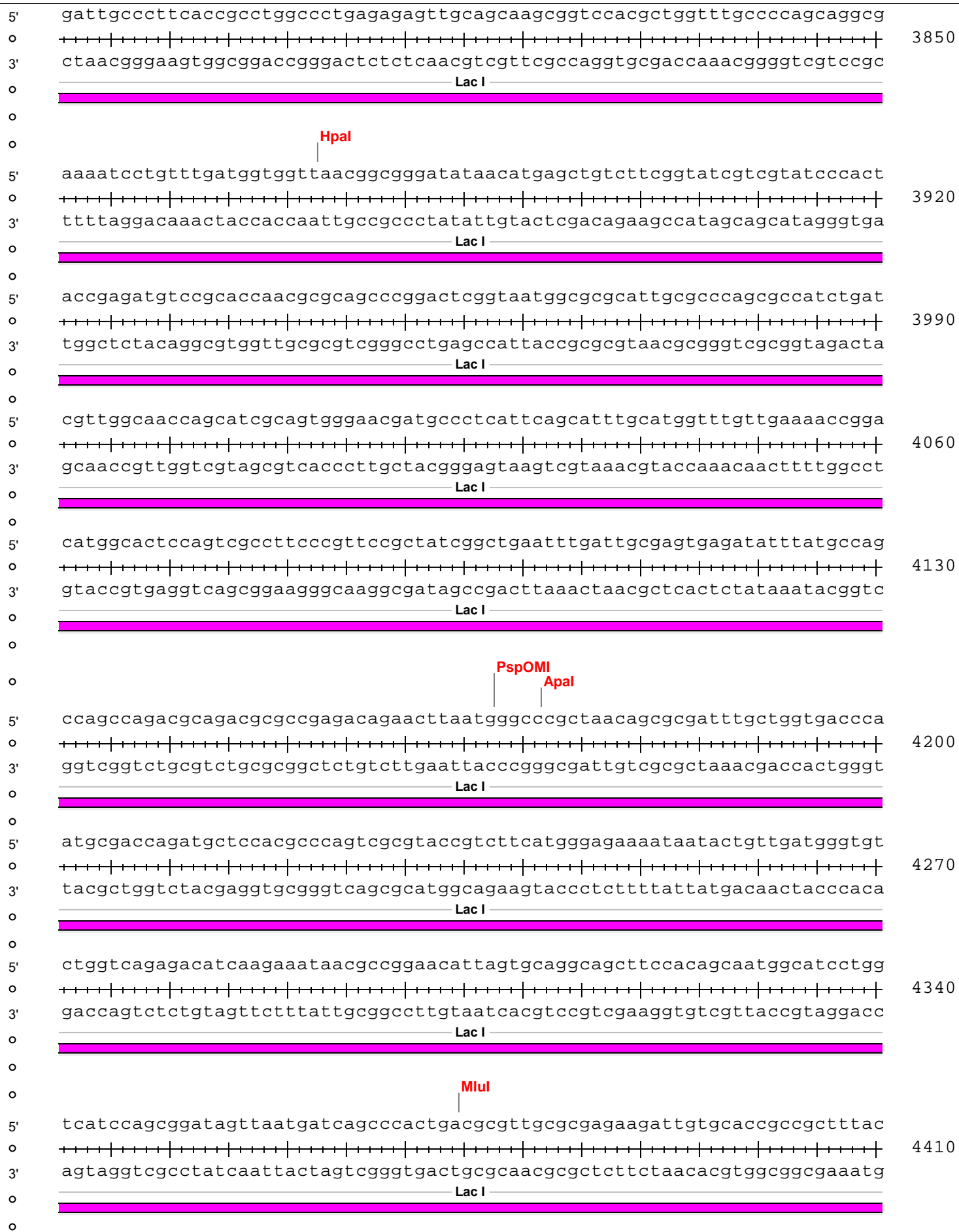


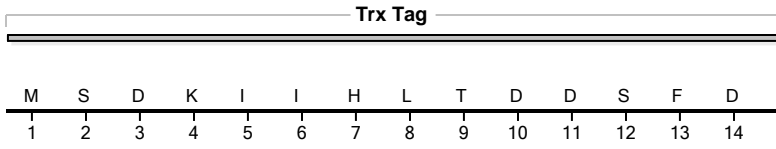
BGT25_T02a1-pET32-DEST



BGT25_T02a1-pET32-DEST

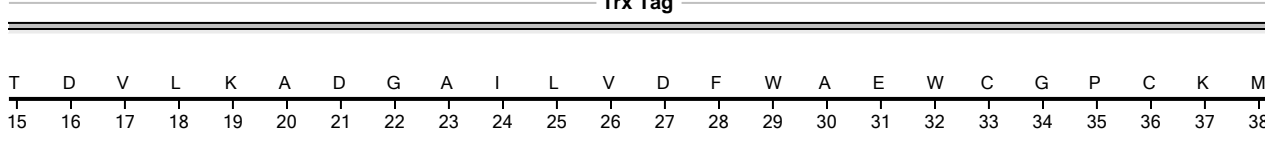
5' gtttaactttaagaaggagatatacatatgagcgcataaaattattcacctgactgacgacagttttgaca
 3' caaattgaaattcttctctatatagtatactcgctattttaataagtggactgactgctgtcaaaactgt

5250



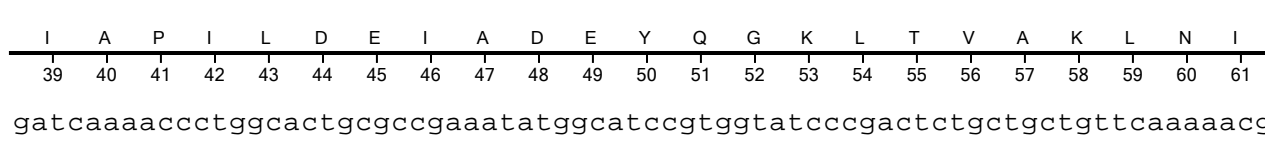
5' cggatgtactcaaagcggacggggcgatcctcgtcgatttctgggcagagtgggtgcggtccgtgcaaaat
