

BGT25_T02a1-pET16-DEST

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70

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210



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280



Ap

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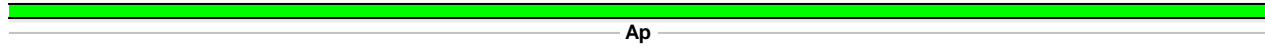
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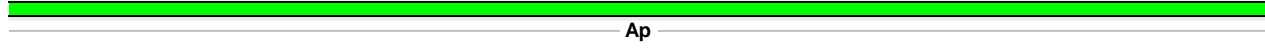
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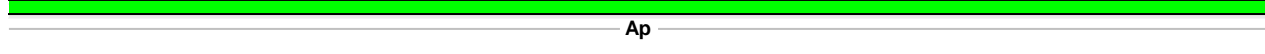
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560



Ap

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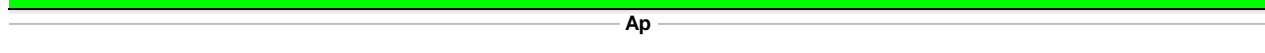
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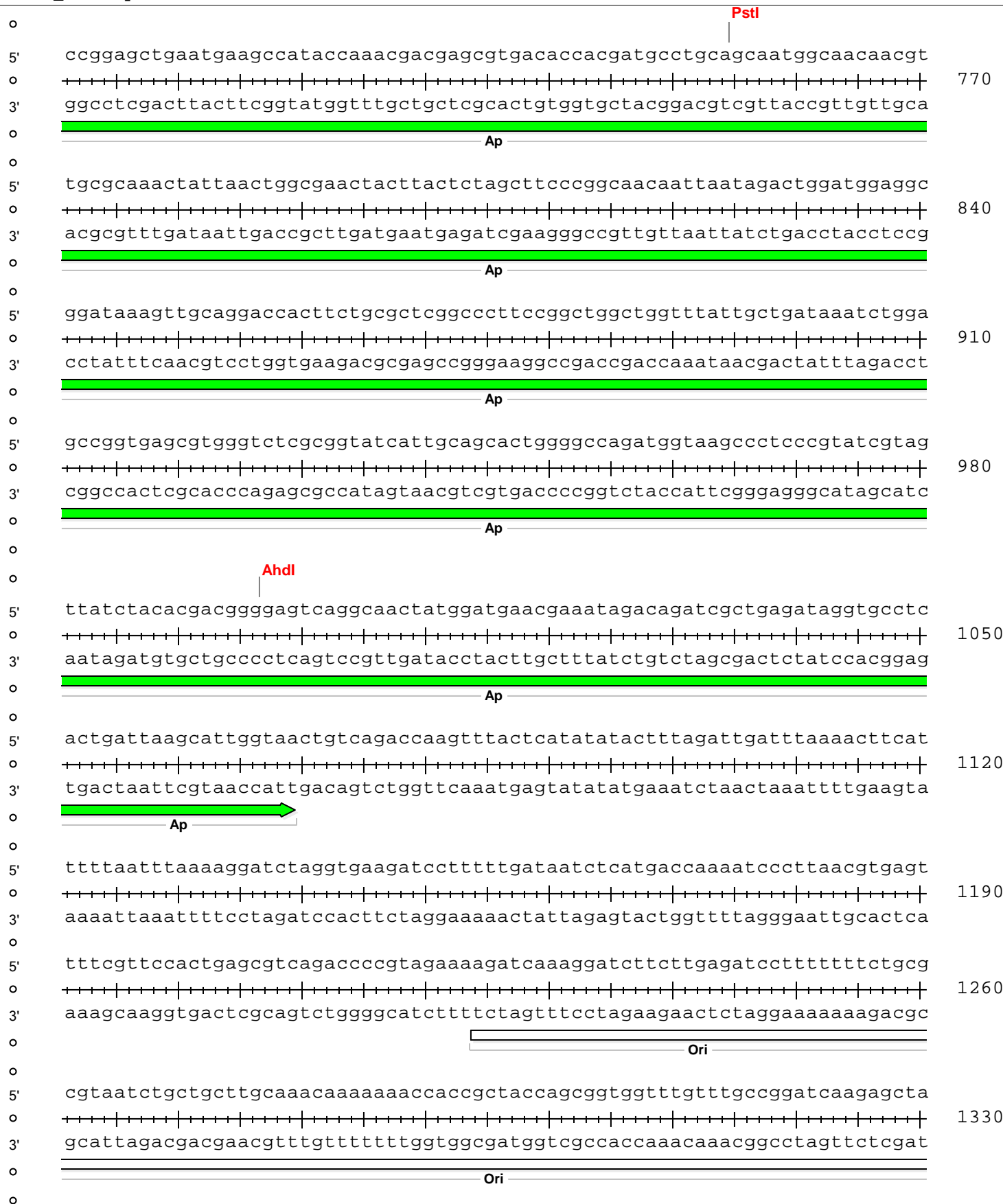
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Ap



