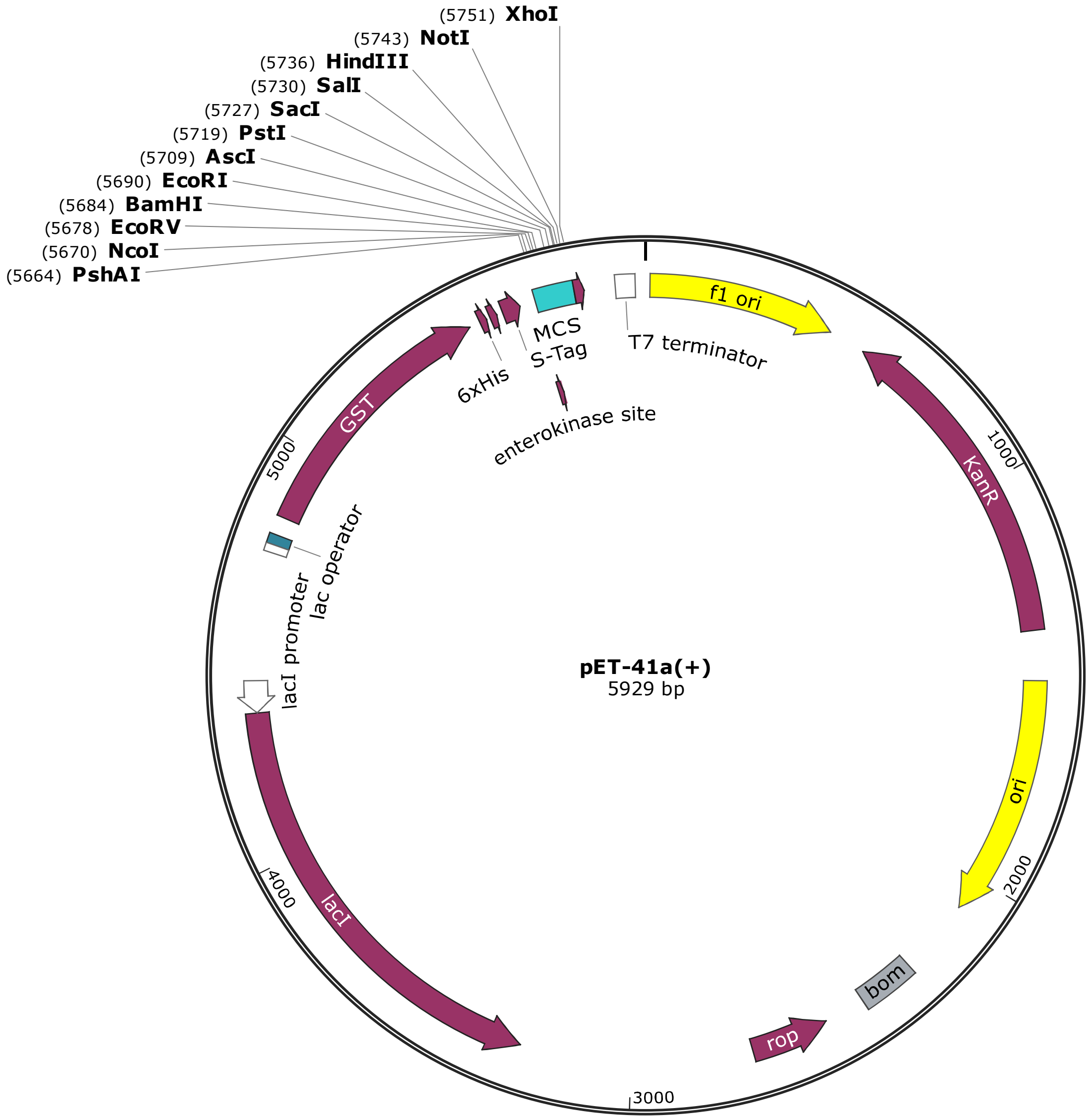

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                                                                              4650
GGTGGTATGGGTGCGGCTTTGTTCGCGAGTACTCGGGCTTCACCGCTCGGGCTAGAAGGGGTAGCCACTACAGCC

