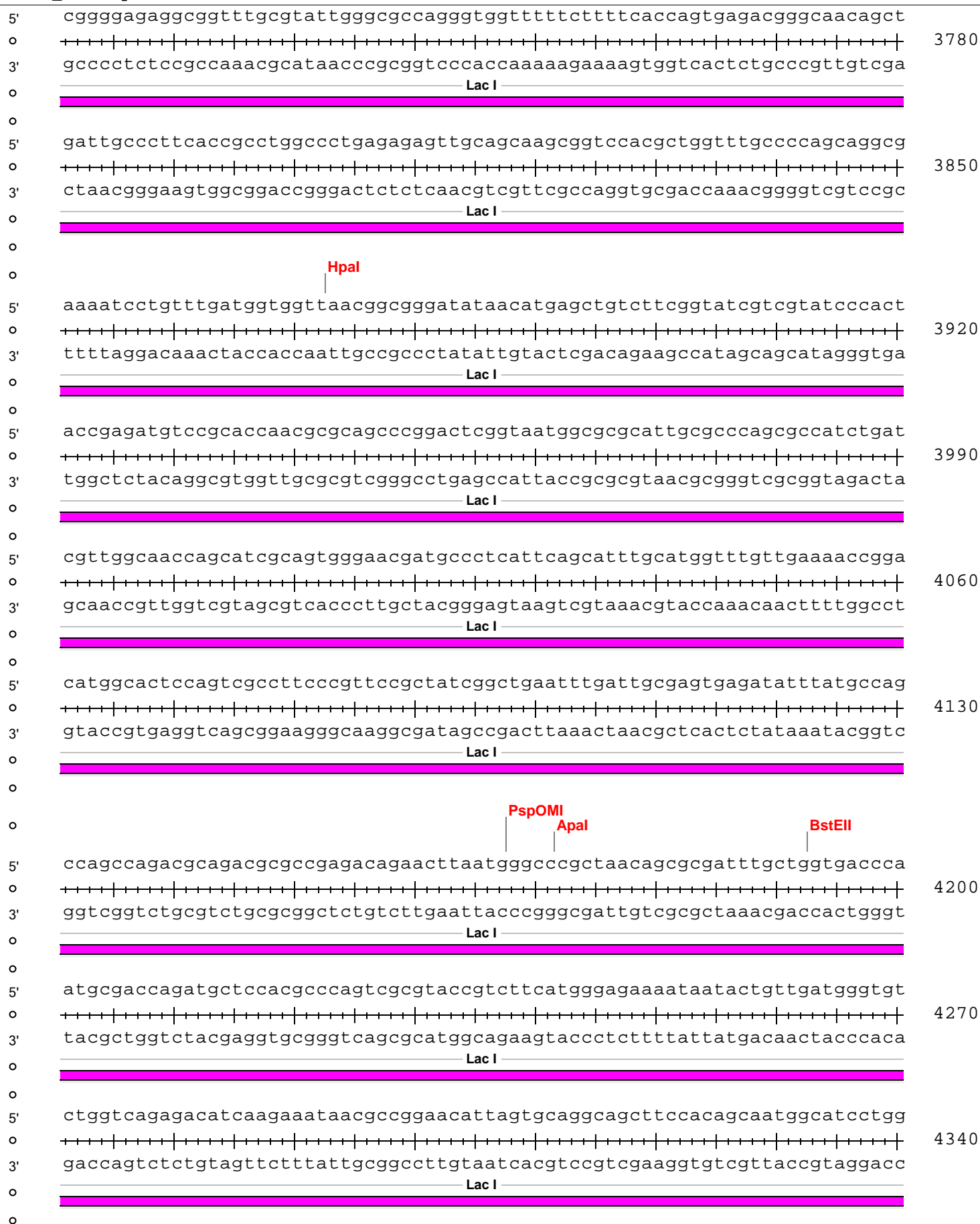


BGT25_T02a2-pET32-DEST



BGT25_T02a2-pET32-DEST



o
 5' accgcacctgtggcgccgggtgatgccggccacgatgctccggcgtagaggatcgagatcgatctcgatc
 o
 3' tggcgtggacaccgcgccactacggccggtgctacgcaggccgcacatctcctagctctagctagagctag

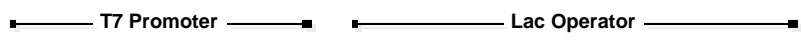
5110

SgrAI

XbaI

o
 5' ccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaataatttt
 o
 3' ggcgctttaattatgctgagtgatatccccttaacactcgctattgttaaggggagatctttattaaa

