

BGT02_T05a-pET32-DEST

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Dralll

AloI'

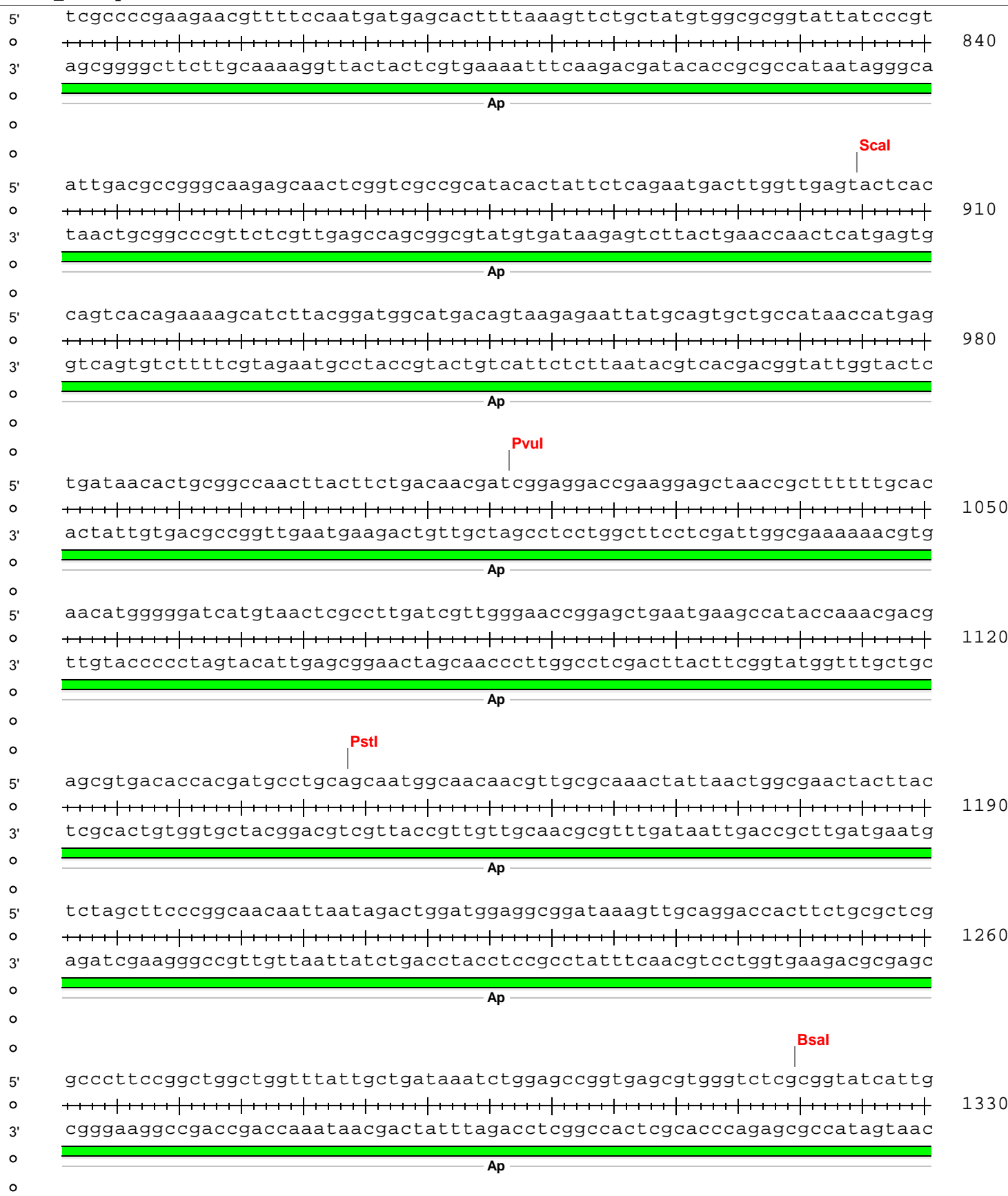