BGT25_T02a1-pET16-DEST

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BstZ17I



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Bpu10I



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FspAI



Lac I



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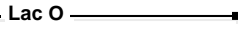
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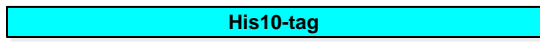
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5320



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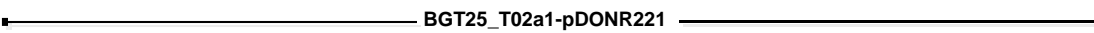
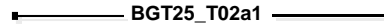
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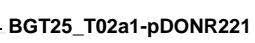
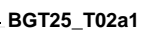
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 3' TAACAGTTCTTGCTCTGCTTCCAGTAGGACGTTACGGAGCGGTCGCACGAGGGGGAACAGCTGATGCACG

5530



I V K N E T K V I L Q C L A S V L P L V D Y V
 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71

BGT25_T02a1-pET16-DEST

Agel

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5600

GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

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5670

GT2?

BGT25_T02a1

BGT25_T02a1-pDONR221

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5740

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BGT25_T02a1

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5810

GT2?

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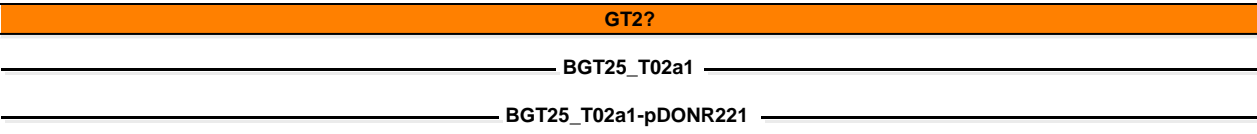
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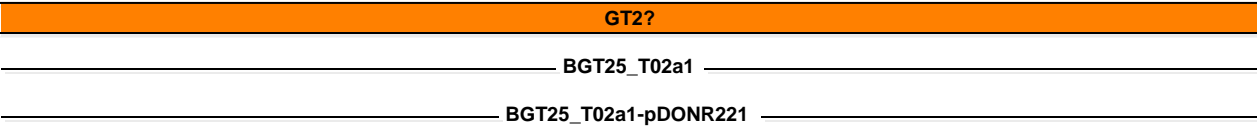


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Bael Bael'

