RIKEN_Clone_ID : IRAL005L16

Lot#: 7566_B5Ae

Vector : pOTB7

Gene	PPIA	
Accession No.	BC000689.2	744 bp
	CDS	498 bp

● Plasmid DNA purification

Date : 2025/01/14　　Culture : LB（25 ug/ml Chloramphenicol） 5 ml –> at 37 deg C over night

Date : 2025/01/15　　Purification : QIAGEN Miniprep kit –> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/01/15

DNA concentration（O.D.）: 133 ng/ul

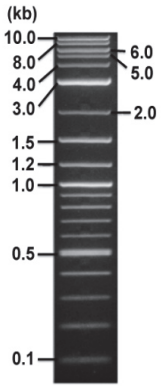
DNA	0.75 ul
Enzyme（BamHI + BglII ）	0.5 + 0.5 ul
Buffer H	1 ul
dH_2O	7.25 ul
Total	10 ul

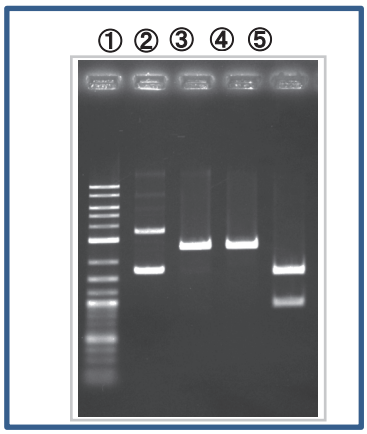
< Size of fragment expected from this clone >

BamHI	2.5 kb
BglII	2.5 kb
BamHI + BglII	1.6kb (Vector)　0.9 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder（NEB#N3200L）





①:Marker
②:uncut
③:BamHI
④:BglII
⑤:BamHI + BglII

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/01/21

DNA（133 ng/ul）	82 ul
10x TE	44 ul
dH_2O	311 ul
Total	436 ul

● Confirmation of the sequence

Date : 2025/01/16

full sequence	IRAL005L16hts01.seq

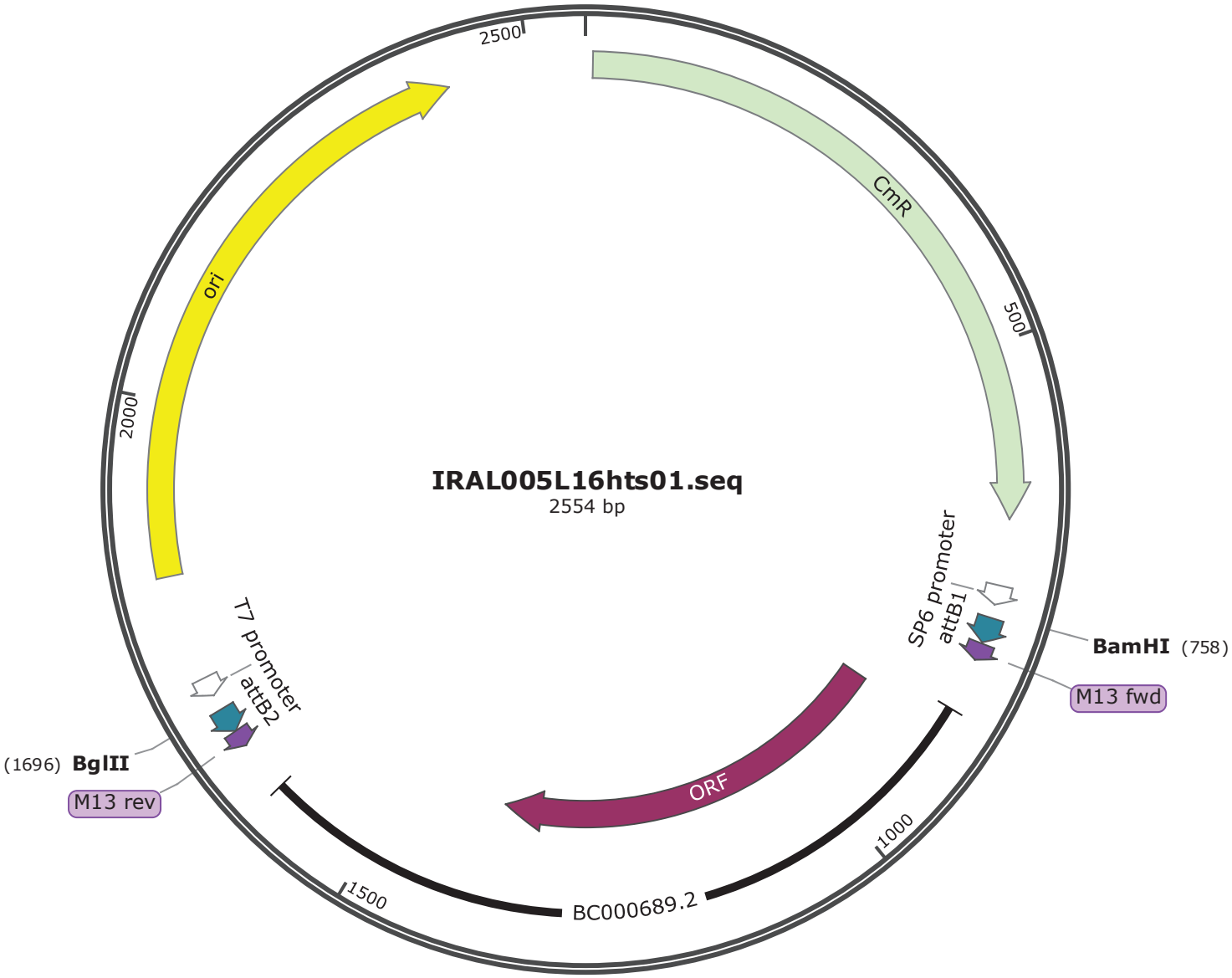
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ng/μl, Volume : μl