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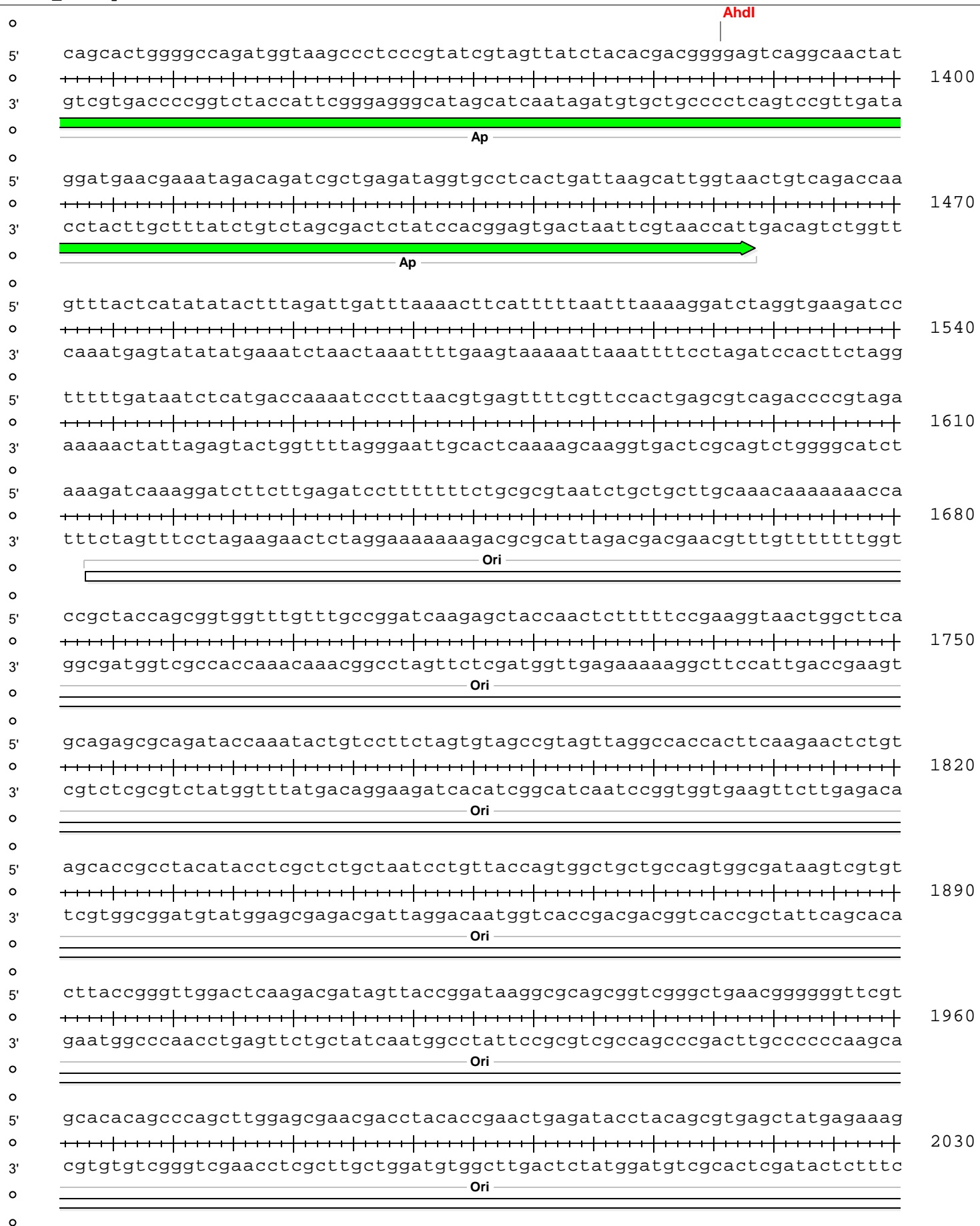
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Ap

