

RIKEN Clone ID : TEx18B07 (PC010724-41)

Lot# : 6078_B4Go

Vector : pET-11a

Locus tag	TTHA0724
Insert size	1302 bp
Product	serine protease

● **Plasmid DNA purification**

Date : _____

Culture : LB (100 ug/ml Ampicillin) 10 ml -> 37°C O/N

Date : _____

Purification : QIAGEN Miniprep kit -> dH₂O 50 ul

● **Digestion by restriction enzyme/Concentration calibration**

Date : _____

DNA concentration (O.D.): _____ ng/ul

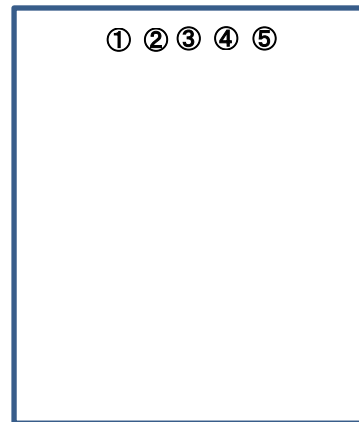
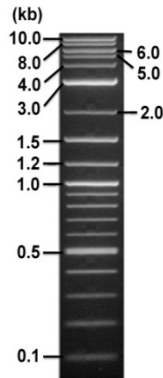
< Size of fragment expected from this clone >

DNA	ul
Enzyme (BglII + EcoRI)	0.5 + 0.5 ul
Buffer H	1 ul
dH ₂ O	ul
Total	10 ul

BglII	5.9, 1.1 kb
EcoRI	7.0 kb
BglII + EcoRI	5.2, 1.1, 0.7 kb

Electrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder



- ①:Marker
- ②:uncut
- ③:BglII
- ④:EcoRI
- ⑤:BglII + EcoRI

● **Adjust plasmid DNA solution to 25 ng/ul**

Date : _____

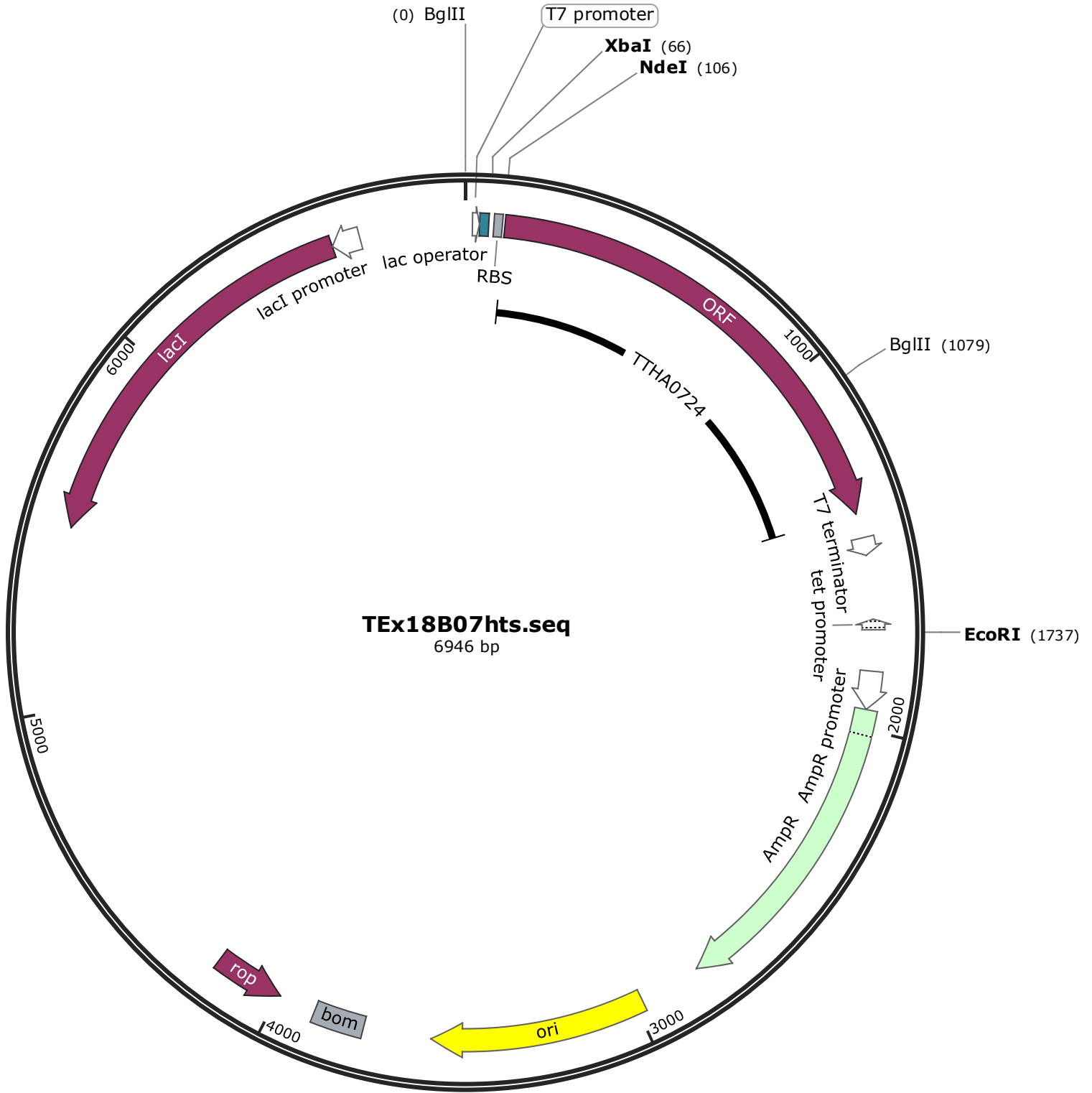
DNA (_____ ng/ul)	ul
10x TE	ul
dH ₂ O	ul
Total	ul

