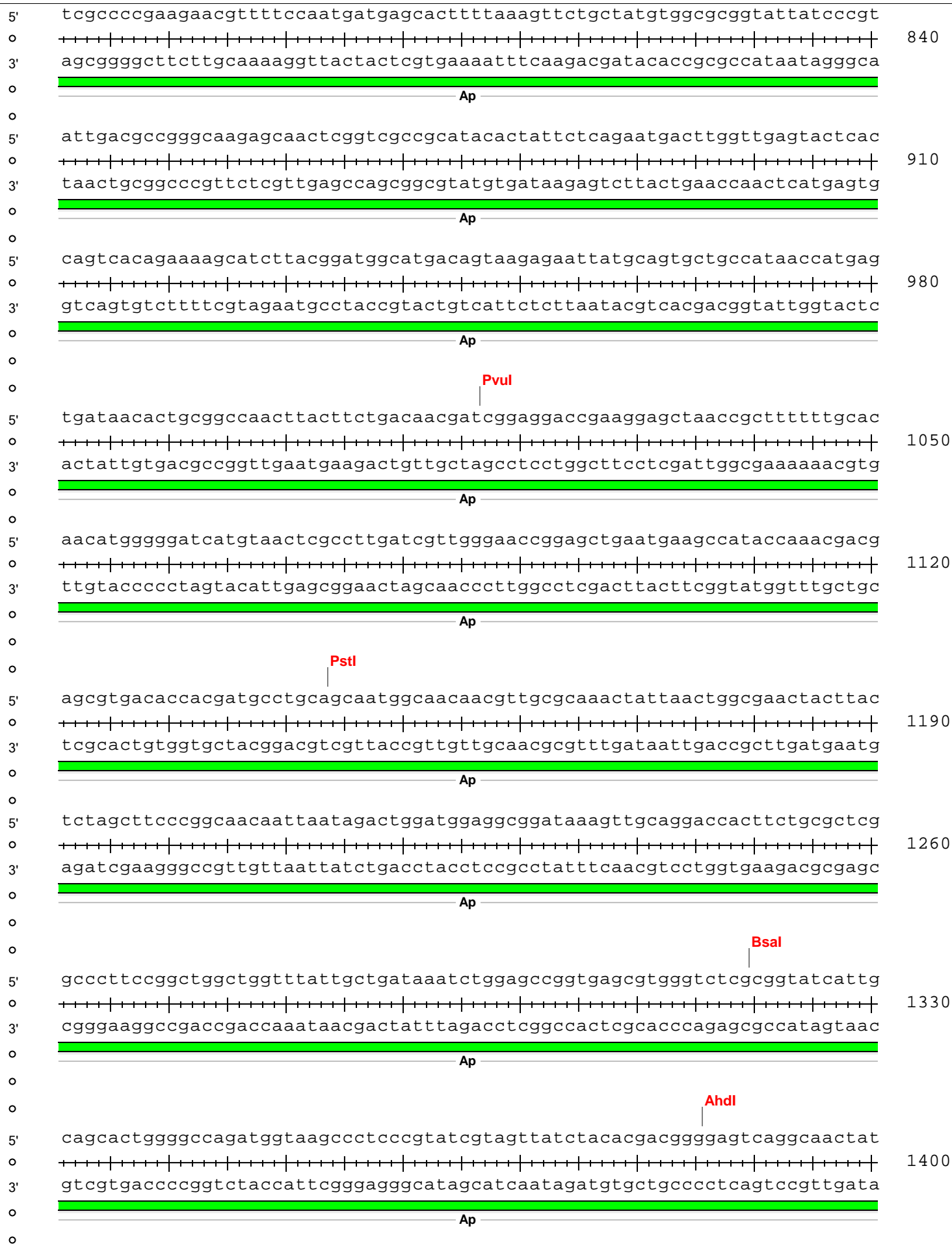


BGH47_B03a-pET32-DEST



BGH47_B03a-pET32-DEST

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 Ap →

5' gtttactcatatatacttttagattgatttaaaacttcatttttaatttaaaggatctaggtgaagatcc
 1540
 3' caaatgagtatatatgaaatctaactaaatgtgaagtaaaaattaaatcttcttagatccacttctagg