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APPROVED BY :


2500
CmR
500
ori
2000
IRAL005L16hts01.seq
2554 bp
SP6 promoter
attB1
BamHI (758)
M13 fwd
T7 promoter
attB2
(1696) BglII
M13 rev
ORF
1000
1500
BC000689.2

BLAST Results

Questions/comments

Blast 2 sequences

Job title: BC000689:Homo sapiens peptidylprolyl isomerase...

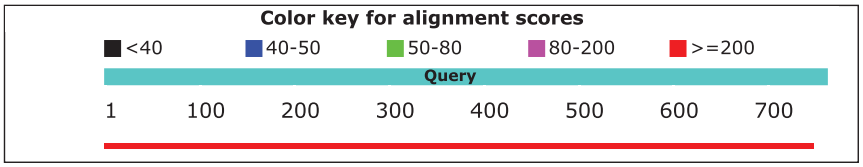
RID SHFUXRZE114 (Expires on 01-17 15:12 pm)

Query ID	BC000689.2	**Subject ID**	lcl|Query_2667655
Description	Homo sapiens peptidylprolyl isomerase A (cyclophilin A), mRNA (cDNA clone MGC:2351 IMAGE:3349335), complete cds	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	744	**Subject Length**	2554
		Program	BLASTN 2.16.1+

IRAL005L16hts01.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	1375	1375	100%	0.0	100.00%	Query_2667655

Alignments

Sequence ID: Query_2667655 Length: 2554 Number of Matches: 1
Range 1: 859 to 1602

Score	Expect	Identities	Gaps	Strand	Frame
1375 bits(744)	0.0()	744/744(100%)	0/744(0%)	Plus/Plus	

