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3' gactatttacgaagttattataacttttcttctcatactcataagttgtaaaggcacagcgggaataa
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+-----+-----+-----+-----+-----+-----+-----+-----+-----+
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Ap

840

910

980

1050

1120

1190

1260

1330

1400

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0
0
0
0
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0
3' caaatgagtatatatgaaatctaactaaattttgaagtaaaaattaaattttcctagatccacttctagg
0
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0
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0
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5' gaccattcatgttgttgcTcaggtcgcagacgttttgcagcagcagtcgcttcacgttcgctcgcgtatc
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5' tcatgcgcaccCGtggggcccgaatgccggcgataatggcctgcttctcgccgaaacgTTtggtggcggg
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3' aacgcgagtgacgggCGaaaggTcagccctttggacagcacggTcgacgtaattacttagccggTTgcgc
0
0
0
Lac I
←

5' cgaggagaggcggtttgctgatttgggcgcaggggtgggttttctttaccagtgagacggggcaacagct
+
3' gcccctctccgccaacgcataaccgcggtcccaccaaagaaaagtggctactctgccggtgtcga
Lac I

5' gattgcccttcaccgcctggccctgagagagttgcagcaagcgggtccacgctgggtttgccccagcaggcg
+
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Lac I

5' aaaatcctgtttgatgggtggttaacggcgggatataacatgagctgtcttcggtatcgtcgtatcccact
+
3' ttttaggacaaactaccaccaattgccgcccctatatgtactcgacagaagccatagcagcatagggtga
Lac I

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Lac I

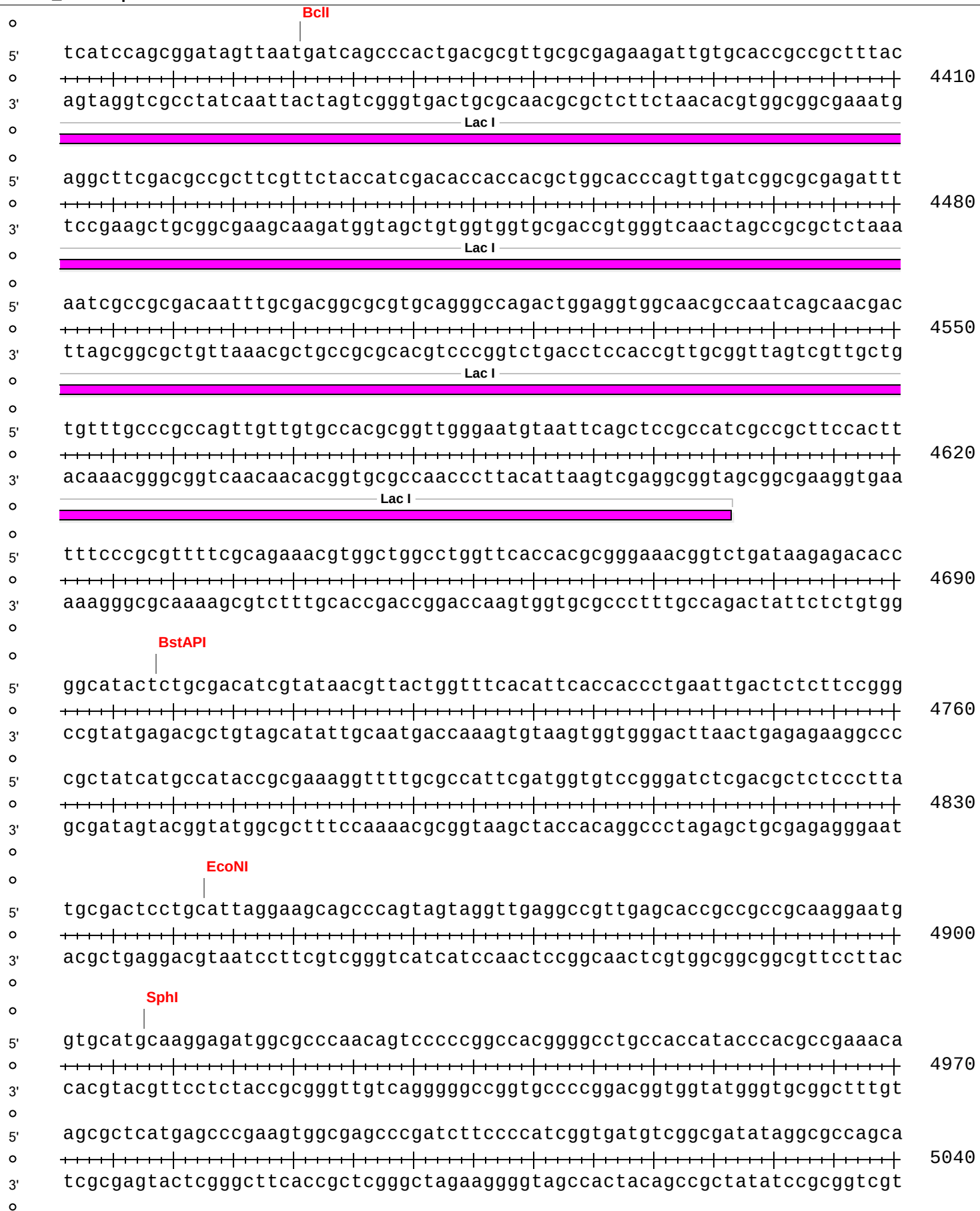
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Lac I

