















BGH02\_B01c-pET32-DEST

5' agcgctcatgagcccgaagtggcgagcccgatcttccccatcggtgatgtcggcgatatagggcggcagca  
 0 ++++++  
 3' tcgcgagtactcgggcttcaccgctcgggctagaaggggtagccactacagccgctatatccgcggtcgt

5040

SgrAI

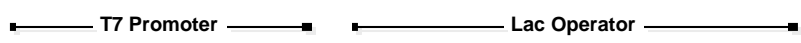
5' accgcacctgtggcgccgggtgatgccggccacgatgcgctccggcgtagaggatcgagatcgatctcgatc  
 0 ++++++  
 3' tggcgtggacaccgcgccactacggccgggtgctacgcaggccgcacatctcctagctctagctagagctag

5110

XbaI

5' ccgcgaaattaatacgaactcactataggggaattgtgagcggataacaattcccctctagaataatttt  
 0 ++++++  
 3' ggcgctttaattatgctgagtgatatccccttaacactcgctattgttaaggggagatctttattaaa

5180



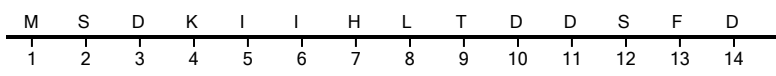
BamHI

BamHI

5' gtttaactttaagaaggagatatacatatgagcgataaaattattcacctgactgacgacagttttgaca  
 0 ++++++  
 3' caaattgaaattcttccctctatatgtataactcgctattttaataagtgactgactgctgtcaaaactgt

5250

Trx Tag

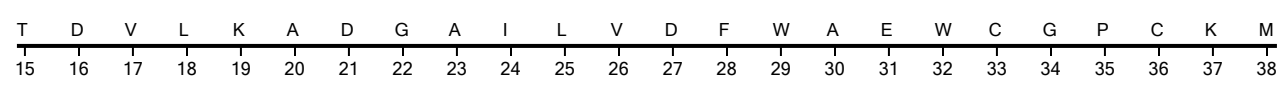


RsrII

5' cggatgtactcaaagcggacggggcgatcctcgtcgatttctgggcagagtgggtgcgggtccgtgcaaaat  
 0 ++++++  
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5320

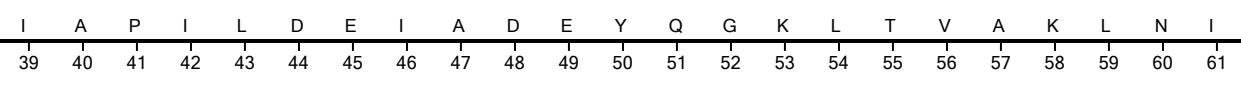
Trx Tag



5' gatcgccccgattctggatgaaatcgctgacgaatatcagggcaaaactgaccggttgcaaaactgaacatc  
 0 ++++++  
 3' cttagcggggctaagacctactttagcgaactgcttataagctcccgtttgactggcaacgttttgactttag

5390

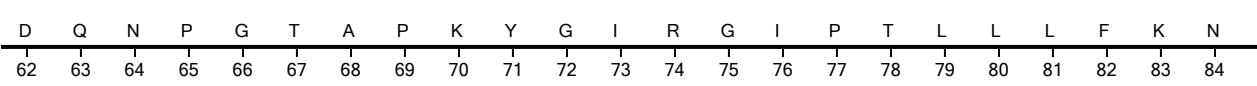
Trx Tag



5' gatcaaaaccctggcactgcgccgaaatatggcatccggtgatcccgactctgctgctgttcaaaaacg  
 0 ++++++  
 3' ctagttttgggaccgtgacgcggctttataccgtaggcaccatagggctgagacgacgacaagtttttgc

5460

Trx Tag





BGH02\_B01c-pET32-DEST

5' gtgaagtggcggcaaccaaaagtgggtgcaactgtctaaaggtcagttgaaagagttcctcgacgctaacct  
 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

