



o  
5' attgacgccgggcaagagcaactcggctcgccgcatacactattctcagaatgacttgggtgagtactcac  
o  
3' taactgccccggttctcgttgagccagcggcgtatgtgataagagtcttactgaaccaactcatgagtg  
o  
Ap  
o

Scal

910

5' cagtcacagaaaagcatcttacggatggcatgacagtaagagaattatgcagtgctgccataacatgag  
o  
3' gtcagtgcttttcgtagaatgcctaccgtactgtcatctcttaatacgtcacgacggatattggtactc  
o  
Ap  
o

980

5' tgataaactgcgccaacttacttctgacaacgatcggaggaccgaaggagctaaccgcttttttgac  
o  
3' actattgtgacgccggttgaatgaagactgttgctagcctcctggcttctcgttggcgaaaaaacgtg  
o  
Ap  
o

PvuI

1050

5' aacatgggggatcatgtaactcgccttgatcggtgggaaccggagctgaatgaagccataccaaacgacg  
o  
3' ttgtaccccctagtagcattgagcggaaactagcaaccctggcctcgacttacttcggtatggtttgctgc  
o  
Ap  
o

1120

5' agcgtgacaccacgatgcctgcagcaatggcaacaacggttgcgcaactattaactggcgaactacttac  
o  
3' tcgcactgtggtgctacggacgctcgttaccggtgttgcaacgcggttgataattgaccgcttgatgaatg  
o  
Ap  
o

PstI

1190

5' tctagcttcccggcaacaattaatagactggatggaggcggataaagttgcaggaccacttctgcgctcg  
o  
3' agatcgaagggccggttgttaattatctgacctacctccgcctatttcaacgtcctggtgaagacgcgagc  
o  
Ap  
o

1260

5' gcccttccggctggctggtttattgctgataaatctggagccggtgagcgtgggtctcgcggtatcattg  
o  
3' cgggaaggccgaccgaccaataacgactatttagacctcggccactcgcacccagagcgcctatagtaac  
o  
Ap  
o

Bsal

1330

5' cagcactggggccagatggtaagccctcccgtatcgtagttatctacacgacggggagtcaggcaactat  
o  
3' gtcgtgaccccggctctaccattcgggagggcatagcatcaatagatgtgctgccctcagtcctgtgata  
o  
Ap  
o

AhdI

1400









0  
5' tcatccagcggatagttaatgatcagcccactgacgcggtgcgcgagaagattgtgcaccgcccgtttac 4410  
0  
3' agtaggtcgcctatcaattactagtcgggtgactgcgcaacgcgctcttctaacacgtggcgcgaaatg  
0  
Lac I

0  
5' aggcttcgacgcccgttcggttctaccatcgacaccaccacgctggcaccagttgatcggcgcgagattt 4480  
0  
3' tccgaagctgcgcgcaagcaagatggtagctgtgggtggtgacaccgtgggtcaactagcccgcgctctaaa  
0  
Lac I

0  
5' aatcgccgcgacaatttgcgacggcgcggtgcagggccagactggaggtggcaacgccaatcagcaacgac 4550  
0  
3' ttagcggcgctgttaaagcgtgccgcgcacgctcccggctgacctccaccggtgcggttagtcggtgctg  
0  
Lac I

0  
5' tgtttgcccgccagttggttgccacgcggttgggaatgtaattcagctccgccatcgcccgttccactt 4620  
0  
3' acaaacgggcggtcaacaacacgggtgcgccaacccttacattaagtcgaggcggtagcggcgaaagtgaa  
0  
Lac I

0  
5' tttcccgcgttttcgcagaaacgtggctggcctgggtcaccacgcgggaaacggtctgataagagacacc 4690  
0  
3' aaagggcgcaaaagcgtctttgcaccgaccggaccaagtgggtgcgccctttgccagactattctctgtgg  
0  
5' ggcatactctgcgacatcgtataacgttactggtttcacattcaccaccctgaattgactctcttcggg 4760  
0  
3' ccgatatgagacgctgtagcatattgcaatgaccaaagtgaagtgggtgggacttaactgagagaaggccc

0  
5' cgctatcatgccataaccgcgaaaggttttgccgcatcgcggtggtggtcgggatctcgacgctctccctta 4830  
0  
3' gcgatagtagcggatggcgctttccaaaacgcggtaagctaccacaggccctagagctgcgagaggggaat  
0  
5' tgcgactcctgcattaggaagcagcccagtagtaggttgaggccggtgagcaccgcccgcgcaaggaatg 4900  
0  
3' acgctgaggacgtaatccttcgctcgggtcatcatccaactccggcaactcgtggcggcgggcgttccttac