CGATATAGGCGCCAGCAACCGCACCTGTGGCGCCGGTGATGCCGGCCACGATGCGTCCGGCGTAGAGGATCGAGA
                                                                              4725
GCTATATCCGCGGTCGTTGGCGTGGACACCGCGGCCACTACGGCCGGTGCTACGCAGGCCGCATCTCCTAGCTCT

TCGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAA
                                                                              4800
AGCTAGAGCTAGGGCGCTTTAATTATGCTGAGTGATATCCCCTTAACACTCGCCTATTGTTAAGGGGAGATCTTT
                     T7 promoter        lac operator

TAATTTTGTTTAACTTTAAGAAGGAGATATACATATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGT
                                                                              4875
ATTAAAACAAATTGAAATTCTTCCTCTATATGTATACAGGGGATATGATCCAATAACCTTTTAATTCCCGGAACA
                                      1           5              10
                                      Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val
                                                           GST

GCAACCCACTCGACTTCTTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATGAGCGCGATGAAGGTGA
                                                                              4950
CGTTGGGTGAGCTGAAGAAAACCTTATAGAACTTCTTTTTATACTTCTCGTAAACATACTCGCGCTACTTCCACT
  15                  20                  25                  30                  35
  Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp
                                     GST
```

```
TAAATGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAA     5025
ATTTACCGCTTTGTTTTTCAAACTTAACCCAAACCTCAAAGGGTTAGAAGGAATAATATAACTACCACTACAATT
 40              45              50              55              60
Lys Trp Arg Asn Lys Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
GST
```

```
ATTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAACATGTTGGGTGGTTGTCCAAAAGAGCG     5100
TAATTGTGTCAGATACCGGTAGTATGCAATATATCGACTGTTCGTGTTGTACAACCCACCAACAGGTTTTCTCGC
 65              70              75              80              85
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg
GST
```

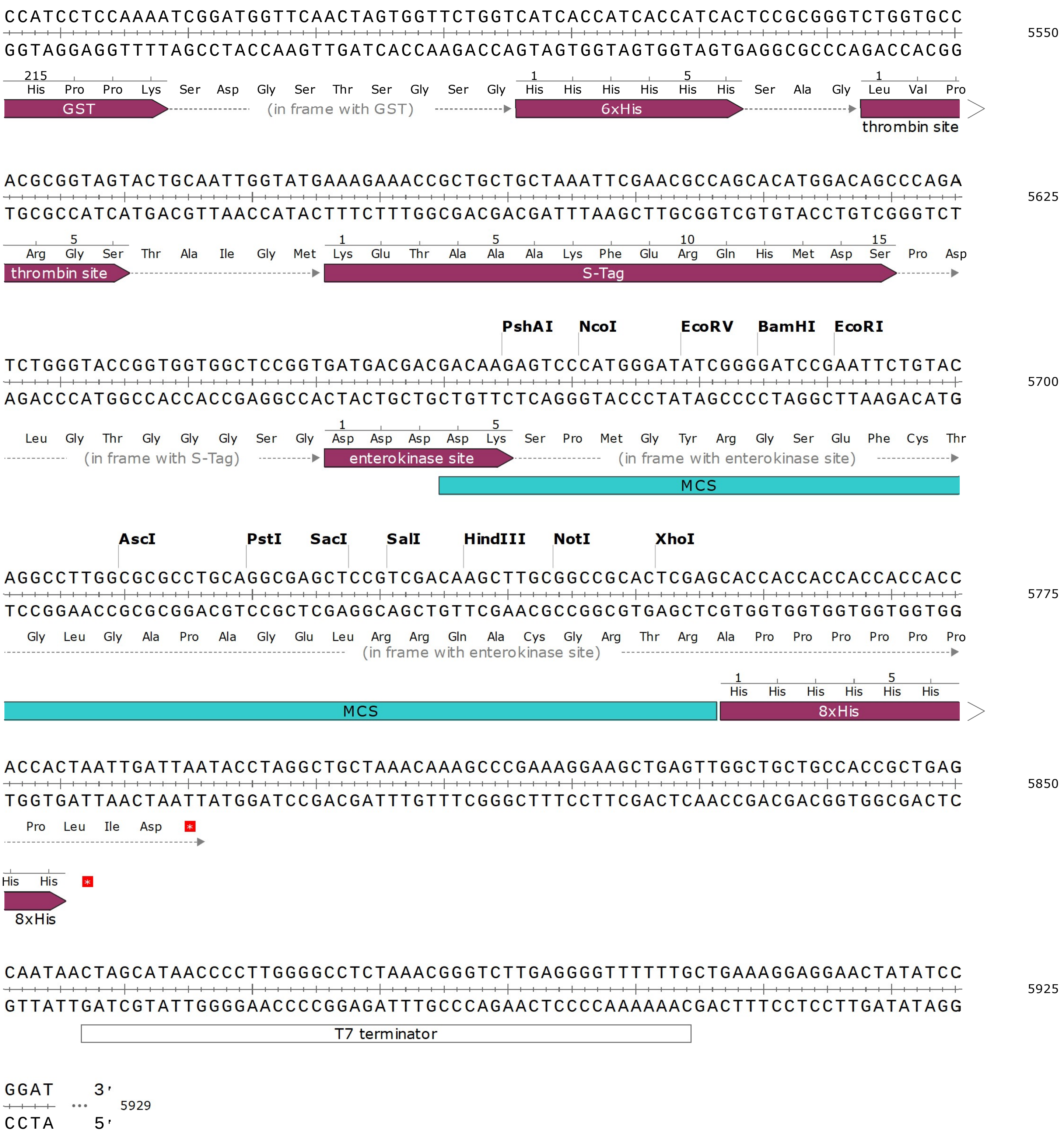
```
TGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTGGATATTAGATACGGTGTTTCGAGAATTGCATATAGTAAAGA     5175
ACGTCTCTAAAGTTACGAACTTCCTCGCCAAAACCTATAATCTATGCCACAAAGCTCTTAACGTATATCATTTCT
 90              95              100             105             110
Ala Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser Lys Asp
GST
```