 3' gcctacatgagtttcgctgccccgctaggagcagctaaagaccctctcaccacgccaggcacgtttta

5320



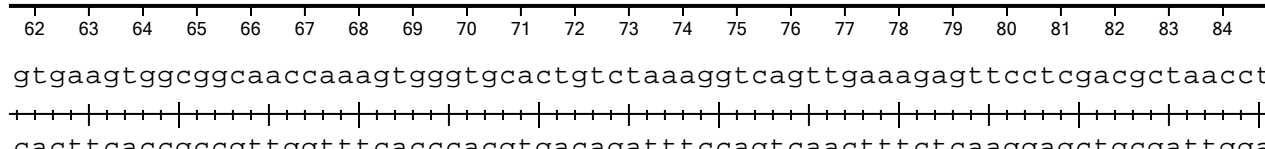
5' gatcgccccgattctggatgaaatcgctgacgaatatcagggcaaaactgaccgttgcaaaactgaacatc
 3' ctagcggggctaagacctactttagcgcactgcttatagtcctcgtttgactggcaacgttttgacttgtag

5390



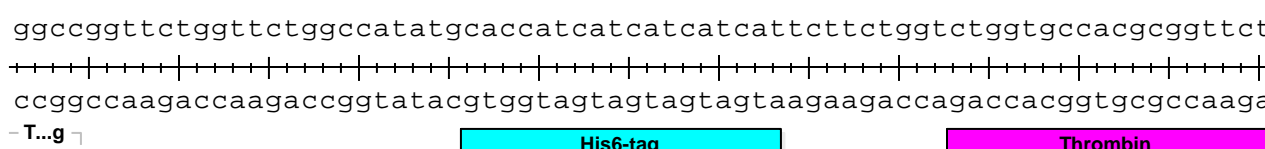
5' gatcaaaaccctggcactgcgcgaaatatggcatccgtgggtatcccgactctgctgctgttcaaaaacg
 3' ctagttttgggaccgtgacgcggctttataccgtaggcaccatagggtgagacgacgacaagtttttgc