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+
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Lac I

5' ccagccagacgcagacgcgcgagacagaacttaatgggcccgcctaacagcgcgatttgctgggtgacca
+
3' ggtcggctctgcgtctgcgcggctctgtcttgaattaccgggagattgtcgcgctaacgaccactgggt
Lac I

5' atgcgaccagatgctccacgcccagtcgcgtaccgtcttcatgggagaaaataatactgttgatgggtgt
+
3' tacgctgggtctacgaggtgcgggtcagcgcgcatggcagaagtaccctcttttattatgacaactaccaca
Lac I

5' ctggtcagagacatcaagaaataacgccggaacattagtgcaggcagcttccacagcaatggcatcctgg
+
3' gaccagtctctgtagttctttattgcggccttgtaatcacgtccgtcgaagggtgctgttacgtaggacc
Lac I



5110

5180

5250

M	S	D	K	I	I	H	L	T	D	D	S	F	D
1	2	3	4	5	6	7	8	9	10	11	12	13	14

5320

T	D	V	L	K	A	D	G	A	I	L	V	D	F	W	A	E	W	C	G	P	C	K	M
15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38

5390

I	A	P	I	L	D	E	I	A	D	E	Y	Q	G	K	L	T	V	A	K	L	N	I
39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61

5460

D	Q	N	P	G	T	A	P	K	Y	G	I	R	G	I	P	T	L	L	L	F	K	N
62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84

5' gtgaagtggcggcaaccaaagtgggtgcactgtctaaaggtcagttgaaagagttcctcgacgctaacct
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' cacttcaccgccgttggtttcaccacgtgacagatttcagtcaactttctcaaggagctgcgattgga
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

The diagram shows a DNA double helix with the following sequence:

Top strand (5' to 3'): ggtatgaaagaaaccgctgctgctaaattcgaacgccagcacatggacagcccagatctgggtaccgacg

Bottom strand (3' to 5'): ccatactttctttggcgacgacgatttaagcttgcggtcgtgtacctgtcgggtctagacccatggctgc

A BglII restriction site is indicated by a red vertical line at position 149, labeled "BglII".

An enzyme binding site is indicated by a pink box labeled "En...e" at the end of the bottom strand.

Below the DNA sequence, a protein sequence is shown with amino acid single-letter codes and their corresponding positions:

Position	Amino Acid
132	G
133	M
134	K
135	E
136	T
137	A
138	A
139	A
140	K
141	F
142	E
143	R
144	Q
145	H
146	M
147	D
148	S
149	P
150	D
151	L
152	G
153	T
154	D