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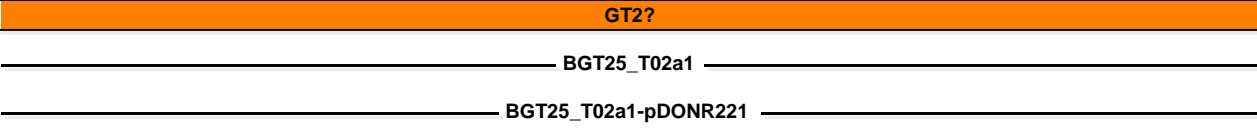
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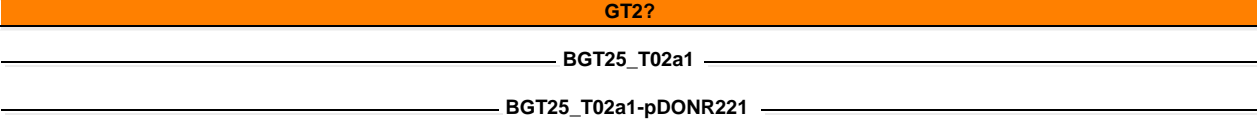
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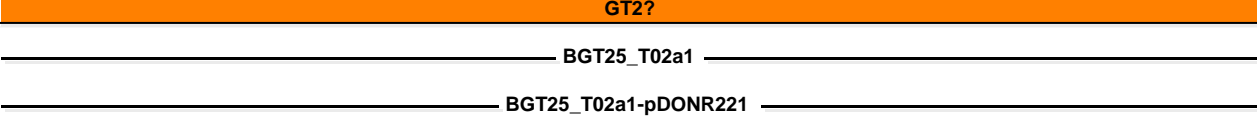
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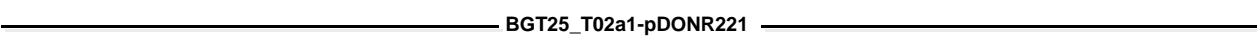
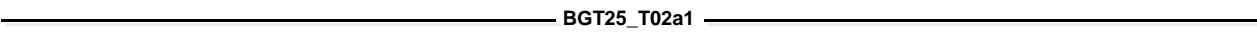


L L E A G N L M A A L G R P F D E V V A A F E R
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BGT25_T02a1-pET16-DEST

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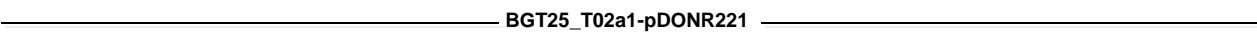
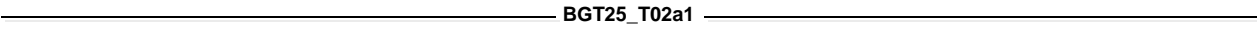
6300



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6370

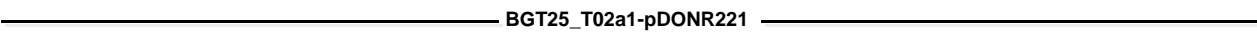
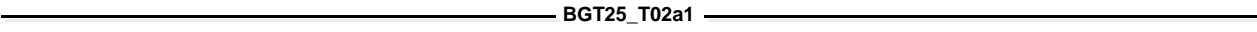


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PasI

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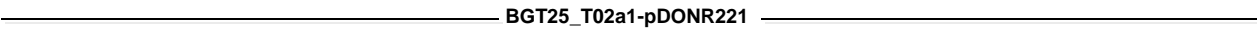
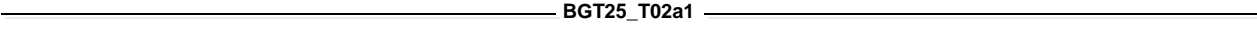
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 3' CCTTAGCGAGCTGCGAACAGATTTTAAACGAGCGGAGGCTGTTTAAACGGACGCCTTTACCGCTTCGCACAC

6510



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6580

GT2?