5460



5' gtgaagtggcggcaaccaaagtgggtgcactgtctaaaggctcagttgaaagagttcctcgacgctaacct
 3' cacttcaccgccggttggtttcaccacgtgacagatttccagtcactttctcaaggagctgcgattgga

5530



5' ggccggttctgggttctggccatatgcaccatcatcatcattcttctgggtctgggtgccacgcggttct
 3' ccggccaagaccaagaccggtatacgtggtagtagtagtaagaagaccagaccacgggtgcgccaaga

5600



5' ggtatgaaagaaaccgctgctgctaaattcgaacgccagcacatggacagcccagatctgggtaccgacg
 3' ccatactttctttggcgacgacgatttaagcttgcggtcgtgtacctgtcgggtctagacccatggctgc

Acc65I
KpnI

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

5670

5' acgacgacaaggccatggcgatATCAACAAGTTTGTACAAAAAAGCAGGCTctgaaaacttgtactttca
 3' tgctgctgttccgggtaccgctaTAGTTGTTCAAACATGTTTTTTCGTCCGAgacttttgaacatgaaagt

Enterokinase attB1 TEV site

BGT25_T02a1-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

5740

5' aggcAGCACCATCGGCCTGTGCATGATTGTCAAGAACGAGACGAAGGTCATCCTGCAATGCCTCGCCAGC
 3' tccgTCGTGGTAGCCGGACACGTACTAACAGTTCTTGCTCTGCTTCCAGTAGGACGTTACGGAGCGGTTCG

T... GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

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

5810

5' GTGCTCCCCCTTGTGCGACTACGTGCTCATCGTCGACACCGGTTCCGAGGACGGCAGCAAGACCTGATAC
 3' CACGAGGGGGAACAGCTGATGCACGAGTAGCAGCTGTGGCCAAGGCTCCTGCCGTGCGTTCTGGACTATG

Agel

GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

5880

5' V L P L V D Y V L I V D T G S E D G T Q D L I
 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224

5' GCGGCTTTCTCGCCGATAACGGTGTCCAAGGCGCTGTCATTGACGAGCCATGGCGGGACTTCGCGTACAA
 3' CGCCGAAAGAGCGGCTATTGCCACAGGTTCCGCGACAGTAACTGCTCGGTACCGCCCTGAAGCGCATGTT

GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

5950

5' R G F L A D N G V Q G A V I D E P W R D F A Y 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

BGT25_T02a1-pET32-DEST

5' CCGGACCTTCGCCCTTGAACGATTGCGTAAAGTCGAGACTGTGCGACTATGCAATGATCATCGACGCGGAC
 0 ++++++
 3' GGCCTGGAAGCGGGAACCTTGCTAACGCATTTTCAGCTCTGACAGCTGATACGTTACTAGTAGCTGCGCCTG

GT2?

0 _____ **BGT25_T02a1** _____

0 _____ **BGT25_T02a1-pDONR221** _____

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

6020

5' GATGTTCTGATCCGGGACGCCGACTTTCGATCCGATCAGGTTCAAGTCGCAGATGGAACACGATTTTATACG
 0 ++++++
 3' CTACAAGACTAGGCCCTGCGGCTGAAGCTAGGCTAGTCCAAGTTCAGCGTCTACCTTGTGCTAAATATGC

GT2?

0 _____ **BGT25_T02a1** _____

0 _____ **BGT25_T02a1-pDONR221** _____

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

6090

5' ACGTCGAGGTGTTACATGGTGGCATTTCGTTTTATCGCCCGCAGATCTGCCGCAACCGTCTGCCGTTTCG
 0 ++++++
 3' TGCAGCTCCACAATGTACCACCGTAAAGCAAATAGCGGGCGTCTAGACGGCGTTGGCAGACGGCAAGCG

GT2?

