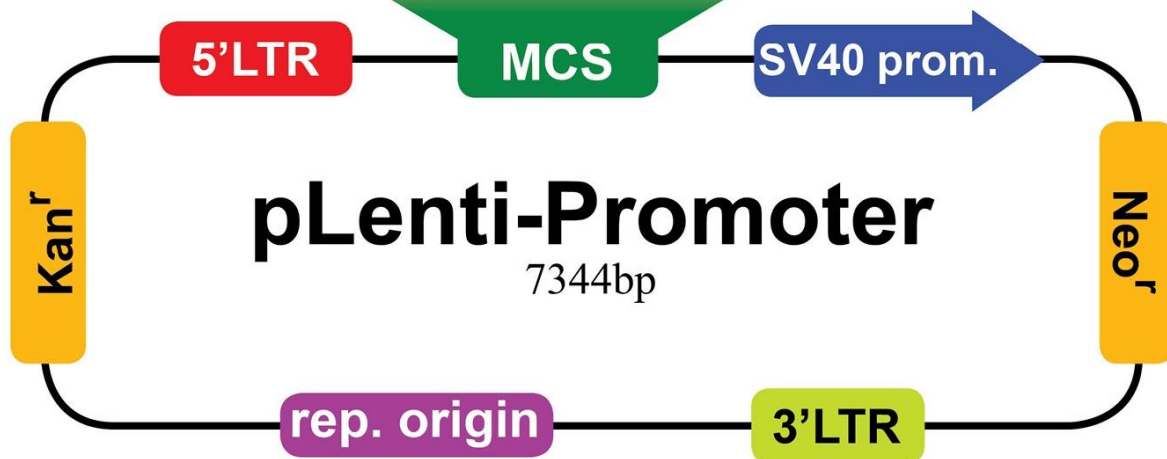


Vector Name	LV013 pLenti-promoter
VectorType	Lentiviral vector
Antibiotic Information	Kanamycin
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Sequence

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Gentaur Molecular Products
Voortstraat 49
1910 Kampenhout, Belgium

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4561 aagcggtaa tacggttatc cacagaaatc ggggataacg caggaagaa catgtgagca
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4741 acaggactat aaagatacca ggcgtttccc cctggaagct cctcgtgocg ctctcctgtt
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5161 agagttgcta gctcttgatc cggcaaaaa accaccgctg gtagcgggtg ttttttgg
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6301 ctgtgctcga cgttgctact gaagcgggaa gggactggct gctattgggc gaagtcagg
6361 ggcaggtatc cctgtcatct cacctgtctc ctgcccagaa agtatccatc atggctgatg
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7141 agagcttgac ggggaaagc ggcgaacgtg gcgagaaag aaggaagaa agcgaagaa
7201 gggggccta gggcgctgga aagtgtagc gtcacgctc gcgtaaccac cacaccgctc
7261 cgcttaatgc gccgctacag ggcgctcca ttcccatc aggatogaat taattcttaa
7321 ttaacatcat caataata cctt

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Text Map

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1 ttttggattgaagccaatagataatgagggggtggagtttgtgacgtggcggggggcgt 60
  AAAACCTAACTTCGGTTATACATTAACCTCCCCACCTCAAACACTGCACCGCCCCCGCA

61 gggaaacggggcgggtgacgtagtagtggcgggaagtgtgatgttgaagtgtggcggaa 120
  CCTTGCCCCGCCACTGCATCATCACACCGCCTTACACTACAACGTTACACCGCCTT

Encap other (162, 310) >>>
|
121 cacatgtaagcgacggatgtggcaaaagtgaacttttgggtgtgcccgggtgtacacagg 180
  GTGTACATTCGCTGCCACACCGTTTCACTGCAAAAACACACCGGGCCACATGTGTCC

181 aagtgacaattttcgcgctgttttagcggatgtttagtaaaatttggcgtaaccgagtt 240
  TTCACTGTTAAAGCGCGCAAAATCCGCCTACAACATCATTTAAACCCGCATTGGCTCA