BGT25_T02a1

procollagen-lysine 5-dioxygenase

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V A N A R F A T G K L P V N E P P K L G A F G
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6650

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

T E S L I D Q H R L V R Q R S L R S R I E G T P
 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445

5' GCGCATCCTGGTGACAATCCTCGCAAAGCAGAAAGAGCCGGCACTGCCGCTGTACCTCGAGTGCATCGAG
 0 ++++++
 3' CGCGTAGGACCACTGTTAGGAGCGTTTCGTCTTTCTCGGCCGTGACGGCGACATGGAGCTCACGTAGCTC

6720

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

R I L V T I L A K Q K E P A L P L Y L E C I E
 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468

5' GCGCTCGACTACCCCAAGGCGTCGATCGTCCTGTACATCAGGACAAACAACAACACCGACAGGACCGAGC
 0 ++++++
 3' CGCGAGCTGATGGGGTTCCGCAGCTAGCAGGACATGTAGTCCTGTTGTTGTTGTTGGCTGTCCTGGCTCG

6790

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

A L D Y P K A S I V L Y I R T N N N T D R T E
 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491

5' ACATACTGCGCGAATGGGTGGAGCGGTTGGTACCTCTATGCCGCGGTTGAATTCGATGCCTCCAACGT
 0 ++++++
 3' TGTATGACGCGCTTACCCACCTCGCGCAACCAGTGGAGATACGGCGCCAACCTAAGCTACGGAGGTTGCA

6860

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

H I L R E W V E R V G H L Y A A V E F D A S N V
 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515

BGT25_T02a1-pET16-DEST

5' GGCCGATAGAGTCGAGCAGTTTGGCGAACACGAATGGAACGAGACGCGCTTCAGGGTGCTTGGCCGAATC
 3' CCGGCTATCTCAGCTCGTCAAACCGCTTGTGCTTACCTTGCTCTGCGCGAAGTCCCACGAACCGGCTTAG

6930

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

A D R V E Q F G E H E W N E T R F R V L G R I
 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538

5' CGCAACATAAGTTTGC GGAAA CTCTCGAACACAGCTGCGATTTCTATTTTCGTTGCCGACGTCGATAAATT
 3' GCGTTGTATTCAAACGCCTTTTGAGAGCTTGTGTGCGACGCTAAAGATAAAGCAACGGCTGCAGCTATTAA

7000

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

R N I S L R K T L E H S C D F Y F V A D V D N
 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561

BmgBI

5' TCGTGCGACCGGCCACGCTACGCGAGCTTGTGCGCGCTCGACGTGCCGATCGTCGCTCCCCTGCTTCGCTC
 3' AGCACGCTGGCCGGT GCGATGCGCTCGAACAGCGCGAGCTGCACGGCTAGCAGCGAGGGGACGAAGCGAG

7070

BGT25_T02a1

procollagen-lysine 5-dioxygenase

BGT25_T02a1-pDONR221

F V R P A T L R E L V A L D V P I V A P L L R S
 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585

XmaI
SmaI

CspCI

5' CATCTCTCCCGGGCAATACTATTCGAACTACCACGCCGAAATCGACGCCAACGGCTACTATATGCAGTGC
 3' GTAGAGAGGGCCCGTTATGATAAGCTTGATGGTGC GGCTTTAGCTGCGGTTGCCGATGATATACGTCACG

7140

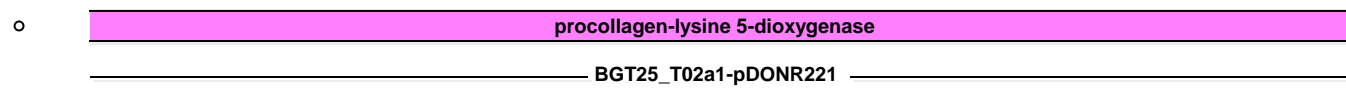
BGT25_T02a1

procollagen-lysine 5-dioxygenase

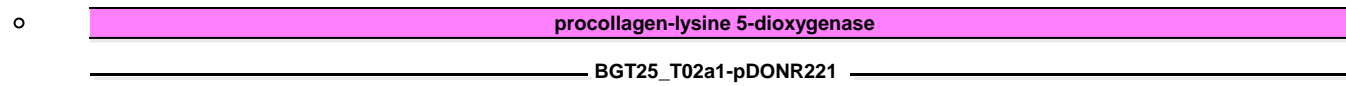
BGT25_T02a1-pDONR221

I S P G Q Y Y S N Y H A E I D A N G Y Y M Q C
 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608