0 _____ **BGT25_T02a1** _____

0 _____ **BGT25_T02a1-pDONR221** _____

D V E V L H G G I S F Y R P Q I C R N R L P F A
 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318

6160

5' CTTCAAGGGCGTCTGCACGAATATCTCGAGGCCCTCCTGGCCATCTCACGCGGGAGACCGCCAAGGGT
 0 ++++++
 3' GAAGTTCCTCCGACGACGTGCTTATAGAGCTCCGGGGAGGACCGGTAGAGTGCGCCCTCTGGCGGTTCCCA

GT2?

0 _____ **BGT25_T02a1** _____

0 _____ **BGT25_T02a1-pDONR221** _____

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

6230

Bael' Bael'

5' TTTCGCGTGGCGACGGGGCGTGGCGGAGCACGCAGTCAAACCCACGAAAGTACCAGGACGACTCGGCCG
 0 ++++++
 3' AAAGCGCACCCTGCCCCGCACCGCCTCGTGCCTCAGTTTTGGGTGCTTTCATGGTCCTGCTGAGCCGGC

GT2?

0 _____ **BGT25_T02a1** _____

0 _____ **BGT25_T02a1-pDONR221** _____

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

6300

BGT25_T02a1-pET32-DEST

5' TTCTTGAAAATGCGCTTGCAACGGAGACCGACCCCTTCTTGTTTCGCGATAACACCTTCTATCTGGCGCA
 6370
 3' AAGAACTTTTACGCGAACGTTGCCTCTGGCTGGGGAAAAGAACAAGCGCTATGTGGAAGATAGACCGCGT

GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

V L E N A L A T E T D P F L V S R Y T F Y L A Q
 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' GAGCTACAGGGATTCCGGCGAGCGTGAAAAATCACTCGCGAACTATCTGAAGCGCGCCGATCTAGGTTTT
 6440
 3' CTCGATGTCCCTAAGGCCGCTCGCACTTTTGTAGTGAGCGCTTGATAGACTTCGCGCGGCTAGATCCAAAA

GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

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

5' TGGGACGAGGAGGTCTATGTCAGCCTGCTTGAGGCGGGCAACCTCATGGCAGCATTGGGGCGGCCATTTCG
 6510
 3' ACCCTGCTCCTCCAGATACAGTCGGACGAACTCCGCCCGTTGGAGTACCGTCGTAACCCCGCCGTAAGC

GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

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

BspMI

5' ACGAGGTCGTTGCCGCCTTTGAGCGCGCGGCGCAGGTCGTCCCCGCCCGCGCGGAGGCTCTACACGCTGC
 6580
 3' TGCTCCAGCAACGGCGGAACTCGCGCGCCGCGTCCAGCAGGGGCGGGCGCGCCTCCGAGATGTGCGACG

GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

D E V V A A F E R A A Q V V P A R A E A L H A A
 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' GAGCCTCTATTGCCGCAACCAGGGCCGGAATGCGGAAGGAACGGAATTTGCGCGTCGAGGGCTCGACCTT
 6650
 3' CTCGGAGATAACGGCGTTGGTCCCAGCCTTACGCCTTCCTTGCCCTTAAACGCGCAGCTCCCAGCTGGAA

GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

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

BGT25_T02a1-pET32-DEST

Pasi

o

5' GTTCAACCCGCGGACTTTTCATTCAGCCCTGGGTTTACGATTACGGACTGCTCGACGAGTTTGCTGTCA
 3' CAAGTTGGGCGGCCTGAAAAGTAAGTCGGGACCCAAATGCTAATGCCTGACGAGCTGCTCAAACGACAGT

6720

GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

o

V Q P A G L F I Q P W V Y D Y G L L D E F 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' ATGCCTACTGGGCAGGCGCCTACCGGGAATCGCTCGACGCTTGTCTAAAATTGCTCGCCTCCGACAAATT
 3' TACGGATGACCCGTCCGCGGATGGCCCTTAGCGAGCTGCGAACAGATTTTAAACGAGCGGAGGCTGTTTAA

6790

GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

o

N A Y W A G A Y R E S L D A C L K L L A S D K L
 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' GCCTGCGGAAATGGCGAAGCGTGTGGTGGCCAACGCTCGCTTCGCCACCGGCAAGCTTCCGGTCAATGAG
 3' CGGACGCCTTTACCGCTTCGCACACCACCGGTTGCGAGCGAAGCGGTGGCCGTTTCAAGGCCAGTTACTC

6860

GT2?