241 aagatttggccattttcgcgggaaaactgaataagaggaagtgaatctgaataattttg 300
  TTCTAAACCGGTTAAAGCGCCCTTTGACTTATCTCCTTCACTTTAGACTTATTTAAAC

301 tgttactcatagcgcgtaatacggcagacctcagcgttagattattgaagcatttatcag 360
  ACAATGAGTATCGCGCATTATGCCCTCTGGAGTCGCGATCTAATAACTTCGTAATAGTC

amp prom (365, 393) <<<
|
361 ggttattgtctcatgagcggatacattttgaatgtatttagaaaaataaacaataggg 420
  CCAATAACAGAGTACTCGCCTATGTATAAATTTACATAAATCTTTTTATTGTTTATCCC

HpaI
|
421 gttccgcgcacatttccccgaaaagtgccacctgacgttaactataacggctcctaaggt 480
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481 gcgaaagctcagatctggatctcccgatcccctatggctogactctcagtaacaatctgctc 540
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541 tgatgcccagatgtaagccagatctgctccctgcttgtgtgttggaggtcgtgagta 600
  ACTACGGCGTATCAATTCGGTCATAGACGAGGGACGAACACACAACCTCCAGGACTCAT

601 gtagcggagcaaaatgaaagctacaacaagcaagcgttaccgacaatgtagtct 660
  CACGGCTCGTTTTAAATTCGATGTTGTTCCGTTCCGAACTGGCTGTTAATTCATCAGA

661 tatgcaatactctttagtcttgaacatggtaacgatgagtttagcaacatgccttaca 720
  ATACGTTATGAGAACATCAGAACGTTGTACCATTTGCTACTCAATCGTTGTACGGAAATGTT

721 ggagagaaaaagcaccgtgcatgccgattgggtggaagtgaaggtgtacgatcgtgcctta 780
  CCTCTCTTTTTCGTTGGCAGTACGGCTAACCCCTTCATTCACCATGCTAGCACGGAAAT

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781 tttaggaaggcaacagacgggtctgacatggattggacgaaccactgaattgccgattgc 840
AATCCTTCGGTTGTCTGCCAGACTGTACCTAACCTGCTTGGTGACTTACGGCGTAAC

HIV-1_5_LTR other (880,1060)>>>

841 agagatatgtatttaagtgcttagctcgatacataaacgggtctctctggttagaccag 900
TCTCTATAACATAAATTCACGGATCGAGCTATGTATTTGCCAGAGACCAATCTGGTC

901 atctgagcctgggagctctctggctaactagggaaaccactgcttaagcctcaataaagc 960
TAGACTCGGACCTCGAGAGACCGATTGATCCCTGGGTGACGAATTCGGAGTTATTTCC

961 ttgccttgagtgtcaagtagtgtgtgcccgtctgtgtgtgactctggtaactagaga 1020
AACGGAACACAGAAAGTTCATCACACACGGGCAGACAACACACTGAGACCATTGATCTCT

1021 tcctcagacccttttagtcagtggtgaaaatctctagcagtgggcccccgaacagggact 1080
AGGGAGTCTGGGAAAATCAGTCACACCTTTTAGAGATCGTCACCGGGCTTGTCCCTGA

1081 tgaagogaagggaaccagaggagctctctcgacgcaggactcggcttctgtaagcgc 1140
ACTTTCGCTTTCCTTTGGTCTCCTCGAGAGAGCTGCGTCTGAGCCGAACGACTTTCGCG

HIV-1_psi_pack other (1171,1215)>>>

1141 gcacggcaagaggcgagggcgcgactggtgagtagcgcacaaaattttgactagcggag 1200
CGTGCGTCTCCGCTCCCGCGCTGACCACTCATGCGGTTTTTAAACTGATCGCCTC

1201 gctagaaggagagatgggtgagagcgtcagtagttaaagcggggagaattagatcgc 1260
CGATCTTCTCTCTACCCAGCTCTCGAGTCATAATTCGCCCTCTTAATCTAGCG