Acc65I

KpnI

5' ggtatgaaagaaaccgctgctgctaaattcgaacgccagcacatggacagcccagatctgggtaccgacg  
 3' ccatactttcttggcgacgacgatttaagcttgcggtcgtgtacctgtcgggtctagacctatggctgc  
 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' acgacgacaaggccatggcgatATCAACAAGTTTGTACAAAAAAGCAGGCTctgaaaacttgtactttca  
 3' tgctgctgttccggtaccgctaTAGTTGTTCAAACATGTTTTTTCGTCCGAgacttttgaacatgaaagt  
 Enterokinase attB1 TEV site

5740

BGH02\_B01c-pDONR221

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' aggcCTTTATCCTAAAGAGAGTGAAACAAGAGAGGTAAAGGATTTGTCAGGAGTGTGGGAGTTTAGAAC  
 3' tccgGAAATAGGATTTCTCTCACTTTGTTCTCTCCATTTCTAAACAGTCCTCACACCCTCAAATCTTGG  
 BGH02\_B01c

5810

BGH02\_B01c-pDONR221

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

BGH02\_B01c-pET32-DEST

5' GAATCTGATAAAAATTATATCCTCATGCCAGTTCCTGCAAGTTTAAACGACATCACACAAGATATTAATT  
 3' CTTAGACTATTTTAAATATAGGAGTACGGTCAAGGACGTTCAAATTTGCTGTAGTGTGTTCTATAATTAA

5880

BGH02\_B01c

BGH02\_B01c-pDONR221

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

AgeI

5' TAAGAGATTATGTTGGCAGAGTATATTATAAAAAATCCTTCTTTATACCGGTTTATTGGAAAGAAAGAAA  
 3' ATTCTCTAATAACAACCGTCTCATATAATATTTTTTAGGAAGAAATATGGCCAAATAACCTTCTTTCTTT

5950

BGH02\_B01c

BGH02\_B01c-pDONR221

L R D Y V G R V Y Y K K S F F I P V Y W K E R N  
 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' TATTTTTTTGAGGGTGGGAGCAGCAGCTCATTTTTCTGAGGTTTATGTAAATGGTAATTTAGTGAATAAA  
 3' ATAAAAAACTCCACCTCGTCTGAGTAAAAAGACTCCAAATACATTTACCATTAATCACTGATTT

6020

BGH02\_B01c

BGH02\_B01c-pDONR221

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

5' CACAAAGGAGGATTTCTTCTTTCGAGGCAGAGATCTCTAAATTTGTAAATTATGGACAAGAAAATATTA  
 3' GTGTTTCTCTCTAAAGAAGGAAAGCTCCGTCTCTAGAGATTTAAACATTTAATACCTGTTCTTTTATAAT

6090

BGH02\_B01c

BGH02\_B01c-pDONR221

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

5' TAGAAATTATGGTAGACAACACTTTAACTTGGGATGTTCTTCTCTCGGAGAATTAAAAGTTATTGAGGA  
 3' ATCTTTAATACCATCTGTTGTGAAATTGAACCCTACAAGAAGGAGGACCTCTTAATTTTCAATAACTCCT

6160

BGH02\_B01c

BGH02\_B01c-pDONR221

I E I M V D N T L T W D V L P P G E L K V I E D  
 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318

BGH02\_B01c-pET32-DEST

NsiI

5' CGAAATGCATCCTAAAGGATATAAGGTTTTGAATTATTATTTTGATTTTTTTAATTACTCTGGAATTCAC  
 3' GCTTTACGTAGGATTTCCCTATATTCCAAAACCTTAATAATAAAACTAAAAAATTAATGAGACCTTAAGTG

6230

BGH02\_B01c

BGH02\_B01c-pDONR221

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

Bsu36I

5' AGGCCTGTGGTAATATATAACCACTCCTAAGGTATATATTAAGATTTTTCTGTTATTACTGAACTAAGTA  
 3' TCCGGACACCATTATATATGGTGAGGATTCCATATATAATTTCTAAAAAGACAATAATGACTTGATTCAT