0  
5' gtgcatgcaaggagatggcgcccaacagtccccggccacggggcctgccaccatacccacgcccgaaaaca 4970  
0  
3' cacgtacgctcctctaccgcgggttgctcagggggccggtgccccggacgggtggatgggtgcggtcttgt  
0  
5' agcgctcatgagcccgaagtggcgagcccgatcttccccatcgggtgatgtcggcgatataggcggccagca 5040  
0  
3' tcgagagtactcgggcttcaccgctcgggctagaaggggtagccactacagccgctatatccgcggtcgt

0  
5' accgcacctgtggcgccgggtgatgccggccacgatgcgtccggcgtagaggatcgagatcgatctcgatc 5110  
0  
3' tggcgtggacaccgcggccactacggccggtgctacgcaggccgcacatctcctagctctagctagagctag

0  
0  
5' accgcacctgtggcgccgggtgatgccggccacgatgcgtccggcgtagaggatcgagatcgatctcgatc 5110  
0  
3' tggcgtggacaccgcggccactacggccggtgctacgcaggccgcacatctcctagctctagctagagctag

SgrAI





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5' ggccggttctggttctggccatcatgcaccatcatcatcattcttctggtctggtgccacgcggttct  
 3' ccggccaagaccaagaccggtatacgtggttagtagtagtaagaagaccagaccacggtgcgccaaga

**MscI**

**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

5600

5' ggtatgaaagaaaccgctgctgctaaattcgaacgccagcacatggacagcccagatctgggtaccgacg  
 3' ccatactttctttggcgacgacgatttaagcttgcggtcgtgtacctgctcggtctagaccatggctgc

**BstBI** **BglII** **Acc65I** **KpnI**

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

5670

5' acgacgacaaggccatggcgatATCAACAAGTTTGTACAAAAAGCAGGCTctgaaaacttgtactttca  
 3' tgctgctgttccggtaccgctaTAGTTGTTCAAACATGTTTTTTCGTCCGAgacttttgaacatgaaagt

**Enterokinase** **attB1** **TEV site**

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5740

5' aggcACGACAACCCCTGGTGGCGCGGCGCGGTTATTTATCAGGTATAACCCCGCAGTTTGATGGATAACC  
 3' tccgTGCTGTTGGGGGACCACCGCGCCGCGCAATAAATAGTCCATATGGGGGCGTCAAACCTACCTATGG

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5810

5' AATGGCGATGGCATTTGGTGATATTCCCGGCATTATCAAAAAGCTCGACTACATCGCCAGCCTGGGTGTGG  
 3' TTACCGCTACCGTAACCACTATAAGGGCCGTAATAGTTTTTCGAGCTGATGTAGCGGTTCGGACCCACACC

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5880

5' N G D G I G D I P G I I K K L D Y I A S L G V  
 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224



## BGH13\_B04a-pET32-DEST

5' AACTTTTTGCGTACCCAGCCAGATTTAAATTACCACTGTCCGCAAGTGC GCGAGCAAATTTTGCAGGAAG  
 3' TTGAAAAACGCATGGGTGGTCTAAATTTAATGGTGACAGGCGTTCACGCGCTCGTTTAAAACGTCTCTC

6300

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

5' TGGAGTTCTGGTTGAAACGCGGCGTGGATGGTTTGC GCCTTGATGCCATTA ACTTCTGCTTTCACGATAA  
 3' ACCTCAAGACCAACTTTGCGCCGCACCTACCAAACGCGGAACTACGTAATTGAAGACGAAAGTGCTATT

6370

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V E F W L K R G V D G L R L D A I N F C F H D K  
 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' GGAATTGCGTTCCAATCCTGCCAAGCCGGAAGCAGAGCGTAAGGGGCGAGGCTTTAAGGAAGACAACCCC  
 3' CCTTAACGCAAGGTTAGGACGGTTCGGCCTTCGTCTCGCATTCCCCGCTCCGAAATTCCTTCTGTTGGGG

6440

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

5' TACGCATTCCAGAAACACATATTTGATAATACCCGCCCGGAAAACCTGGCTTTCCTGGAGTCCTTGCGCC  
 3' ATGCGTAAGGTCTTTGTGTATAAACTATTATGGGCGGGCCTTTTGGACCGAAAGGACCTCAGGAACGCGG