NruI

1261 gatgggaaaaattcggttaagccaggggaaagaaaaataaaattaaaacatatag 1320
CTACCTTTTTTAAGCCAATTCGGTCCCTTTCTTTTTTATATTTAATTTTGTATATC

1321 tatgggcaagcaggagctagaacgattcgcagtagtaacccctgctgtagaacaatcag 1380
ATACCGTTCGTCCTCGATCTTGCTAAGCGTCAATTAGGACCGGACAATCTTTGTAGTC

1381 aagcctgtagacaaactaggacagctacaacccctcagacaggatcagaagaac 1440
TTCCGACATCTGTTTATGACCCTGTCGATGTTGGTAGGGAAGTCTGCTAGTCTTCTTG

1441 ttagatcattatataatacagtagcaaccctctattgtgtgcatcaaggatagagataa 1500
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1501 aagacaccaaggaagctttagacaagatagaggaagagcaaaaacaaagtaagaccaccg 1560
TTCTGTGGTTCCTCGAAATCTGTTCTATCTCTCTCTCGTTTTGTTTTTATTCTGGTGGC

1561 cacagcaagcgcgctgactctcagacctggaggagagatagaggacaattgagaag 1620
GTGTCGTTCCGGCGACTAGAAGTCTGGACCTCCTCCTTATACTCCCTGTTAACTCTTC

1621 tgaattataataataaagtagtaaaaattgaaccattaggagtagcaccaccaaggc 1680
ACTTAATATATTTATATTTTATCATTTTTTAACCTGGTAATCCTCATCGTGGGTGGTCCG

RRE reg (1723,1956)>>>

1681 aaagagaagagtggtgcagagagaaaaagagcagtgagggaataggagctttgttccttg 1740
TTTCTCTTCTCACCGTCTCTTTTTTCTCGTCACCTTATCCTCGAAACAGGAACC

ORF_2 rf (2) (1766,2467)>>>

1741 gttcttgggagcagcaggaagcaactatgggagcagcgtcaatgacgctgacggtacagge 1800
CAAGAACCTCGTCGCTTTCGTGATACCGCGTGCAGTTACTGCGACTGCCATGTCCG

1801 cagacaattattgtctggtatagtgacgagcagacaatttggctgagggctattgagge 1860
GTCTGTTAATAACAGACCATATCACGTCGTCGTTGTTAAACGACTCCCGATAACTCCG

1861 gcaacagcactctgttgcaactcacagtctgggcaatcaagcagctccaggaagaatcct 1920
CGTTGTCGTAGACAACGTTGAGTGTGAGACCCCGTAGTTGTCGAGGTCGGTCTTCTAGGA

1921 ggctgtggaagatacctaaggaatcaacagctcctgggatttggggttctctggaaga 1980
CCGACACCTTTCTATGATTTCTAGTTGTCGAGGACCCCTAAACCCCAACGAGACCTTT

1981 actcatttgcaccactgctgtgcttggaaatgctagttggagtaataaatctctggaaca 2040
TGAGTAAACGTTGGTACGACACGGAACCTTACGATCAACCTCATTATTTAGAGACCTTGT

2041 gatttggaaatcacacgacctggatggagtgaggacagagaaattaacaattacacaagcct 2100
CTAAACCTTAGTGTGCTGGACCTACCTCACCCTGCTCTTTAATTGTTAATGTTGTCGAA

2101 aatacactccttaattgaagaatcgcaaaaccagcaagaaagaatgaacaagaattatt 2160
TTATGTGAGGAATTAACCTTCTAGCGTTTTGGTCTGTTCTTTTCTTACTTGTCTTAATAA

2161 ggaattagataaatgggcaagtttgggaattggtttaaacaatacaaatggctgtggta 2220
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2221 tataaaattattcataatgatagtagggccttggtaggtttaaagaatagttttgtgt 2280
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2281 actttctatagtagaatagagtaggagggatattcaccattatcgtttcagaccacct 2340