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 1610
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5' aaagatcaaaggatcttcttgagatcctttttctgcgcgtaactctgctgcttgcaaacaaaaaacca
 1680
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 Ori

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 1750
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 Ori

5' gcagagcgcagataccaataactgtccttctagtgtagccgtagttaggccaccacttcaagaactctgt
 1820
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 Ori

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 Ori

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 Ori

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 Ori

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 Ori

BGH47_B03a-pET32-DEST

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 ++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
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 Ori
 =====
 =====

2170

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 ++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
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 Ori
 =====
 =====>

2240

5' acggttctggccttttGctggccttttGctcacatgttctttcctgcggttatcccctgattctgtggat
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2310

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2380

SapI

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 ++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
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2450

BstZ17I

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2520

Tth111I

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2590

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2660

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2730

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2800

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 ++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
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2870

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o	Lac I	
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o
5110

SgrAI

XbaI

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5180

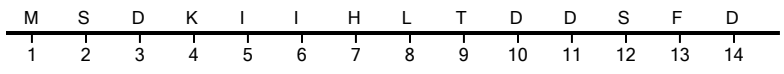


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o
5250

BamI

BamI'

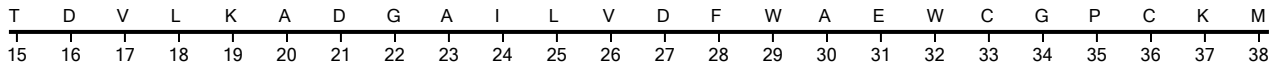
Trx Tag



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o
5320

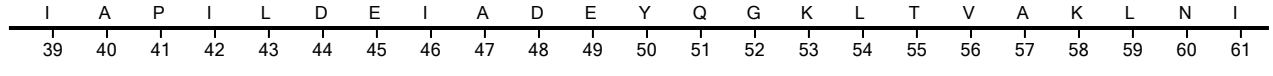
RsrII

Trx Tag



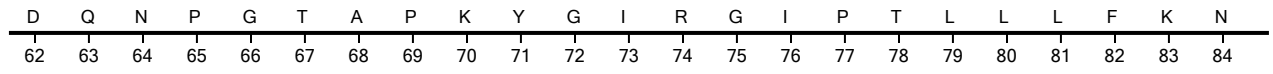
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o
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o
5390

Trx Tag



5' gatcaaaaccctggcactgcgCCGAAATATGGCATCCGTGGTATCCCGACTCTGCTGCTGTTCAAAAACG
o
3' ctagttttgggaccgtgacgCGGCTTTATACCCTAGGCACCATAGGGCTGAGACGACGACAAGTTTTTGC
o
5460

Trx Tag



BGH47_B03a-pET32-DEST

5' gtgaagtggcggcaaccaaaagtgggtgcaactgtctaaaggtcagttgaaagagttcctcgcagcctaact
 0 ++++++
 3' cacttcaccgcccgttggtttcaccacgtgacagatttccagtcaactttctcaaggagctgcgattgga

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

MscI

5' ggccggttctggttctggccatatgcaccatcatcatcattcttctggtctggtgccacgcggttct
 0 ++++++
 3' ccggccaagaccaagaccggtatacgtggtagtagtagtaagaagaccagaccacggtgcgccaaga

5600

-T...g 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

BstBI

BglII

5' ggtatgaaagaaaccgctgctgctaaattcgaacgccagcacatggacagcccagatctgggtaccgacg
 0 ++++++
 3' ccatactttcttggcgacgacgatttaagcttgcggtcgtgtacctgtcgggtctagacctatggctgc

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

NcoI

5' acgacgacaaggccatggcgaTATCAACAAGTTTGTACAAAAAAGCAGGCTctgaaaacttgtactttca
 0 ++++++
 3' tgctgctgttccggtaccgctaTAGTTGTTCAAACATGTTTTTTCGTCCGAgacttttgaacatgaaagt