5180



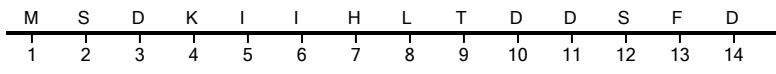
BamHI

BamHI'

o
 5' gtttaactttaagaaggagatatacatatgagcggataaaattattcacctgactgacgacagttttgaca
 o
 3' caaattgaaattcttctctatatagtatactcgctattttaataagtgactgactgctgtcaaaactgt

5250

Trx Tag

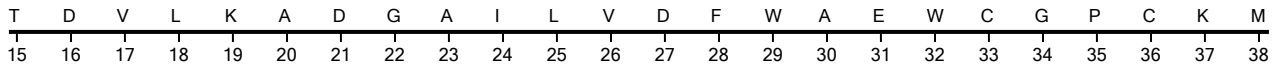


RsrII

o
 5' cggatgtactcaaagcggacggggcgatcctcgtcgatttctgggcagagtggtgctgggtccgtgcaaaat
 o
 3' gcctacatgagtttcgctgccccgctaggagcagctaaagaccgctctcaccacgccaggcaggtttta

5320

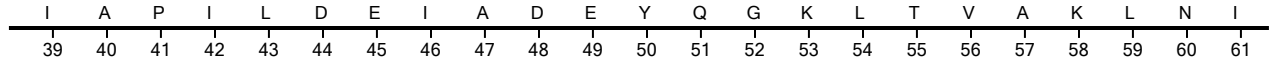
Trx Tag



o
 5' gatcgccccgattctggatgaaatcgctgacgaatatcagggcaaactgaccgttgcaaaactgaacatc
 o
 3' ctagcggggctaagacctactttagcgcactgcttatagtcccgtttgactggcaacgttttgacttgtag

5390

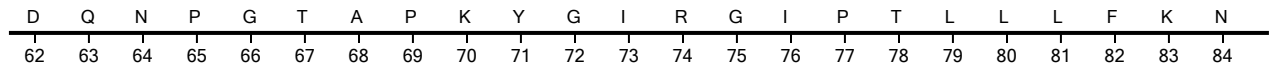
Trx Tag



o
 5' gatcaaaaccctggcactgcgccgaaatatggcatccgtggatcccgactctgctgctgttcaaaaacg
 o
 3' ctagttttgggaccgtgacgcggctttataccgtaggcaccatagggctgagacgacgacaagtttttgc

5460

Trx Tag



BGT25_T02a2-pET32-DEST

5' gtgaagtggcggcaaccaaagtgggtgcaactgtctaaagggtcagttgaaagagttcctcgcagcctaact
 0 ++++++
 3' cacttcaccgcccgttggtttcaccacgtagacagatttccagtcactttctcaaggagctgcgattgga
 0
 0
 0

5530

Trx Tag

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

5' ggccggttctgggttctggccatatgcaccatcatcatcattcttctgggtctgggtgccacgcggttct
 0 ++++++
 3' ccggccaagaccaagaccggtatacgtggtagtagtagtaagaagaccagaccacgggtgcgccaaga
 0
 0
 0

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

His6-tag

Thrombin

BstBI

Acc65I

KpnI

5' ggatgaaagaaaccgctgctgctaaattcgaacgccagcacatggacagcccagatctgggtaccgacg
 0 ++++++
 3' ccatactttctttggcgacgacgatttaagcttgcggtcgtgtacctgtcgggtctagacctatggctgc
 0
 0
 0

5670

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

5' acgacgacaaggccatggcgatATCAACAAGTTTGTACAAAAAAGCAGGCTctgaaaacttgtactttca
 0 ++++++
 3' tgctgctgttccggtaccgctaTAGTTGTTCAACATGTTTTTTCGTCCGAgacttttgaacatgaaagt
 0
 0
 0

5740

Enterokinase

attB1

TEV site

BGT25_T02a2-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

5' aggcAGCACCATCGGCCTGTGCATGATTGTCAAGAACGAGACGAAGGTCATCCTGCAATGCCTCGCCAGC
 0 ++++++
 3' tccgTCGTGGTAGCCGGACACGTAACAGTTCTTGCTCTGCTTCCAGTAGGACGTTACGGAGCGGTCG
 0
 0
 0

5810

BGT25_T02a2

BGT25_T02a2-pDONR221

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

BGT25_T02a2-pET32-DEST

Agel

5' GTGCTCCCCCTTGTCTGACTACGTGCTCATCGTCTGACACCGGTTCCGAGGACGGCACGCAAGACCTGATAC
 3' CACGAGGGGGAACAGCTGATGCACGAGTAGCAGCTGTGGCCAAGGCTCCTGCCGTGCGTTCTGGACTATG