3601 ctttacgggtatcgccgctcccattcgagcgcacgctctctatcgctctcttgacgag 3660
GAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAAGTCTGCTC

3661 ttctcttgagcgggactctggggttcgatattagacaaggcagctgtagatcttagccac 3720
AAGAAGACTCGCCCTGAGACCCCAAGCTATAATCTGTTCCGTCGACATCTAGAATCGGTG

delta_U3 other (3743,3795)>>>
|

3721 tttttaaaagaaaaggggggactggaagggctaatcactoccaaagacaagatctg 3780
AAAAATTTCTTTCCCCCTGACCTTCCCGATTAAGTGAGGGTGTGTTCTGTTCTAGAC

HIV-1_5_LTR other (3796,3976)>>>
|

3781 ctttttgcttgactgggtctctctggttagaccagatctgagcctgggagctctctg 3840
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3841 taactaggaaccactgcttaagcctcaataaagcttgcttgagtgcttcaagtagtg 3900
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3901 tgtgccctgctgtgtgactctgtaactagagatccctcagacccttttagctcagtg 3960
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3961 tggaaaaatcttagcagtagtagttcatgtcatcttattattcagatattataacttgca 4020
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4021 aagaaatgaatatcagagagtgagaggaacttgctttaaaccgctgatcagcctcgact 4080
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SmaI
|
XmaI
| |

4081 gtgccttctagttgccagccatctgttgttggccggggcgatcgctgcccctcccccg 4140
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4141 gccttcctgaccctggaagtgccactcccactgtccttctcctaataaaatgaggaaat 4200
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4201 tgcctcgcattgtctgagtaggtgtcattctattctggggggtggggggggcaggacag 4260
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4261 caagggggaggattggaagacaaatagcagggcatgctggggatgcggtgggctctatg 4320
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ClaI
|

4321 ttctgaggcggaaagaaccagcagatcgatctgcatctatgtcgggtgcccggagaaagg 4380
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4381 taatgaaatggcattatgggtattatgggtctgcattatgaatcgcccaacgatccccg 4440
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4441 tgtgaaataccgcacagatgctgaaggagaaaaataccgcatcaggcgtctctccgcttcc 4500
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4501 tgcctcactgactcgtcgcctcgggtcttggctcggcgagcgggtatcagctcactca 4560
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4561 aagggcggtaatacggttatccacagaatcaggggataacgcaggaaagaacatgtgagca 4620
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pBR322 origin (4656,5275)<<<
|

4621 aaaggccagcaaaaggccaggaaccgtaaaaggccgctgtgctggcgttttccatagg 4680
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4681 ctccgccccctgacgagcatcaaaaaatcgagcgtcaagttagaggtggcgaaccgg 4740
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4741 acaggactataaagataaccaggcgtttccccctggaagctcccctcgtgctctctctg 4800
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4801 ccgaccctgcccgttacggataccctgctcgcctttctccttcgggaagcgtggcgctt 4860
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5041 agcagagcaggtatgtaggggtgtacagagttcttgaagtggcctaactacggc 5100

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5101 tacactagaaggacagtatttggatctctgctctctgctgaagccagttaccttcggaaaa 5160
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5341 tcaaaaaggatcttcaactagatccttttaaatataaataagagttttaaatacaatctaa 5400
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5701 agtagtccgagtaaatagtttgcgcaacggttggtaaaggatcttccactagatcc 5760
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5761 ttttcagtagaaagccagctccgcagaaacggtgctgaccccggatgaatgtcagctact 5820
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5821 gggctatctggacaagggaaaaacgcaagcgaagagaaagcaggtagcttgcagtgggc 5880
CCGATAGACTGTTCCCTTTTGGCTTCGCGTTCTCTTTCGTCATCGAACGTCACCCG