● **Shipping**

- Conc. : 25 ng/μl, Volume : 40 μl
- Conc. : _____ ng/μl, Volume : _____ μl

APPROVED BY :





BLAST Results

[Questions/comments](#)

Blast 2 sequences

Job title: Nucleotide Sequence

RID [ANW9YN5F114](#) (Expires on 08-02 10:21 am)

Query ID Icl|Query_3291041
 Description None
 Molecule type dna
 Query Length 1302

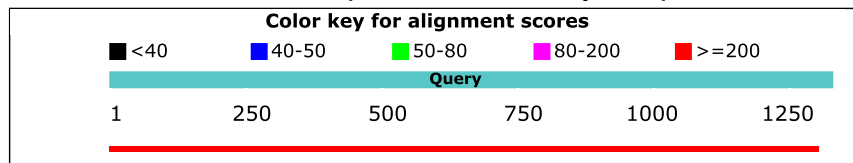
Subject ID Icl|Query_3291043
 Description None
[See details](#)
 Molecule type dna
 Subject Length 6946
 Program BLASTN 2.16.0+

TTHA0724

TEx18B07hts.seq

[Graphic Summary](#)

Distribution of the top 1 Blast Hits on 1 subject sequences



[Dot Matrix View](#)

[Descriptions](#)

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	2399	2399	100%	0.0	99.92%	Query_3291043

[Alignments](#)

Sequence ID: Query_3291043 Length: 6946 Number of Matches: 1
 Range 1: 108 to 1409

Score	Expect	Identities	Gaps	Strand	Frame
2399 bits(1299)	0.0()	1301/1302(99%)	0/1302(0%)	Plus/Plus	

Features:

Query 1	ATGAAGCGCCTGCTCTTTGGGGCCCTTTTCTCTCCACGGCCCTCCTCCTCACGGCCTGT	60	6 G>A
Sbjct 108	ATGAAACGCCTGCTCTTTGGGGCCCTTTTCTCTCCACGGCCCTCCTCCTCACGGCCTGT	167	
Query 61	CCCCAGACCCACCGCCGCCGTGAACCCCGCCGAGTCCCGGTAGGTCCCCTGCGGGTG	120	
Sbjct 168	CCCCAGACCCACCGCCGCCGTGAACCCCGCCGAGTCCCGGTAGGTCCCCTGCGGGTG	227	
Query 121	CAGAGCCTGGATGCTCCTTCTAAGCTGCACGGTTTGGGAAGCTTAAAGGGGAGTTCGTT	180	
Sbjct 228	CAGAGCCTGGATGCTCCTTCTAAGCTGCACGGTTTGGGAAGCTTAAAGGGGAGTTCGTT	287	
Query 181	CCGGGAGAAGTCAATGAGTGCACAAACAGGCTTTCCCTTCAGAGCTTGCAGGCTCA	240	
Sbjct 288	CCGGGAGAAGTCAATGAGTGCACAAACAGGCTTTCCCTTCAGAGCTTGCAGGCTCA	347	
Query 241	GGAGTAGAGCCCAAGGCCAGCTCGCCCTGGACGTAATCAAGGTGAAGGTTCCCATGGG	300	
Sbjct 348	GGAGTAGAGCCCAAGGCCAGCTCGCCCTGGACGTAATCAAGGTGAAGGTTCCCATGGG	407	
Query 301	GAGGAGAAAGTCCGAGCGGAAGCTCTTTGCGGGCGGGTGCTCAGTATGTCAGCCCAAC	360	
Sbjct 408	GAGGAGAAAGTCCGAGCGGAAGCTCTTTGCGGGCGGGTGCTCAGTATGTCAGCCCAAC	467	

Query 361 TACGTTTACCGGCCTTTGCGGGCTCCGAATGACCTCTATTACCCCGATCAAAGCGCTAC 420
 Sbjct 468 TACGTTTACCGGCCTTTGCGGGCTCCGAATGACCTCTATTACCCCGATCAAAGCGCTAC 527
 Query 421 TTGAATCGGTGGTGGCGCTTAGAAAAGCGCTTGGGACTTCAGCACAGGCAGGGGATGCCCG 480
 Sbjct 528 TTGAATCGGTGGTGGCGCTTAGAAAAGCGCTTGGGACTTCAGCACAGGCAGGGGATGCCCG 587
 Query 481 CCCCTTGTGGCCGTGCTAGACACGGGAGTTCTTGCCACAGGACTTTAGGCCAGCAAG 540
 Sbjct 588 CCCCTTGTGGCCGTGCTAGACACGGGAGTTCTTGCCACAGGACTTTAGGCCAGCAAG 647
 Query 541 TACCTCCCGCCGGGTTAACCTGGACGTGGCTGACGGAGATGCCAATCCCACGGACGAC 600
 Sbjct 648 TACCTCCCGCCGGGTTAACCTGGACGTGGCTGACGGAGATGCCAATCCCACGGACGAC 707
 Query 601 TCGGCTCCCAACAATGGGGGCATGGTTAGAGGTGGCCTCGGTCTGGGGCCGGATACC 660
 Sbjct 708 TCGGCTCCCAACAATGGGGGCATGGTTAGAGGTGGCCTCGGTCTGGGGCCGGATACC 767
 Query 661 AACAACTCTAAGGGAATAGCAGGAACCTACCTGGGGTGGATACGTTGTTCCAATCAAGTT 720
 Sbjct 768 AACAACTCTAAGGGAATAGCAGGAACCTACCTGGGGTGGATACGTTGTTCCAATCAAGTT 827
 Query 721 TTCTACCGGGTGGTGGAGCCAGTATGAAACCTTTTCAAGGGGGTTCGGTTAGCCCGC 780
 Sbjct 828 TTCTACCGGGTGGTGGAGCCAGTATGAAACCTTTTCAAGGGGGTTCGGTTAGCCCGC 887
 Query 781 CAACTGGGGGCCAGGTCATCAACATTTGCTGGGGGTAAAGACTATGACGAGGTTCTG 840
 Sbjct 888 CAACTGGGGGCCAGGTCATCAACATTTGCTGGGGGTAAAGACTATGACGAGGTTCTG 947
 Query 841 GATGAGGAGCTGGCCGGGCTCGGAACGAGGGGAGGGTTATTGTAGCTGCGGCGGAAAC 900
 Sbjct 948 GATGAGGAGCTGGCCGGGCTCGGAACGAGGGGAGGGTTATTGTAGCTGCGGCGGAAAC 1007
 Query 901 TACGAGACCGGGAATGGGGACCGGTTATGTTCCCTGCCAGCAGCCCAACTCTCGCT 960
 Sbjct 1008 TACGAGACCGGGAATGGGGACCGGTTATGTTCCCTGCCAGCAGCCCAACTCTCGCT 1067
 Query 961 GTGGGTGCGGTAGATCTCCTTAAAAGCGGGCGAATTTTTCGGCCTATGGCCCGAGCTT 1020
 Sbjct 1068 GTGGGTGCGGTAGATCTCCTTAAAAGCGGGCGAATTTTTCGGCCTATGGCCCGAGCTT 1127
 Query 1021 GACCTAATGGTCCAGGGTGGAGGTTTTGGCGGCAGGCCCTCAGGCAACTATCGCTTT 1080
 Sbjct 1128 GACCTAATGGTCCAGGGTGGAGGTTTTGGCGGCAGGCCCTCAGGCAACTATCGCTTT 1187
 Query 1081 GTGAGCGGACCTCTTTGGCTAGCCCATCGTGGCCGGGGTGGTGGCCCTACATGAGC 1140
 Sbjct 1188 GTGAGCGGACCTCTTTGGCTAGCCCATCGTGGCCGGGGTGGTGGCCCTACATGAGC 1247
 Query 1141 AAGTACGCCAGCGAGCGGAAGGCGTGGCCTAGCCCGGACCAGGCTACCAATGCCTCATC 1200
 Sbjct 1248 AAGTACGCCAGCGAGCGGAAGGCGTGGCCTAGCCCGGACCAGGCTACCAATGCCTCATC 1307
 Query 1201 AACACCGCCGAGGACCTAGGGCTTCCGGTGGGACCCGGAATACGGCTTCGGCTGGTC 1260