5880

BGT25_T02a2

BGT25_T02a2-pDONR221

V L P L V D Y V L I V D T G S E D G T Q D L I
 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224

5' GCGGCTTTCTCGCCGATAACGGTGTCCAAGGCGCTGTCATTGACGAGCCATGGCGGGACTTCGCGTACAA
 3' CGCCGAAAGAGCGGCTATTGCCACAGGTTCCGCGACAGTAACTGCTCGGTACCGCCCTGAAGCGCATGTT

5950

BGT25_T02a2

BGT25_T02a2-pDONR221

R G F L A D N G V Q G A V I D E P W R D F A Y N
 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248

5' CCGGACCTTCGCCCTTGAACGATTGCGTAAAGTCGAGACTGTCTGACTATGCAATGATCATCGACGCGGAC
 3' GGCCGTGGAAGCGGGAACCTTGCTAACGCATTTACAGCTCTGACAGCTGATACGTTACTAGTAGCTGCGCCTG

6020

BGT25_T02a2

BGT25_T02a2-pDONR221

R T F A L E R L R K V E T V D Y A M I I D A D
 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271

5' GATGTTCTGATCCGGGACGCCGACTTCGATCCGATCAGGTTCAAGTCGCAGATGGAACACGATTTATACG
 3' CTACAAGACTAGGCCCTGCGGCTGAAGCTAGGCTAGTCCAAGTTTACGCGTCTACCTTGTGCTAAATATGC

6090

BGT25_T02a2

BGT25_T02a2-pDONR221

D V L I R D A D F D P I R F K S Q M E H D L Y
 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294

Zral AatII

5' ACGTCGAGGTGTTACATGGTGGCATTTCGTTTTATCGCCCGCAGATCTGCCGCAACCGTCTGCCGTTTCGC
 3' TGCAGCTCCACAATGTACCACCGTAAAGCAAATAGCGGGCGTCTAGACGGCGTTGGCAGACGGCAAGCG

6160

BGT25_T02a2

BGT25_T02a2-pDONR221

D V E V L H G G I S F Y R P Q I C R N R L P F A
 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318

BGT25_T02a2-pET32-DEST

5' CTTC AAGGGCGTCCTGCACGAATATCTCGAGGCCCTCCTGGCCATCTCACGCGGGAGACCGCCAAGGGT
 0 ++++++
 3' GAAGTCCC GCAGGACGTGCTTATAGAGCTCCGGGGAGGACCGGTAGAGTGCGCCCTCTGGCGGTTCCCA

----- BGT25_T02a2 -----
 ----- BGT25_T02a2-pDONR221 -----

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

6230

Bael

Bael'

5' TTTCGCGTGGCGACGGGGCGTGGCGGAGCACGCAGTCAAACCCACGAAAGTACCAGGACGACTCGGCCG
 0 ++++++
 3' AAAGCGCACCGCTGCCCCGCACCGCCTCGTGCCTCAGTTTTGGGTGCTTTCATGGTCTCTGCTGAGCCGGC

----- BGT25_T02a2 -----
 ----- BGT25_T02a2-pDONR221 -----

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

6300

5' TTCTTGAAAATGCGCTTGCAACGGAGACCGACCCCTTCTTGTTTCGCGATACACCTTCTATCTGGCGCA
 0 ++++++
 3' AAGAACTTTTACGCGAACGTTGCCTCTGGCTGGGGAAAGAACAAGCGCTATGTGGAAGATAGACCGCGT

----- BGT25_T02a2 -----
 ----- BGT25_T02a2-pDONR221 -----

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

6370

5' GAGCTACAGGGATTCCGGCGAGCGTGAAAAATCACTCGCGAACTATCTGAAGCGCGCCGATCTAGGTTTT
 0 ++++++
 3' CTCGATGTCCCTAAGGCCGCTCGCACTTTT TAGTGAGCGCTTGATAGACTTCGCGCGGCTAGATCCAAAA

----- BGT25_T02a2 -----
 ----- BGT25_T02a2-pDONR221 -----

S Y R D S G E R E K S L A N Y L K R A D L G F
 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411

6440

BseRI

5' TGGGACGAGGAGGTCTATGTCAGCCTGCTTGAGGCGGGCAACCTCATGGCAGCATTGGGGCGGCCATTTCG
 0 ++++++
 3' ACCCTGCTCCTCCAGATACAGTCGGACGAACTCCGCCCGTTGGAGTACCGTCGTAACCCCGCCGGTAAGC

----- BGT25_T02a2 -----
 ----- BGT25_T02a2-pDONR221 -----

W D E E V Y V S L L E A G N L M A A L G R P F
 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434

6510

