

BGT02_T01a-pET32-DEST

5' ctggtcagagacatcaagaaataacgccggaacattagtgaggcagcttccacagcaatggcatcctgg
 0 ++++++
 3' gaccagtctctgtagttctttattgccccttgaatcacgtccgtcgaagggtgcgttacccgtaggacc

4340

Lac I



5' tcatccagcggatagttaatgatcagcccactgacgcgcttgccgcgagaagattgtgcaccgccgctttac
 0 ++++++
 3' agtaggtcgcctatcaattactagtcgggtgactgcccgaacgcgctcttctaacacgtggcggcgaaatg

4410

Lac I



5' aggcttcgacgccgcttcggttctaccatcgacaccaccacgctggcaccagttgatcggcgcgagattt
 0 ++++++
 3' tccgaagctgcccgaagcaagatggtagctgtgggtggcgcaccgtgggtcaactagccgcgctctaaa

4480

Lac I



5' aatcgccgcgacaatttgccgacggcgcgctgcagggccagactggaggtggcaacgccaatcagcaacgac
 0 ++++++
 3' ttagcggcgcgctgttaaaccgctgcccgcgcacgtcccggctctgacctccaccggtgcccgttagtcggtgctg

4550

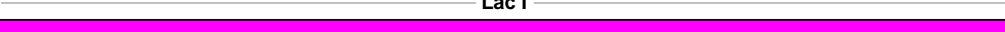
Lac I



5' tgtttgcccgcagttgttgtgcccacgcggttgggaatgtaattcagctccgccatcgccgcttccactt
 0 ++++++
 3' acaaacgggcgggtcaacaacacgggtgcccgaacccttacattaagtcgaggcggtagcggcgaagggtgaa

4620

Lac I



5' tttcccgcgttttcgagaaacgtggctggcctgggtcaccacgcgggaaacggtctgataagagacacc
 0 ++++++
 3' aaagggcgcaaaagcgtctttgcaccgaccggaccaagtggtgcccctttgccagactattctctgtgg

4690

BstAPI



5' ggcatactctgcgacatcgtataacgttactggtttcacattcaccaccctgaattgactctcttccggg
 0 ++++++
 3' ccgatatgagacgctgtagcatattgcaatgaccaaagtgtaagtggtgggacttaactgagagaaggccc

4760

5' cgctatcatgccataaccgcgaaaggttttgcgccattcgatgggtgtccgggatctcgacgctctccctta
 0 ++++++
 3' gcgatagtacggatggcgctttccaaaacgcggttaagctaccacaggccctagagctgagagagggaat

4830

EcoNI



5' tgcgactcctgcattaggaagcagcccagtagtaggttgaggccggtgagcaccgcccgcaagggaatg
 0 ++++++
 3' acgctgaggacgtaatccttcgctcgggtcatcatccaactccggcaactcgtggcggcggcgttcccttac

4900

SphI



5' gtgcatgcaaggagatggcgcccaacagtccccggccacggggcctgccaccatacccacgccgaaaca
 0 ++++++
 3' cacgtacgttcctctaccgcgggttgctcagggggccggtgccccgacgggtggatgggtgcccgtttgt

4970

BGT02_T01a-pET32-DEST

5' gtgaagtggcggcaaccaaaagtgggtgcaactgtctaaaggtcagttgaaagagttcctcgacgctaact
 3' cacttcaccgcccgttggtttcaccacgtgacagatttccagtcaactttctcaaggagctgcgattgga
 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

5' ggccggttctggttctggccatatgcaccatcatcatcattcttctggtctggtgccacgcggttct
 3' ccggccaagaccaagaccggtatacgtggtagtagtagtaagaagaccagaccacggtgcgccaaga
 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
 3' ccatacttcttggcgacgacgatttaagcttgcggtcgtgtacctgtcgggtctagacctatggctgc
 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' acgacgacaaggccatggcgatATCAACAAGTTTGTACAAAAAGCAGGCTctgaaaacttgtactttca
 3' tgctgctgttccggtaccgctaTAGTTGTTCAAACATGTTTTTTCGTCCGAgacttttgaacatgaaagt
 Enterokinase attB1 TEV site

5740

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

BsmI

5' aggcACAAATGATCATAGAATGCTGTGGTTGTGGTTCCTGCGTACAACGAAGAAAAACGTTTGTCCGCA
 3' tccgTGTTTACTAGTATCTTACGACAGCCAACCAAGGACGCATGTTGCTTCTTTTTGCAAACAGGCGT
 BGT02_T01a BGT02_T01a-pDONR221