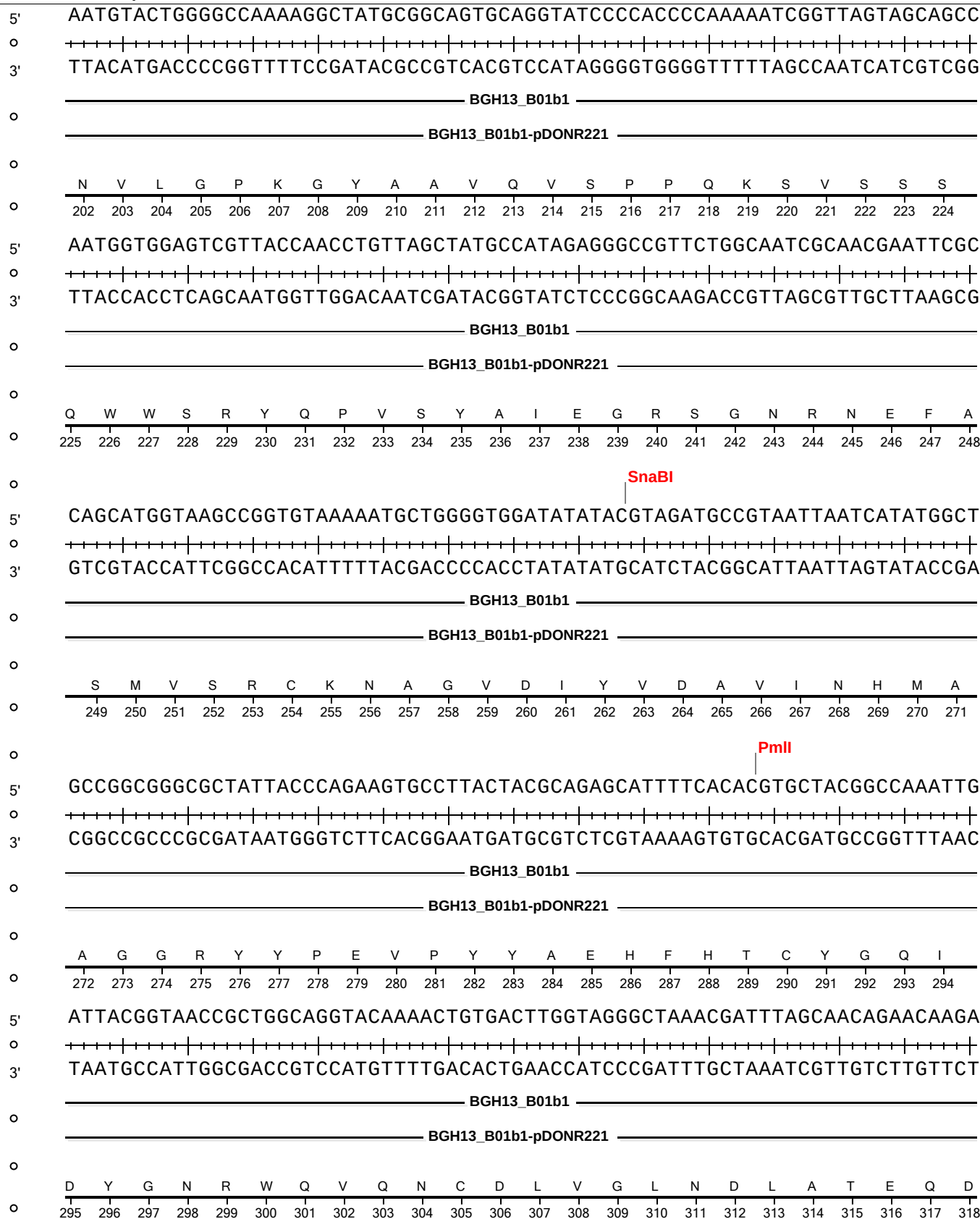
5' aggcCAACCGCGAACCGCGTTTCGTTCAATTTGTTTCAATGGCAGTGGAAACGATATTGCTAGCGAGTGC₁₇₉AA
3' tccgGTTGGCGCTTGGCGCAAGCAAGTAAACAAGCTTACCGTCACCTTGCTATAACGATCGCTCACGCTT