BGT25_T02a1

procol...enase

BGT25_T02a1-pDONR221

o

P A E M A K R V V A N A R F A T G K L P V N E
 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551
 5' CCGCCGAAACTTGGGGCGTTCGGGACCGAGAGCTTGATCGACCAGCACAGGCTTGTCCGGCAGCGGTTCGT
 3' GGCGGCTTTGAACCCCGCAAGCCCTGGCTCTCGAACTAGCTGGTTCGTGTCCGAACAGGCCGTCGCCAGCA

6930

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

o

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

BGT25_T02a1-pET32-DEST

5' TGCGGTCGCGCATCGAGGGCACGCCGCGCATCCTGGTGACAATCCTCGCAAAGCAGAAAGAGCCGGCACT
 0 ++++++
 3' ACGCCAGCGCGTAGCTCCCGTGCGGCGCGTAGGACCACTGTTAGGAGCGTTTCGTCTTTCTCGGCCGTGA

7000

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

L R S R I E G T P R I L V T I L A K Q K E P A L
 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' GCCGCTGTACCTCGAGTGCATCGAGGCGCTCGACTACCCCAAGGCGTCGATCGTCCTGTACATCAGGACA
 0 ++++++
 3' CGGCGACATGGAGCTCACGTAGCTCCGCGAGCTGATGGGGTTCCGCAGCTAGCAGGACATGTAGTCCTGT

7070

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

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

5' AACAAACACCGACAGGACCGAGCACATACTGCGCGAATGGGTGGAGCGCGTTGGTCACCTCTATGCCG
 0 ++++++
 3' TTGTTGTTGTGGCTGTCCTGGCTCGTGTATGACGCGCTTACCCACCTCGCGCAACCAGTGGAGATACGGC

7140

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

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

5' CGGTTGAATTTCGATGCCTCCAACGTGGCCGATAGAGTCGAGCAGTTTGGCGAACACGAATGGAACGAGAC
 0 ++++++
 3' GCCAACTTAAGCTACGGAGGTTGCACCGGCTATCTCAGCTCGTCAAACCGCTTGTGCTTACCTTGCTCTG

7210

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

A V E F D A S N V A D R V E Q F G E H E W N E T
 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' GCGCTTCAGGGTGCTTGGCCGAATCCGCAACATAAGTTTGC GGAAA CTCTCGAACACAGCTGCGATTTTC
 0 ++++++
 3' CGCGAAGTCCCACGAACCGGCTTAGGCGTTGTATTCAAACGCCTTTTGAGAGCTTGTGTGCTGACGCTAAAG