```
CTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTCGAAGATCGTTTATGTCA     5250
GAAACTTTGAGAGTTTCAACTAAAAGAATCGTTCGATGGACTTTACGACTTTTACAAGCTTCTAGCAAATACAGT
 115             120             125             130             135
Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His
GST
```

```
TAAAACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGATGTTGTTTTATA     5325
ATTTTGTATAAATTTACCACTAGTACATTGGGTAGGACTGAAGTACAACATACTGCGAGAACTACAACAAAATAT
 140             145             150             155             160
Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr
GST
```

```
CATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAAAAAACGTATTGAAGCTATCCCACAAAT     5400
GTACCTGGGTTACACGGACCTACGCAAGGGTTTTAATCAAACAAAATTTTTTGCATAACTTCGATAGGGTGTTTA
 165             170             175             180             185
Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile
GST
```

```
TGATAAGTACTTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGA     5475
ACTATTCATGAACTTTAGGTCGTTCATATATCGTACCGGAAACGTCCCGACCGTTCGGTGCAAACCACCACCGCT
 190             195             200             205             210
Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp
GST
```



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ACGCGGTAGTACTGCAATTGGTATGAAAGAAACCGCTGCTGCTAAATTCGAACGCCAGCACATGGACAGCCCAGA   5625
TGCGCCATCATGACGTTAACCATACTTTCTTTGGCGACGACGATTTAAGCTTGCGGTCGTGTACCTGTCGGGTCT

TCTGGGTACCGGTGGTGGCTCCGGTGATGACGACGACAAGAGTCCCATGGGATATCGGGGATCCGAATTCTGTAC   5700
AGACCCATGGCCACCACCGAGGCCACTACTGCTGCTGTTCTCAGGGTACCCTATAGCCCCTAGGCTTAAGACATG

AGGCCTTGGCGCGCCTGCAGGCGAGCTCCGTCGACAAGCTTGCGGCCGCACTCGAGCACCACCACCACCACCACC   5775
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CAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGGAACTATATCC   5925
GTTATTGATCGTATTGGGGAACCCCGGAGATTTGCCCAGAACTCCCCAAAAAACGACTTTCCTCCTTGATATAGG

GGAT    3' ... 5929
CCTA    5'
```