Ap

BGT02_T05a-pET32-DEST





BGT02_T05a-pET32-DEST

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o		
	FspAI	
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 0

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 0 ----- Lac I -----
 0

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 0 ----- Lac I -----
 0

0
 0 **HpaI**
 0 |
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 0 ----- Lac I -----
 0

0
 0 **BssHII**
 0 |
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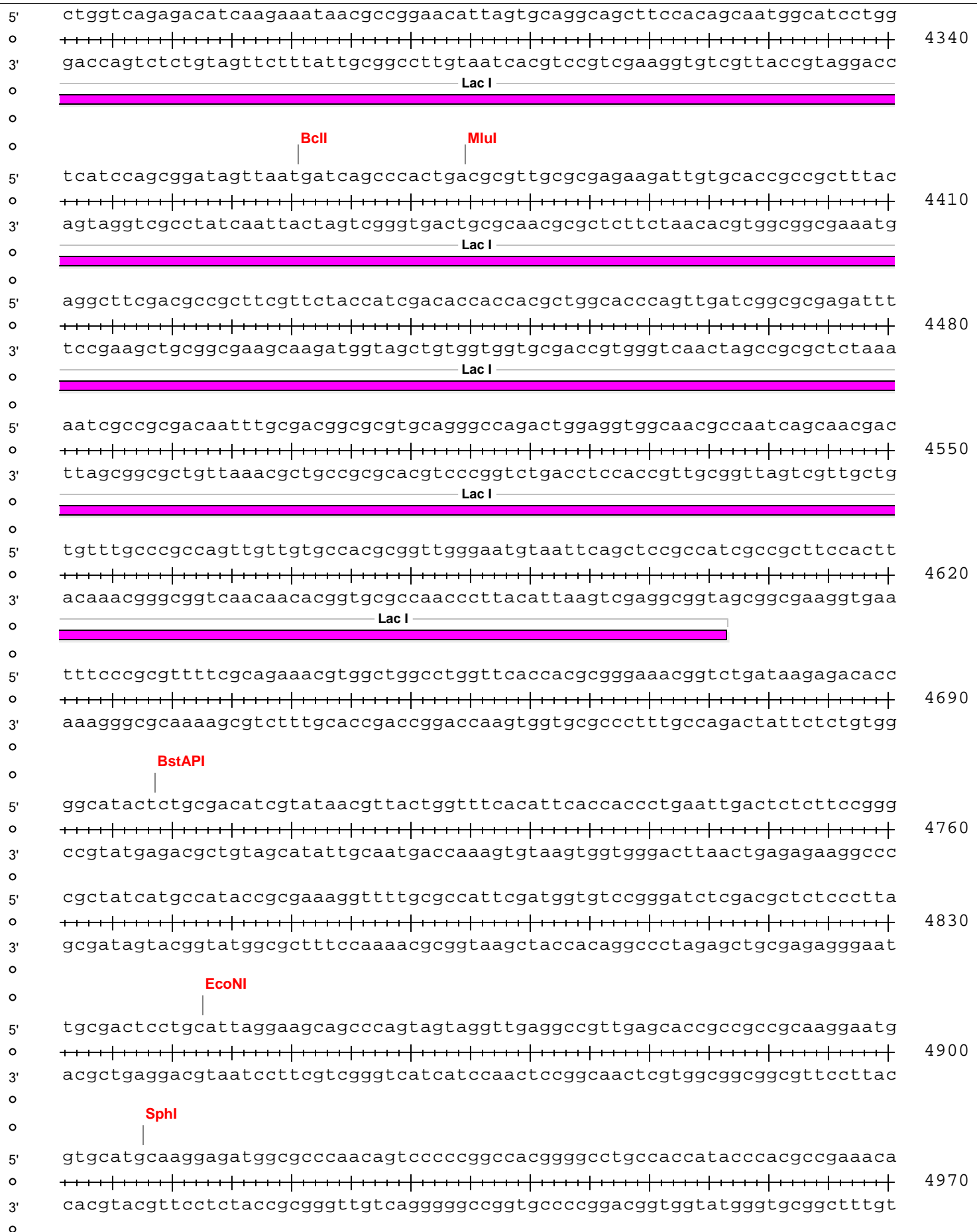
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BGT02_T05a-pET32-DEST



BGT02_T05a-pET32-DEST

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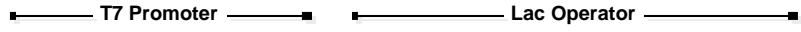
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5110

XbaI

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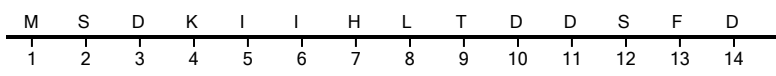
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BamHI