 **BGH13_B01b1**

BGH13_B01b1-pDONR221

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

BGH13_B01b1-pET32-DEST



5880

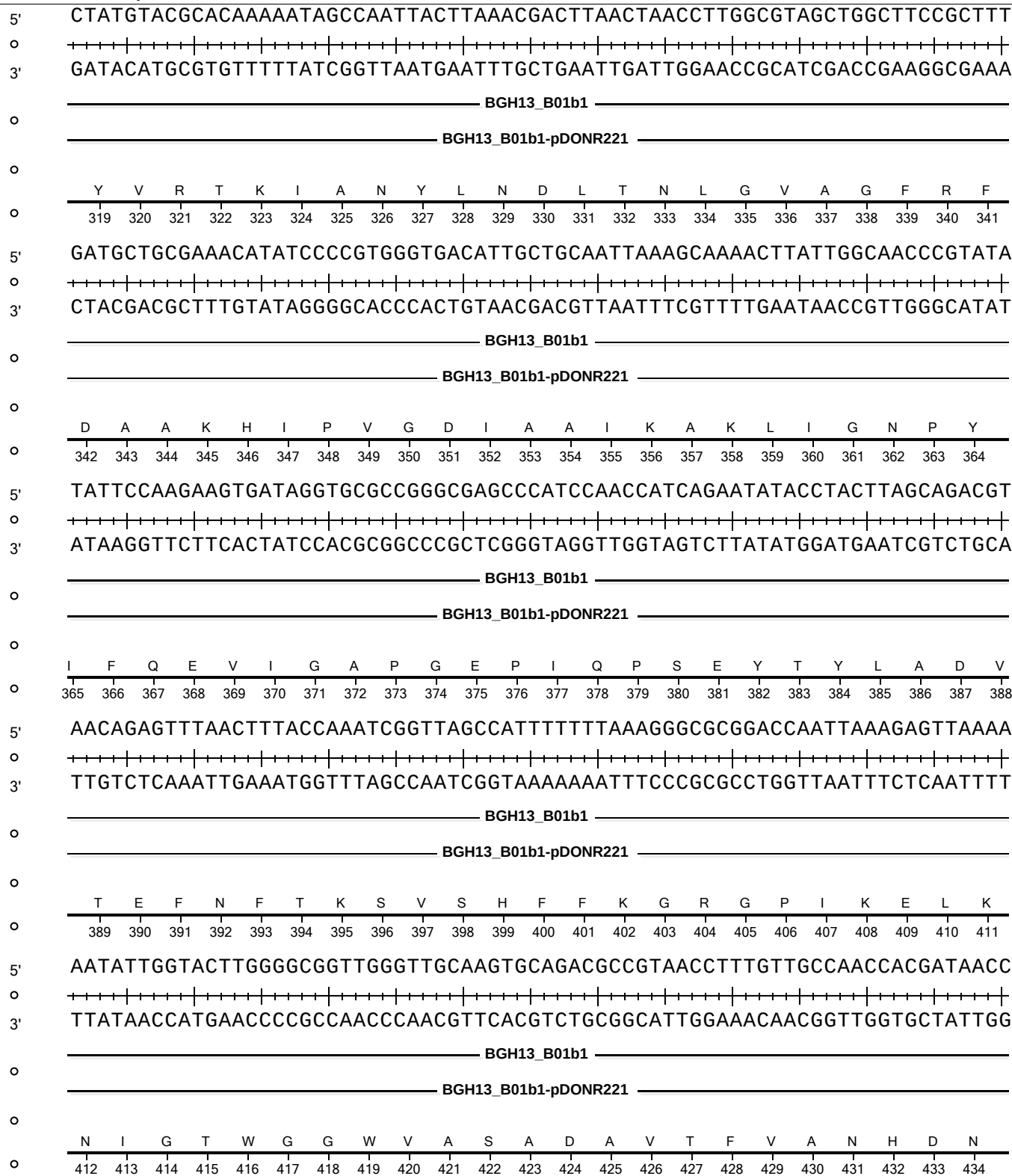
5950

6020

6090

6160

BGH13_B01b1-pET32-DEST



6230

6300

6370

6440

6510

5' AGCGCCAGGATACAACAACACCATTTACCCATAAAGATGGTGATAAACCGAATACTATGGCGCACGTATT
+
3' TCGCGGTCCTATGTTTGTGTGGTAATGGGTATTTCTACCACTATTGGCGTTATGATACCGCGTGCATAA
BGH13_B01b1
BGH13_B01b1-pDONR221

Q R Q D T N N T I T H K D G D N R N T M A H V F
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' TATGCTGGGCTGGCCCTATGGGTACCCTAAAGTAATGTCTAGTTATGAGTGGTACGATCACGACCAAGGC
+
3' ATACGACCCGACCGGGATACCCATGGGATTTTCATTACAGATCAATACTCACCATGCTAGTGCTGGTTCGG
BGH13_B01b1
BGH13_B01b1-pDONR221

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

5' CCTCCCGCCACGGTGCTAGCAGCTGTAACAGCGGCTGGTTATGTGAACACCGCACGCCAGCTATCGCCA
+
3' GGAGGGCGGGTGCCACGATCGTCGACATTGTCGCCGACCAATACACTTGTGGCGTGCGGTCGATAGCGGT
BGH13_B01b1
BGH13_B01b1-pDONR221

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

5' ATATGGTTGCTTTTCGCAATTTCACTGCAGACGAATTTTCGCGTAACCAACTATTGGGATAACGGCAACAA
+
3' TATACCAACGAAAAGCGTTAAAGTGACGTCTGCTTAAAGCGCATTGGTTGATAACCCTATTGCCGTTGTT
BGH13_B01b1
BGH13_B01b1-pDONR221

N M V A F R N F T A D E F R V T N Y W D N G N N
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' TCAAATAGCTTGGGGCCGAGGCGGCAAGGGTTTGTAGTTATAAATATGGAAGGCAACAATTTAACCCGT
+
3' AGTTTATCGAACCCCGGCTCCGCCGTTTCCCAAACATCAATATTTATACCTTCCGTTGTTAAATTGGGCA
BGH13_B01b1
BGH13_B01b1-pDONR221

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

BGH13_B01b1-pET32-DEST