7280

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

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

BGT25_T02a1-pET32-DEST

o

5' TATTTTCGTTGCCGACGTCGATAATTTTCGTGCGACCGGCCACGCTACGCGAGCTTGTTCGCGCTCGACGTGC

o

3' ATAAAGCAACGGCTGCAGCTATTAAGCACGCTGGCCGGTTCGATGCGCTCGAACAGCGCGAGCTGCACG

BmgBI

7350

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

Y F V A D V D N F V R P A T L R E L V A L D V

692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714

o

5' CGATCGTCGCTCCCCTGCTTCGCTCCATCTCTCCCGGGCAATACTATTCGAACTACCACGCCGAAATCGA

o

3' GCTAGCAGCGAGGGGACGAAGCGAGGTAGAGAGGGCCCGTTATGATAAGCTTGATGGTTCGCGCTTTAGCT

XmaI
SmaI

7420

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

P I V A P L L R S I S P G Q Y Y S N Y H A E I D

715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738

o

5' CGCCAACGGCTACTATATGCAGTGCATCAATATGGGTGGGTGCTCAACCGCCACGTGCGCGCATTATC

o

3' GCGGTTGCCGATGATATACGTCACGCTAGTTATACCCACCCACGAGTTGGCGGTGCACGCGCCGTAATAG

PmlI

7490

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

A N G Y Y M Q C D Q Y G W V L N R H V R G I I

739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761

o

5' GAGATGCCGCTTGTGCACTGCACCTATCTTGTCCGCGCCGACGTAAGTCCCGAAGTACATACGAGGACG

o

3' CTCTACGGCGAACACGTGACGTGGATAGAACAGGCGCGGCTGCATGACGGGCTTGACTGTATGCTCCTGC

7560

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

E M P L V H C T Y L V R A D V L P E L T Y E D

762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784

BGT25_T02a1-pET32-DEST

5' CGACATCGCGCTACGAGTACGTGATCTTTGCCGACAGCGCCCGCAAGGCCGGCATCGTCCAGTATATGGA
 0 ++++++
 3' GCTGTAGCGCGATGCTCATGCACTAGAAACGGCTGTCGCGGGCGTTCGCGCCGTAGCAGGTCATATACCT

7630

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

A T S R Y E Y V I F A D S A R K A G I V Q Y M D
 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808

5' TAACCGACAAGTCTATGGCTACATCACCTTCGGCGATGGCCAATATTATGTGAGTGACGGGATCGAGCGC
 0 ++++++
 3' ATTGGCTGTTTCAGATACCGATGTAGTGGAAGCCGCTACCGGTTATAATACTCACTGCCCCTAGCTCGCG

7700

BGT25_T02a1

procollagen-lysine 5-dioxygenase

GT25?

BGT25_T02a1-pDONR221

N R Q V Y G Y I T F G D G Q Y Y V S D G I E R
 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831

5' GCCCCGAGCGCTGTTGCACGGTGCCGGCGACACGCCGGTATTCCTGCGCCACGCCTCCGGGCGCCGTAC
 0 ++++++
 3' CGGGCTCGCGACAACGTGCCACGGCCGCTGTGCGGCCATAAGTGACGGCGGTGCGGAGGCCCGCGGCATG

7770

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

A R A L L H G A G D T P V F T A A T P P G A V
 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854

5' CGATGCCAGATCGACATGTCGAGCCGCCGCAAATTCACCTAATAAACTTGGACAGCAGCGTCGAGCGCTG
 0 ++++++
 3' GCTACGGTCTAGCTGTACAGCTCGGCGGCGTTTAAAGTGATTATTTGAACCTGTCGTGCGAGCTCGCGAC

7840

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

P M P D R H V E P P Q I H L I N L D S S V E R W
 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878

BGT25_T02a1-pET32-DEST

SgrDI

5' GCGCAAATATCAAGATAGGAATCCTCATCTAGCCGCCAATACAATTCGGGTATCGGCCGTCGACGGAGCA
 3' CGCGTTTATAGTTCTATCCTTAGGAGTAGATCGGCGGTTATGTTAAGCCCATAGCCGGCAGCTGCCTCGT

7910

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

R K Y Q D R N P H L A A N T I R V S A V D G A
 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901

5' TCCCTCGATAGGTGACCTTGCAAGCCTTGGTGGACGATGGAGTGATTGCCGAGGATTGCGGGTATCTGC
 3' AGGGAGCTATCCAGCTGGAACGTTTCGGAACCACCTGCTACCTCACTAACGGCTCCTAACGCCCATAGACG

7980

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

S L D R S T L Q A L V D D G V I A E D C G Y L
 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924

5' CGGGCGCATTGGGATGTGCTCTATCGCACATCAACTTGTGGAAGTTAGCGGTATCCGAGAAGCGGCCAAT
 3' GCCCGCGTAACCTACACGAGATAGCGTGTAGTTGAACACCTTCAATCGCCATAGGCTCTTCGCCGGTTA

8050

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

P G A L G C A L S H I N L W K L A V S E K R P I
 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948