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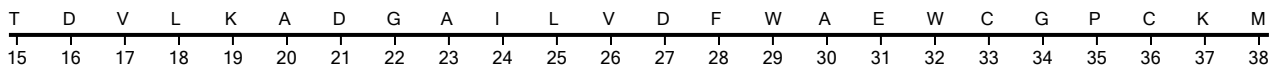


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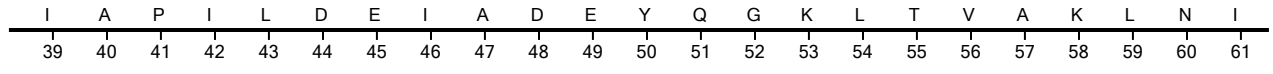
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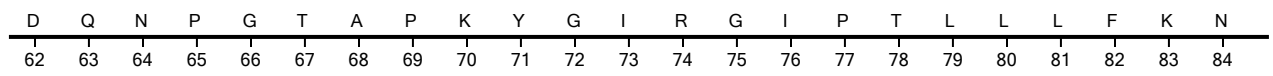
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5460

Trx Tag



BGT02_T05a-pET32-DEST

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 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
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MscI

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 3' ccggccaagaccaagaccgggtatacgtggtagtagtagtaagaagaccagaccacgggtgcgccaaga
 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
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BstBI

BglII

Acc65I

KpnI

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 En...e

5670

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NcoI

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 Enterokinase attB1 TEV site

5740

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 BGT02_T05a

5810

BGT02_T05a-pDONR221

G L N F L S I F L L T Y G V L A I S H I A F Q
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BGT02_T05a-pET32-DEST

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5880

BGT02_T05a

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5950

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6020

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 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271

Bsu36I

5' TTGATTGAAAAAGTCTATAACACTTATCAATCAAATCAAATGTAAAATTTTATTGCCTGAGGAAAACA
 3' AACTAACTTTTTTCAGATATTGTGAATAGTTAGTTTAGTTTACAAATTTTAAAATAACGGACTCCTTTTGT

6090

BGT02_T05a

BGT02_T05a-pDONR221

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

5' AAGGCAAACGTCACCTGTCAAAAACCTTGGATTTGATATTGCTAAGGCGATATTATTGTCACAGTGGATTC
 3' TTCCGTTTGCAGTGACAGTTTTTGAACCTAAACTATAACGATTCCCGCTATAATAACAGTGTACCTAAG

6160

BGT02_T05a

BGT02_T05a-pDONR221

K G K R H C Q K L G F D I A K G D I I V T V D S
 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_T05a-pET32-DEST

5' AGATACCTTACTACATGATGAGAATGCAGTTGAAAAATTAATTCAGCGTTTTGCTTATAAGAACGTTGGG
 3' TCTATGGAATGATGTACTACTCTTACGTCAACTTTTTAATTAAGTCGCAAACGAATATTCTTGCAACCC

6230

BGT02_T05a

BGT02_T05a-pDONR221

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

BmgBI

SnaBI

5' GCTGTCACTGGTGATGTTTCGAGTCGAAAACAAAAATACGAATATCTTAACACGTCTGATTACGTATCGCT
 3' CGACAGTGACCACTACAAGCTCAGCTTTTGT'TTTTATGCTTATAGAATTGTGCAGACTAATGCATAGCGA

6300

BGT02_T05a

BGT02_T05a-pDONR221

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

5' ATTGGACTGCGTTTCACCAAGAGCGAGCAGCTCAAAGCCGCTTTCACGTTGTAATGTGTTGTTCTGGACC
 3' TAACCTGACGCAAAGTGGTTCTCGCTCGTTCGAGTTTCGGCGAAAGTGCAACATTACACAACAAGACCTGG

6370

BGT02_T05a

BGT02_T05a-pDONR221

Y W T A F H Q E R A A Q S R F H V V M C C S G P
 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' GTTTTCAGCCTATCGTAAAGAAATAATTGACAAAGTCAAAGAGAAATACATTACACAATATTTCTTAGGC
 3' CAAAAGTCGGATAGCATTCTTTATTAAGTGTTCAGTTTCTCTTTATGTAATGTGTTATAAAGAATCCG