5740

Enterokinase attB1 TEV site

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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' aggcCAAGCGGAGTTATCGCTAAGCGTCAAACAGGAATTTATCAGATCCTGGGATGCTTACAAACGATAC
 0 ++++++
 3' tccgGTTTCGCTCAATAGCGATTTCGCAGTTTGTCTTAAATAGTCTAGGACCTACGAATGTTTGCTATG

5810

T... BGH47_B03a
BGH47_B03a-pDONR221

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 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201

Psrl

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5880

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BGH47_B03a-pDONR221

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

Psrl'

Nsil

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3' AAAGCGTCTAACTACGTATATCGTGGTACTTTCACTACCCGGAGGTCTTTGTCCGGTCTCTGTAACCTCTT

5950

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BGH47_B03a-pDONR221

I S Q I D A Y S T M K V M G L Q K Q A R D I E K
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' GTTTGTAAACAGATAGTTGCAACTTTGACATAGACGTTTACGTAAAGACCTTTGATGTCAATAATCGCGTA
3' CAAACATTGTCTATCAACGTTGAAACTGTATCTGCAAATGCATTTCTGGAAACTACAGTTATTAGCGCAT

6020

BGH47_B03a

BGH47_B03a-pDONR221

F V T D S C N F D I D V Y V K T F D V N N R 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' CTGGGAGGACTCTTATACATGTACTCCTGCACACACCAGCCTAAAATACTGGAACGCGCAAGAGACTTTG
3' GACCCTCCTGAGAATATGTACATGAGGACGTGTGTGGTTCGGATTTTATGACCTTGCGCGTTCTCTGAAAC

6090

BGH47_B03a

BGH47_B03a-pDONR221

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

5' GAGATCGCCTCTTAAAAGCTTTCAGATCACCGACAGGAATCCCCTATTACTGGGTCAATCTGAAAACCGG
3' CTCTAGCGGAGAATTTTCGAAAGTCTAGTGGCTGTCTTAGGGGATAATGACCCAGTTAGACTTTTGGCC

6160

BGH47_B03a

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G D R L L K A F R S P T G I P Y Y W V N L K T G
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BGH47_B03a-pET32-DEST

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 6230
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K V K G E K V N T A E A A A Y T L E M G I L S
 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341

5' TATTACACAAAGGACCCGAAATATTATCAGGCGGCGAGGAAAGCGACAGAAGCCATATAACGGCAGACGCT
 6300
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Y Y T K D P K Y Y Q A A R K A T E A I Y G R R
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5' CAGCCCTCAACCTTACCGGCAACATCATCAACAATGAAACCGGTGACTGGCTGGAAACCATCAGTTGTAT
 6370
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S A L N L T G N I I N N E T G D W L E T I S C I
 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' CGGCGCAGGAGGCAGCGCTTACTATGAAAAGTATGCTGAAAACATGGCTCCTGTTTAAAGATGAAGCACTG
 6440
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G A G G S A Y Y E S M L K T W L L F K D E A L
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5' AAAGAAATGTGGGAGAAAACCATTACAGCCGTACATCAGTATAACGCAGAAGAAAGTGACACCGCAATAT
 6510
 3' TTTCTTTACACCTCTTTTGGTAATGTCGCGCATGTAGTCATATTGCGTCTTCTTTCACCTGTGGCGTTATA

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BGH47_B03a-pDONR221

K E M W E K T I T A V H Q Y N A E E S D T A I
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BGH47_B03a-pET32-DEST

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0 ++++++
3' CCATGGCGTCTTGCCTGTACATAAGTCCCCTTTGTTTCTTATGTTGACGCTGTCCAATGCTGCGTAAGGA

6580

BGH47_B03a

BGH47_B03a-pDONR221

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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' GCCAGCTCTTTTATGTATCGATAATGATGCAGAACAGGCAGCCAGGGTACACCGGACCTGGAATAATCTC
0 ++++++
3' CGGTCGAGAAAATACATAGCTATTACTACGTCTTGTCCGTCGGTCCCATGTGGCCTGGACCTTATTAGAG

6650

BGH47_B03a

BGH47_B03a-pDONR221

P A L L C I D N D A E Q A A R V H R T W N N L
459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481