5810

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

BGT02_T01a-pET32-DEST

5' TCTTTAGAGGTTCTTTGTGAAAAGGTCGGGCTGTTTTCCCTCGTTTTGAAATATTGTCGTGGATGATG
 0 ++++++
 3' AGAAATCTCCAAGAAACACTTTTCCAGCCCGACAAAAAGGGAGCAAACTTTAATAACAGCACCTACTAC

5880

BGT02_T01a

BGT02_T01a-pDONR221

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

5' GTAGTACCGATAAAACAGCGGATATCGTTATGACCCATAGCCGAAAATATTCGGATGTCCGCCTTATTCG
 0 ++++++
 3' CATCATGGCTATTTTGTGCGCTATAGCAATACTGGGTATCGGCTTTTATAAGCCTACAGGCGGAATAAGC

5950

BGT02_T01a

BGT02_T01a-pDONR221

G S T D K T A D I V M T H S R K Y S D V R L I R
 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248

Agel

5' TTATGAAAAAACCGGGGCAAAGGCTATGCTGTTTCGTACCGGTGTATTGGCTGCAAAGGGCGATTTTCGTG
 0 ++++++
 3' AATACTTTTTTTGGCCCCGTTTCCGATACGACAAGCATGGCCACATAACCGACGTTTCCCGCTAAAGCAC

6020

BGT02_T01a

BGT02_T01a-pDONR221

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

5' TTGTTTCAGCGATGCCGACTTATCAACACCTATCGAAGAGGTTGAGAAGTTGTTTGGTGCCTCGCGGATG
 0 ++++++
 3' AACAAAGTCGCTACGGCTGAATAGTTGTGGATAGCTTCTCCTCAACTCTTCAACAAACCACGTGAGCGCCTAC

6090

BGT02_T01a

BGT02_T01a-pDONR221

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

Ajul'

Ajul

5' GAGCCGATGTCGCTATAGGGTCGCGGGCTGTGCGCCAATCGCTGATTCTAAAGAGTCAGCCTCTTTACCG
 0 ++++++
 3' CTCGGCTACAGCGATATCCCAGCGCCCGACACGCGGTTAGCGACTAAGATTTCTCAGTCGGAGAAATGGC

6160

BGT02_T01a

BGT02_T01a-pDONR221

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

BGT02_T01a-pET32-DEST

5' TATGGTGATGGGGAAAAC TTTTAATAAATTTGTACAGCTGCTGGCGATCCCCGGTATTTTAGATACGCAA
 6230
 3' ATACCACTACCCCTTTTGAAAATTATTTAAACATGTCGACGACCGCTAGGGGCCATAAAATCTATGCGTT

BGT02_T01a

BGT02_T01a-pDONR221

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

5' TGCGGATTTAAGCTTTTTCACGCGTTCTGCCGCTTTAAATCTTTTCAGAGATTGTCGCATTGATGGTTTTG
 6300
 3' ACGCCTAAATTCGAAAAGTGC GCAAGACGGCGAAATTTAGAAAAGTCTCTAACAGCGTAACTACCAAAC

BGT02_T01a

BGT02_T01a-pDONR221

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

5' GTTTCGATGTGGAGTTCTTTTCTTGC GCGTAAAAGAGGCATGGATATACGCGAGATTGGCGTAAGCTG
 6370
 3' CAAAGCTACACCTCCAAGAAAAAGAACGCGCATTTTCTCCGTACCTATATGCGCTCTAACCGCATTCGAC

BGT02_T01a

BGT02_T01a-pDONR221

G F D V E V L F L A R K R G M D I R E I G V S W
 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' GGTCAATTCACCCGATAGCAAAGTACATCCCATCGTTGATTCGGCACGTATGCTCCAAGATTTGGTTGTT
 6440
 3' CCAGTTAAGTGGGCTATCGTTTCATGTAGGGTAGCAACTAAGCCGTGCATACGAGGTTCTAAACCAACAA

BGT02_T01a

BGT02_T01a-pDONR221

V N S P D S K V H P I V D S A R M L Q D L V V
 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411

5' ATTGCGAGACATGCGTTGTTGGGGGATTACGGGGATTTAAGATTGCCACAAGCTAAAATCGAAACAGTAT
 6510
 3' TAAGCGTCTGTACGCAACAACCCCTAATGCCCTAAATTTCTAACGGTGTTTCGATTTTAGCTTTGTCATA

BGT02_T01a

BGT02_T01a-pDONR221

I R R H A L L G D Y G D L R L P Q A K I E T V
 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434