6510

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

5' AGTTAATGGATCGTTATCCCGGGACGGTAACCCTCGGTGAAATTT CAGCCGAGGACTCCCTGAAAACCAT  
 3' TCAATTACCTAGCAATAGGGCCCTGCCATTGGGAGCCACTTTAAAGTCGGCTCCTGAGGGACTTTTGGTA

6580

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Q L M D R Y P G T V T L G E I S A E D S L K T M  
 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458

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5' GGCGGAATACACCTCCGGTAACGACCGTTTGCATATGGCGTATAGCTTTGAACTGCTGGTCGATAAGTTA  
 3' CCGCCTTATGTGGAGGCCATTGCTGGCAAACGTATACCGCATATCGAAACTTGACGACCAGCTATTCAAT

6650

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

BbvCI

5' TCCGGCAACTATATCCGCAATACGGTGGAAACCCTGGAAGCCAATTTGGCTGAGGGCTGGCCCTGTTGGT  
 3' AGGCCGTTGATATAGGCGTTATGCCACCTTTGGGACCTTCGGTTAAACCGACTCCCGACCGGACAACCA

6720

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S G N Y I R N T V E T L E A N L A E G W P C W  
 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504

5' CTATAGGCAACCACGATGTGGTGGCATTATGTGCGGTTGGGGCGGTGAGGCACAATCCCCGAACTCGC  
 3' GATATCCGTTGGTGCTACACCACGCTAAATACAGCGCAACCCCGCCACTCCGTGTTAGGGGGCTTGAGCG

6790

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S I G N H D V V R F M S R W G G E A Q S P E L A  
 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' CAAAACCCTCAATGCCATGCTGCTTTCATTGCGCGGCAGTGTGTGTAGCTATCAGGGGGAAGAACTGGGT  
 3' GTTTTGGGAGTTACGGTACGACGAAAGTAACGCGCCGTCACACACATCGATAGTCCCCCTTCTTGACCCA

6860

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

5' TTGACAGAAGCGGATATCCAGCAGCATGAGTTGCAAGATCCCTATGGTATTACCTTCTGGCCTCGCTTCA  
 3' AACTGTCTTCGCCATAGGTCGTCGTAACGTTCTAGGGATACCATAATGGAAGACCGGAGCGAAGT

6930

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

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Pasi

5' AGGGGCGCGATGGATGTAGAACGCCAATGCCCTGGGACTCATCCCTGGAATACGCGGGATTTTCCAGTGC  
 3' TCCCCGCGCTACCTACATCTTGCGGTTACGGGACCCCTGAGTAGGGACCTTATGCGCCCTAAAAGGTCACG

7000

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

5' AAAACCATGGCTACCCGTATCGGCAAAACACCTGGCGCTCTCCATCGATAAACAGGAAAGCAATCAGGCA  
 3' TTTTGGTACCGATGGGCATAGCCGTTTTGTGGACCGGAGAGGTAGCTATTTGTCCTTTTCGTTAGTCCGT

7070

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BGH13\_B04a-pDONR221

K P W L P V S A K H L A L S I D K Q E S N Q A  
 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621

5' TCTGTGCTGAACGCCTATCGCCATTTTATGCAGTGGCGTAAAACGCAAGCTGCCCTGCGCTTTGGTGGCA  
 3' AGACACGACTTGCGGATAGCGGTAAAATACGTCACCCGATTTTTCGTTTCGACGGGACGCGAAACCACCGT

7140

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BGH13\_B04a-pDONR221

S V L N A Y R H F M Q W R K T Q A A L R F G G  
 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644

5' TTGAATTTCTCTCCAGTAGTGAATCTCATTTGGTGTGTTGTTTCGTCGCCATGGCAATGAGGCGCTATTGTG  
 3' AACCTAAAGAGAGGTCATCACTTAGAGTAAACCACAAACAAGCAGCGGTACCGTTACTCCGCGATAACAC

7210

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BGH13\_B04a-pDONR221

I E F L S S S E S H L V F V R R H G N E A L L C  
 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668

5' TGGATTTAATTTTCAGTGCCAGCCTGCCGTTATTGAGTTGGGACAAGTGTGTTGGCCTGGAGTCAATAACC  
 3' ACCTAAATTAAGTACGCGGTCGGACGGCAATAACTCAACCCTGTTCAACCCGGACCTCAGTTATTGG

7280

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BGH13\_B04a-pDONR221

G F N F S A Q P A V I E L G Q V L G L E S I T  
 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691