BsiWI

5' TGGAACAGTATGGGATGATTCCGATGATCTACGACTTCCGCCGGCAGCATATCACGGCAGCAGCGTACG
0 ++++++
3' ACCTTTGTCATACCCTACTAAGGCTACTAGATGCTGAAGGCGGCCGTCGTATAGTGCCGTCGTGCGCATGC

6720

BGH47_B03a

BGH47_B03a-pDONR221

W K Q Y G M I P M I Y D F R R Q H I T A A A Y
482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504

5' ACCTGAATCCCGAGATCATCGAGTCAGCCTGGTACCTGTATGATTACACAAAAGATAACCGCCTATCAGCA
0 ++++++
3' TGGACTTAGGGCTCTAGTAGCTCAGTCGGACCATGGACATACTAATGTGTTTTTCTATGGCGGATAGTCGT

6790

BGH47_B03a

BGH47_B03a-pDONR221

D L N P E I I E S A W Y L Y D Y T K D T A Y Q Q
505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528

5' GATGGGCAGACAGTACTACAGCGACATATTGCAGTATTGCAGGGCAGGCGCCGCATTCACCTGGCGTAATG
0 ++++++
3' CTACCCGTCTGTCATGATGTCGCTGTATAACGTCATAACGTCCCGTCCGCGGGCGTAAGTGACCGCATTAC

6860

BGH47_B03a

BGH47_B03a-pDONR221

M G R Q Y Y S D I L Q Y C R A G A A F T G V M
529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551

BGH47_B03a-pET32-DEST

5' GATATCAGAAGTAAACAGCAGCAGAAATAAAATGCCGGTCTATTTCTTTGCAACAACAATGAAATACCTGT
 0 ++++++
 3' CTATAGTCTTCATTTGTCGTCGTCTTATTTTACGCCAGATAAAGAAACGTTGTTGTTACTTTATGGACA

6930

BGH47_B03a

BGH47_B03a-pDONR221

D I R S K Q Q Q N K M P V Y F F A T T M K Y L
 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574

BspMI

5' ACCTGCTCTTTACACCAGACAGTGGATTGAATACGCTTGATTACGTATTCACAGCAGAAGGAAACCCGTT
 0 ++++++
 3' TGGACGAGAAATGTGGTCTGTCACCTAACTTATGCGAACTAATGCATAAGTGTCTCTTCCTTTGGGCAA

7000

BGH47_B03a

BGH47_B03a-pDONR221

Y L L F T P D S G L N T L D Y V F T A E G N P F
 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598

ZraI AatII

5' TAAAACGGATGAATTCAAAGCGGCAGAAACAGCCAGACGTCTGGGCATTAATCAGTAGGACCCAGCTTTC
 0 ++++++
 3' ATTTTGCCTACTTAAGTTTCGCCGTCTTTGTCGGTCTGCAGACCCGTAATTAGTCATCCTGGGTCGAAAG

7070

BGH47_B03a

attB2

BGH47_B03a-pDONR221

K T D E F K A A E T A R R L G I N Q
 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617

BamHI EcolCRI SacI Sall NotI EagI PspXI XhoI

5' TTGTACAAAGTGGTTGATatcggatccgaattcgagctccgtcgacaagcttgcggccgcactcgagcac
 0 ++++++
 3' AACATGTTTCACCAACTAtagcctaggcttaagctcgaggcagctgttcgaacgccggcgtgagctcgtg

7140

attB2

5' caccaccaccactgagatccggctgctaacaaagccgaaaggaagctgagttggctgctgccaccg
 0 ++++++
 3' gtggtggtggtggtgactctaggccgacgattgtttcgggctttccttcgactcaaccgacgacggtggc

7210

5' ctgagcaataactagcataaaccccttggggcctctaaacgggtcttgaggggttttttgctgaaaggagg
 0 ++++++
 3' gactcgttattgatcgtattggggaaccccgagatttgcccagaactccccaaaaaacgactttcctcc

7280

T7 Terminator

5' aactatatccggat
 0 ++++++
 3' ttgatataggccta

7294