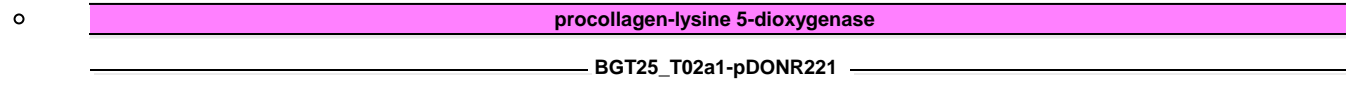
o
5' GATCAATATGGGTGGGTGCTCAACCGCCACGTGCGCGGCATTATCGAGATGCCGCTTGTGCACTGCACCT 7210
o
3' CTAGTTATACCCACCCACGAGTTGGCGGTGCACGCGCCGTAATAGCTCTACGGCGAACACGTGACGTGGA
BGT25_T02a1



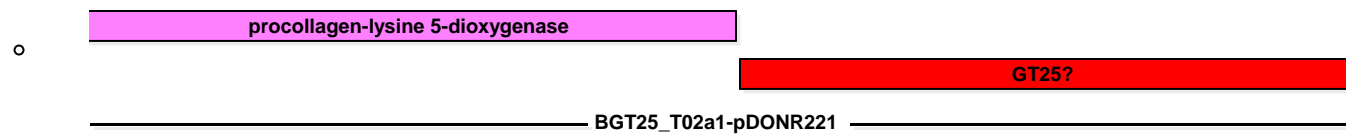
o
D Q Y G W V L N R H V R G I I E M P L V H C T
o
609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631
5' ATCTTGTCCGCGCCGACGTACTGCCCGAAGTACATACGAGGACGCGACATCGCGCTACGAGTACGTGAT 7280
o
3' TAGAACAGGCGCGGCTGCATGACGGGCTTGACTGTATGCTCCTGCGCTGTAGCGCGATGCTCATGCACTA
BGT25_T02a1



o
Y L V R A D V L P E L T Y E D A T S R Y E Y V I
o
632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655
5' CTTTGCCGACAGCGCCCGCAAGGCCGCGCATCGTCCAGTATATGGATAACCGACAAGTCTATGGCTACATC 7350
o
3' GAAACGGCTGTCGCGGGCGTTCCGGCCGTAGCAGGTCATATACCTATTGGCTGTTTCAGATACCGATGTAG
BGT25_T02a1



o
F A D S A R K A G I V Q Y M D N R Q V Y G Y I
o
656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678
5' ACCTTCGGCGATGGCCAATATTATGTGAGTGACGGGATCGAGCGCGCCCGAGCGCTGTTGCACGGTGCCG 7420
o
3' TGGAAGCCGCTACCGGTTATAATACTCACTGCCCTAGCTCGCGCGGGCTCGCGACAACGTGCCACGGC
BGT25_T02a1



o
T F G D G Q Y Y V S D G I E R A R A L L H G A
o
679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701

BGT25_T02a1-pET16-DEST

5' GCGACACGCCGGTATTCACTGCCGCCACGCCTCCGGGCGCCGTACCGATGCCAGATCGACATGTCGAGCC
 0 ++++++
 3' CGCTGTGCGGCCATAAGTGACGGCGGTGCGGAGGCCCGCGGCATGGCTACGGTCTAGCTGTACAGCTCGG

7490

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

G D T P V F T A A T P P G A V P M P D R H V E P
 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725

5' GCCGCAAATTCACCTAATAAACTTGGACAGCAGCGTCGAGCGCTGGCGCAAATATCAAGATAGGAATCCT
 0 ++++++
 3' CGGCGTTTAAGTGGATTATTTGAACCTGTCGTCGCAGCTCGCGACCGCGTTTATAGTTCTATCCTTAGGA