6440

BGT02_T05a

BGT02_T05a-pDONR221

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

5' GAAAATTGTACCTATGGAGATGACCGTCATTTGACAAATTTGGTTCTTGAAGAAGGCCATGACGTTGCCT
 3' CTTTTAACATGGATACCTCTACTGGCAGTAAACTGTTTAAACCAAGAAGTCTTCCGGTACTGCAACGGA

6510

BGT02_T05a

BGT02_T05a-pDONR221

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

BGT02_T05a-pET32-DEST

Bael

Bael'

5' TCCACAGAGATAGTAGAGTTTATACTTTTGTACCTGAAACAATTCGTGGATATATCAAACAGCAAGTACG
 3' AGGTGTCTCTATCATCTCAAATATGAAAACATGGACTTTGTTAAGCACCTATATAGTTTGTCTGTTTCATGC

6580

BGT02_T05a

BGT02_T05a-pDONR221

F H R D S R V Y T F V P E T I R G Y I K Q Q V R
 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' ATGGAATAAAAGCTTCTATCGTGAGATGCTTTGGACAATTAAGTTTGCACCTAAACGTCATTTTTATATG
 3' TACCTTATTTTCGAAGATAGCACTCTACGAAACCTGTTAATTCAAACGTGGATTTCAGTAAAAATATAC

6650

BGT02_T05a

BGT02_T05a-pDONR221

W N K S F Y R E M L W T I K F A P K R H F Y M
 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481

5' CTTTATGATTTGGTCATGCAATTTATCTTACCGTTTATGTTGGTTGTATCATTAATTGCTATGGCTGTCC
 3' GAAATACTAAACCAGTACGTTAAATAGAAATGGCAAATACAACCAACATAGTAATTAACGATACCGACAGG

6720

BGT02_T05a

BGT02_T05a-pDONR221

L Y D L V M Q F I L P F M L V V S L I A M A V
 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504

5' AAACAATTTTCATATCATGATTTAGGACATTTCTATCATTATTTGCTTGTTTTGATTCTGATCGCTATTTT
 3' TTTGTTAAAGTATAGTACTAAATCCTGTAAAGATAGTAATAAACGAACAAAATAAGACTAGCGATAAAA

6790

BGT02_T05a

BGT02_T05a-pDONR221

Q T I S Y H D L G H F Y H Y L L V L I L I A I F
 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' CCGTTCACTGTATGGTATTTATCGAACTAAAGACATTGGATTTTACTCTTTGTTTATATGGCTTTATG
 3' GGCAAGTGACATAACCATAAATAGCTTGATTTCTGTAACTAAAAATGAGAAACAAAATATACCGAAATAC

6860

BGT02_T05a

BGT02_T05a-pDONR221

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

BGT02_T05a-pET32-DEST

5' CACGTAATAATTCTATTACCTGTTTCGATTCTATGCACTATTTCACATTGAAATCGACAAAATGGGGAACGC
 3' GTGCATGATTAAGATAATGGACAAGCTAAGATACGTGATAAGTGTAACTTTAGCTGTTTTACCCCTTGCG

6930

BGT02_T05a

BGT02_T05a-pDONR221

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

BamHI EcoRI EcoICRI SacI Sall

5' GATAGGACCCAGCTTTCTTGTACAAAGTGGTTGATatcggatccgaattcgagctccgctcgacaagcttg
 3' CTATCCTGGGTGCGAAAGAACATGTTTCACCAACTAtagcctaggcttaagctcgaggcagctggttcgaac

7000

attB2

BGT02_T0...pDONR221

R
 575 576

NotI EagI PspXI XhoI Aval BmeT110I

5' cggccgcactcagagcaccaccaccaccactgagatccggctgctaacaaagcccgaaggagctga
 3' gccggcgtgagctcgtggtggtggtggtgactctaggccgacgattgtttcgggctttccttcgact

7070

BipI

5' gttggctgctgccaccgctgagcaataactagcataacccttgggcctctaaacgggtcctgaggggt
 3' caaccgacgacggtggcgactcgttattgatcgtattggggaaccccggagattgcccagaactcccca

7140

T7 Terminator

5' tttttgctgaaaggaggaactatatccggat
 3' aaaaacgactttcctccttgatataggccta

7171

T7...r