6300

BGH02\_B01c

BGH02\_B01c-pDONR221

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

5' ATAATTCTGCATTGGTAAAGTACAGTATTGAAAGTGAAGTAATAATTTTCAAGTTATTTTAAGAGATAA  
 3' TATTAAGACGTAACCATTTTCATGTCATAACTTTCACTTCCATTATTAAGTTCAATAAAATTTCTCTATT

6370

BGH02\_B01c

BGH02\_B01c-pDONR221

N N S A L V K Y S I E S E G N N F Q V I L R 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' AGATAAAAATATAGTAGCAGAGAATTTTGGTAAATCAGGAGTTTGTAGAGGTAAAAAATCCAAAATTATGG  
 3' TCTATTTTTATATCATCGTCTCTTAAAACCATTTAGTCCTCAAAATCTCCATTTTTTAGGTTTAAATACC

6440

BGH02\_B01c

BGH02\_B01c-pDONR221

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

5' GAGCCTGGAAATCCTTATCTATATAATTTAGAGATTAAACTTTTGGAAAAAGACAACCTTTGATATTTATA  
 3' CTCGGACCTTTAGGAATAGATATATTAATCTCTAATTTGAAAACCTTTTTCTGTTGAACTATAAATAT

6510

BGH02\_B01c

BGH02\_B01c-pDONR221

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





BGH02\_B01c-pET32-DEST

5' TATTTCTGGATTTTCATTCTGATCCTCCCTTAATGTTTACAGAGGAGTATCAACAAGAGATGATTA AAAAGA  
 3' ATAAAGACCTAAAGTAAGACTAGGAGGGAATTACAAATGTCTCCTCATAGTTGTTCTCTACTAATTTTCT

7280

BGH02\_B01c

BGH02\_B01c-pDONR221

I S G F H S D P P L M F T E E Y Q Q E M I K R  
 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691

5' TTTGTGGGAGTTCTTGACAGGCTTGATTTTGTGTGGGAGAGCATATTTGGAATTTTGCTGATTTTATGA  
 3' AAACACCCTCAAGAACTGTCCGAATAAAACAACACCCTCTCGTATAAACCTTAAAACGACTAAAATACT

7350

BGH02\_B01c

BGH02\_B01c-pDONR221

F V G V L D R L D F V V G E H I W N F A D F M  
 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714

5' CGAAACAGAGTATAACGAGGGTAGTGGCAATAAGAAAGGGGTTTTTACAAGGAATAGACAGCCTAAAAT  
 3' GCTTTGTCTCATATTGCTCCCATCACCCGTTATTCTTTCCCAAAAATGTTTCTTATCTGTCTGGATTTTA

7420

BGH02\_B01c

BGH02\_B01c-pDONR221

T K Q S I T R V V G N K K G V F T R N R Q P K M  
 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738

5' GGTGGCTCATT TTTTGAAAGAGAGATGGAGTAAATTACCTGATTTTGGGAAAAATAGGACCCAGCTTTC  
 3' CCACCGAGTAAAAACTTTCTCTCTACCTCATTTAATGGACTAAAAACCCTTTTATCCTGGGTCGAAAG

7490

BGH02\_B01c

attB2

BGH02\_B01c-pDONR221

V A H F L K E R W S K L P D F W E K  
 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757

BamHI

EcoRI  
SacI

Sall

HindIII

NotI  
EagI

PspXI  
XhoI  
AvaI  
BmeT110I

5' TTGTACAAAGTGGTTGATatcggatccgaattcgaagctccgctcgacaagcttgcgcccgcaactcgagcac  
 3' AACATGTTTACCAACTAtagcctaggcttaagctcgaggcagctgttcgaacgccggcgtgagctcgtg

7560

attB2

5' caccaccaccactgagatccggctgctaacaagcccgaaaggaagctgagttggctgctgccaccg  
 3' gtggtggtggtggtgactctaggccgacgattgtttcgggctttccttcgactcaaccgacgacggtggc

7630