7560

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

P Q I H L I N L D S S V E R W R K Y Q D R N P
 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748

SgrDI

5' CATCTAGCCGCCAATACAATTCGGGTATCGGCCGTCGACGGAGCATCCCTCGATAGGTGCGACCTTGCAAG
 0 ++++++
 3' GTAGATCGGCGGTTATGTTAAGCCATAGCCGGCAGCTGCCTCGTAGGGAGCTATCCAGCTGGAACGTTTC

7630

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

H L A A N T I R V S A V D G A S L D R S T L Q
 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771

5' CCTTGGTGGACGATGGAGTGATTGCCGAGGATTGCGGGTATCTGCCGGGCGCATTGGGATGTGCTCTATC
 0 ++++++
 3' GGAACCACCTGCTACCTCACTAACGGCTCCTAACGCCCATAGACGGCCCGGTAACCCTACACGAGATAG

7700

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

A L V D D G V I A E D C G Y L P G A L G C A L S
 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795

5' GCACATCAACTTGTGGAAGTTAGCGGTATCCGAGAAGCGCCAATTACCATTTTCGAGGACGACGTCTAC
 0 ++++++
 3' CGTGTAGTTGAACACCTTCAATCGCCATAGGCTCTTCGCCGGTTAATGGTAAAAGCTCCTGCTGCAGATG

7770

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

H I N L W K L A V S E K R P I T I F E D D V Y
 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818

BGT25_T02a1-pET16-DEST

o
 5' GCCTACCTCTTCGAAAGCGGCTTATTCCGTTTCCTGGGACTGGAGTGGTCCTCGAGGATGAGGGCATCGA
 o
 3' CGGATGGAGAAGCTTTCGCCGAATAAGGCAAAGGACCTGACCTCACCAGGAGCTCCTACTCCCCTAGCT

8120

AbsI

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

C L P L R K R L I P F P G T G V V L E D E G I D
 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935

o
 5' CTGCGCAATGTCCGCGGTGTATGACTCGATGCATGCGTTCGTCTGCATGCCGCCACTGGTCATTCACGAC
 o
 3' GACGCGTTACAGGCGCCACATACTGAGCTACGTACGCAAGCAGACGTACGGCGGTGACCAGTAAGTGCTG

8190

NsiI

BGT25_T02a1

GT25?

BGT25_T02a1-pDONR221

C A M S A V Y D S M H A F V C M P P L V I H D
 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958

o
 5' GACGAGCAGGCATCAGATCGGGAAGTCGCGAATCGGCAGTAGGACCCAGCTTCTTGTACAAAGTGGTTG
 o
 3' CTGCTCGTCCGTAGTCTAGCCCTTCAGCGCTTAGCCGTCATCCTGGGTCGAAAGAACATGTTTCACCAAC

8260

BGT25_T02a1

attB2

GT25?

BGT25_T02a1-pDONR221

D E Q A S D R E V A N R Q
 959 960 961 962 963 964 965 966 967 968 969 970 971 972

o
 5' ATtcgaggatccggctgctaacaagcccgaaggaagctgagttggctgctgccaccgctgagcaataa
 o
 3' TAagctcctagggcgacgattgtttcgggctttccttcgactcaaccgacgacggtggcgactcgttatt

8330

BamHI

BlnI

T7 Terminator

o
 5' ctagcataacccttggggcctctaaacgggtcttgaggggttttttgctgaaaggaggaactatatccg
 o
 3' gatcgtattggggaaccccgagatttgcccagaactccccaaaaaacgactttcctccttgatataggc

8400

T7 Terminator

o
 5' gatatcccgcaagaggcccggcagtaccggcataaccaagcctatgcctacagcatccagggtgacggtg
 o
 3' ctatagggcggttctccgggcccgtcatggccgatttggttcggatagcggatgctcgtaggtcccactgccac

8470