Sbjct 1308 AACACCGCCGAGGACCTAGGGCTTCCGGTGGGACCCGGAATACGGCTTCGGCTGGTC 1367
 Query 1261 CGGGCCGACCGGGCGATGACGGACACCACCTACTGCTTCCCC 1302
 Sbjct 1368 CGGGCCGACCGGGCGATGACGGACACCACCTACTGCTTCCCC 1409

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RIKEN Clone ID : TEx18B07 (PC010724-41)

開始Stock :

作業開始日 B4Go QA 93588 保管場所

作業者 古谷・124 Page

Locus tag	TTHA0724
Product	serine protease
lot. No.	6078_B4Go

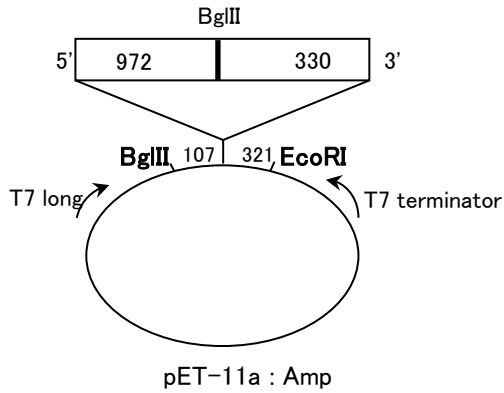


提供担当者確認印



承認印

● 予想 Vector_MAP



● 構造確認

BglIII + EcoRI cut での予想バンドサイズ

Vector : 5213 bp

Insert : 1079, 651 bp

● 配列確認

シーケンス反応はベタインを入れる事

業務准拠 (提供担当チェックリスト)

- 構造チェック(泳動写真確認)
- 配列決定
- 濃度調製 (25 ng/ul)



共同作業印

(承認担当チェックリスト)

- 構造チェック(泳動写真確認)判定
- 配列確認判定

クローンの質

- y : 構造確認・予想サイズと異なる
- z : Insert 情報が異なる
- p : 問題なく検定終了

<MEMO>

HTS解析実施