5' TACCATTTTCGAGGACGACGTCTACTCGTCGTTCAACTTTCTTGAGGAGTCGACTCGCATTTCTGTCCATG
 3' ATGGTAAAAGCTCCTGCTGCAGATGAGCAGCAAGTTGAAAGAACTCCTCAGCTGAGCGTAAGACAGGTAC

8120

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

T I F E D D V Y S S F N F L E E S T R I L S M
 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971

5' GCTCCAGAGAACTGGGATATGGTAAAGTGGGATTCAATTTGACCCTCTATTCCTGTGGTTGAACTTCG
 3' CGAGGTCTCTTGACCCTATAACCATTTACCCCTAAGTTAAAGCTGGGAGATAAGGACACCAACTTGAAGC

8190

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

A P E N W D M V K W G F N F D P L F L W L N F
 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994

BGT25_T02a1-pET32-DEST

5' ATTTCTCCAAAGCCAAGCTGGAGTTCTACAACCGACAACACAAACAGATTCCGGCCCAATTTCAATCTGA
 3' TAAAGAGTTTCGGTTCGACCTCAAGATGTTGGCTGTTGTGTTTGTCTAAGGCCGGGTTAAAGTTAGACT

8260

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

D F S K A K L E F Y N R Q H K Q I P A Q F Q S E
 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018

SpeI

5' AACCTATCCGCGATCTCTTATCCGACTAGTCCATTCCCTTTGGTGCAATGGCTTATTCAGTAACTCCAAGG
 3' TTGGATAGGCGCTAGAGAATAGGCTGATCAGGTAAGGAAACCACGTTACCGAATAAGTCATTGAGGTTCC

8330

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

T Y P R S L I R L V H S F G A M A Y S V T P R
 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041

5' GGAGCTCAAGTACTTCTTGAAAAATGCCTACCTCTTCGAAAGCGGCTTATTCCGTTTCTGGGACTGGAG
 3' CCTCGAGTTTCATGAAGAACTTTTTACGGATGGAGAAGCTTTCGCCGAATAAGGCAAAGGACCCTGACCTC

8400

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

G A Q V L L E K C L P L R K R L I P F P G T G
 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064

AbsI

NsiI

5' TGGTCCCTCGAGGATGAGGGCATCGACTGCGCAATGTCCGCGGTGTATGACTCGATGCATGCGTTTCGTCTG
 3' ACCAGGAGCTCCTACTCCCGTAGCTGACGCGTTACAGGCGCCACATACTGAGCTACGTACGCAAGCAGAC

8470

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

V V L E D E G I D C A M S A V Y D S M H A F V C
 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088

BGT25_T02a1-pET32-DEST

5' CATGCCGCCACTGGTCATTCACGACGACGAGCAGGCATCAGATCGGGAAGTCGCGAATCGGCAGTAGGAC
 3' GTACGGCGGTGACCAGTAAGTGCTGCTGCTCGTCCGTAGTCTAGCCCTTCAGCGCTTAGCCGTCATCCTG

8540

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

M P P L V I H D D E Q A S D R E V A N R Q .
 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110

BamHI

NotI

5' CCAGCTTTCTTGTACAAAGTGTTGATatcggatccgaattcgagctccgtcgacaagcttgcgggccgca
 3' GGTCGAAAGAACATGTTTCACCAACTAtagcctaggcttaagctcgaggcagctgttcgaacgccggcgt

8610

attB2

BGT...21

5' ctcgagcaccaccaccaccactgagatccggctgctaacaaagcccgaaaggaagctgagttggctg
 3' gagctcgtggtggtggtggtgactctaggccgacgattgtttcgggctttccttcgactcaaccgac

8680

BipI

5' ctgccaccgctgagcaataactagcataacccttggggcctctaaacgggtcttgaggggttttttgct
 3' gacggtggcgactcgttattgatcgtattggggaaccccgagatttgcccagaactccccaaaaaacga

8750

T7 Terminator

5' gaaaggaggaactatatccggat
 3' ctttcctccttgatataggccta

8773