NEOKAN prom (5928, 5977) >>>

|

5881 ttacatggcagatagctagactggcggttttatggacagcaagcgaaccggaattgccag 5940
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5941 ctggggcgccctctggtaagttgggaagccctgcaaaagtaaacggatggctttctcgc 6000
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6001 cgccaaggatctgatggcgaggggatcaagctctgatcaagagacaggatgaggatcgt 6060
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NTP_II marker (6069, 6857) >>>

|

ORF_3 rf (3) (6066, 6860) >>>

| |

6061 ttgcgatgtgaaagaatggattgacgcaggttctccggcggcttgggtggagagc 6120
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6121 tattcggctatgactgggcacaacagacaatcggctgctctgatgcccggctgttccggc 6180
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6181 tgtcagcagggggcgcccggttcttttgcgaagaccgacctgtccgggtgcctgaatg 6240
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6241 aactgcaagcagggcagcggcgtatcgtggctggccacgagggcgttcccttgcgcag 6300
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6301 ctgtgctcagcttgtcactgaagcgggaagggactggtgctattggggogaagtgcgg 6360
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6361 ggcagatctctgtcactcacttgcctcctgcccagaaagatccatcatggctgatg 6420
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6421 caatgcggcggctgcatacgttgatccggctacctgcccattcgaccaccaagcgaac 6480
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6481 atcgatcagcagcagctactcggatggaagccggtcttgcgatcaggatgatctgg 6540
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6541 acgaagagcatcagggctcgcgcccagcgaactgttgcagggctcaaggcagcagc 6600
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6601 ccgacggcagagatctcgtcgtgacctgagcagctgctgctgctgcaatcagtggtg 6660
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6661 aaaatggccgcttttctggattcatcgactgtggccggtgggtgtggcggaccgctatc 6720
 TTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAG
 6721 aggacatagcgttggctaccctgatattgctgaagagcttggcggcgaatgggctgacc 6780
 TCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGG
 6781 gttctctgctgtttacggtatcgccgctcccgattcgcagcgcacatgccttctatcgcc 6840
 CGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGG
 6841 ttcttgacgagttcttctgaattttgttaaaattttgttaaatcagctcatttttaac 6900
 AAGAACTGCTCAAGAAGACTTAAACAATTTTAAAAACAATTTAGTCGAGTAAAAAATTG
 6901 caataggccgaaatcggaacatccctataaaatcaaaagaatagaccgcataggggtg 6960
 GTTATCCGGCTTAGCCGTTGTAGGGAATATTTAGTTTTCTTATCTGGCGCTATCCCAAC

 f1 origin(6965,7270)<<<
 |
 6961 agtgttgttccagtttgaacaagagtccactattaagaactggactccaactgcaaa 7020
 TCACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGACCTGAGGTTGCAGTTT
 7021 gggcgaaaaacgctctatcaggcggatggcccactcgtgaaccatcacccaaatcaagt 7080
 CCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACCTTGGTAGTGGGTTTAGTTCA
 7081 tttttcggctcaggtgcccgaagctctaaatcggaaccctaaaggagcccccgattt 7140
 AAAACCGCCAGCTCCACGGCATTTCGAGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAA
 7141 agagcttgacgggaaagccggcgaacgtggcgagaaggaagggaagaaagcgaaaagga 7200
 TCTCGAATGCCCCCTTTCGGCCGCTTGACCCGCTCTTTCCTTCCCTTCTTTCGCTTTCT
 7201 gggcgctagggcgctggcaagtgtagcggctcagctgcgcgtaaccaccaaccgcg 7260
 CGCCCGGATCCCGCGACCGTTCACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGC
 7261 cgcttaatgcgcgctacagggcgcgtccattcgccattcaggatcgaattaattcttaa 7320
 CGAATTACCGGGCGATGTCCTCCGCGCAGGTAAGCGGTAAGTCCTAGCTTAATTAAGAATT

 7321 ttaacatcatcaataataacatt 7344
 AATTGTAGTAGTTATTATATGGAA

Features

5'-LTR
 Start: 670 End: 1151
 Original Location Description:
 670..1151
 Neomycin
 Start: 2875 End: 3669
 Original Location Description:
 2875..3669
 3'-LTR
 Start: 3771 End: 4059
 Original Location Description:
 3771..4060