Features:

```
CDS:Peptidylprolyl i  1                       M  V  N  P  T  V  F  F  D  I  A  V  D
Query                 1    GGAAAACCGTGTACTATTAGCCATGGTCAACCCCACCGTGTTCTTCGACATTGCCGTCGA  60
Sbjct                 859  ............................................................  918

CDS:Peptidylprolyl i  14     G  E  P  L  G  R  V  S  F  E  L  F  A  D  K  V  P  K  T  A
Query                 61   CGGCGAGCCCTTGGGCCGCGTCTCCTTTGAGCTGTTTGCAGACAAGGTCCCAAAGACAGC  120
Sbjct                 919  ............................................................  978

CDS:Peptidylprolyl i  34     E  N  F  R  A  L  S  T  G  E  K  G  F  G  Y  K  G  S  C  F
Query                 121  AGAAAATTTTCGTGCTCTGAGCACTGGAGAGAAAGGATTTGGTTATAAGGGTTCCTGCTT  180
Sbjct                 979  ............................................................  1038

CDS:Peptidylprolyl i  54     H  R  I  I  P  G  F  M  C  Q  G  G  D  F  T  R  H  N  G  T
Query                 181  TCACAGAATTATTCCAGGGTTTATGTGTCAGGGTGGTGACTTCACACGCCATAATGGCAC  240
Sbjct                 1039 ............................................................  1098

CDS:Peptidylprolyl i  74     G  G  K  S  I  Y  G  E  K  F  E  D  E  N  F  I  L  K  H  T
Query                 241  TGGTGGCAAGTCCATCTATGGGGAGAAATTTGAAGATGAGAACTTCATCCTAAAGCATAC  300
Sbjct                 1099 ............................................................  1158

CDS:Peptidylprolyl i  94     G  P  G  I  L  S  M  A  N  A  G  P  N  T  N  G  S  Q  F  F
Query                 301  GGGTCCTGGCATCTTGTCCATGGCAAATGCTGGACCCAACACAAATGGTTCCCAGTTTTT  360
Sbjct                 1159 ............................................................  1218
```

```
CDS:Peptidylprolyl i  114    I  C  T  A  K  T  E  W  L  D  G  K  H  V  V  F  G  K  V  K
Query                361    CATCTGCACTGCCAAGACTGAGTGGTTGGATGGCAAGCATGTGGTGTTTGGCAAAGTGAA  420
Sbjct                1219   ............................................................  1278

CDS:Peptidylprolyl i  134    E  G  M  N  I  V  E  A  M  E  R  F  G  S  R  N  G  K  T  S
Query                421    AGAAGGCATGAATATTGTGGAGGCCATGGAGCGCTTTGGGTCCAGGAATGGCAAGACCAG  480
Sbjct                1279   ............................................................  1338

CDS:Peptidylprolyl i  154    K  K  I  T  I  A  D  C  G  Q  L  E
Query                481    CAAGAAGATCACCATTGCTGACTGTGGACAACTCGAATAAGTTTGACTTGTGTTTTATCT  540
Sbjct                1339   ............................................................  1398

Query                541    TAACCACCAGATCATTCCTTCTGTAGCTCAGGAGAGCACCCCTCCACCCCATTTGCTCGC  600
Sbjct                1399   ............................................................  1458

Query                601    AGTATCCTAGAATCTTTGTGCTCTCGCTGCAGTTCCCTTTGGGTTCCATGTTTTCCTTGT  660
Sbjct                1459   ............................................................  1518

Query                661    TCCCTCCCATGCCTAGCTGGATTGCAGAGTTAAGTTTATGATTATGAAATAAAAACTAAA  720
Sbjct                1519   ............................................................  1578

Query                721    TAACaaaaaaaaaaaaaaaaaaa  744
Sbjct                1579   ........................  1602
```

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BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_021130:Homo sapiens peptidylprolyl isomerase...

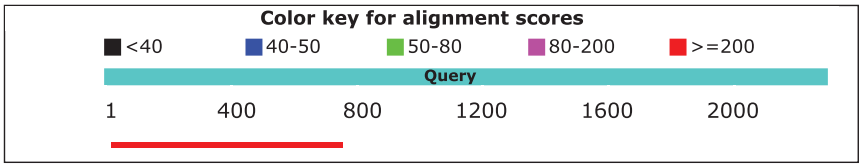
RID SE13RZA4114 (Expires on 01-16 07:42 am)

Query ID NM_021130.5
Description Homo sapiens peptidylprolyl isomerase A (PPIA), transcript variant 1, mRNA
Molecule type nucleic acid
Query Length 2237

Subject ID BC000689.2
Description Homo sapiens peptidylprolyl isomerase A (cyclophilin A), mRNA (cDNA clone MGC:2351 IMAGE:3349335), complete cds
See details
Molecule type nucleic acid
Subject Length 744
Program BLASTN 2.16.1+

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
Homo sapiens peptidylprolyl isomerase A (cyclophilin A), mRNA (cDNA clone MGC:2351 IMAGE:3349335), complete cds	1341	1341	32%	0.0	100.00%	BC000689.2

Alignments

Homo sapiens peptidylprolyl isomerase A (cyclophilin A), mRNA (cDNA clone MGC:2351 IMAGE:3349335), complete cds
Sequence ID: **BC000689.2** Length: 744 Number of Matches: 1
Range 1: 1 to 726

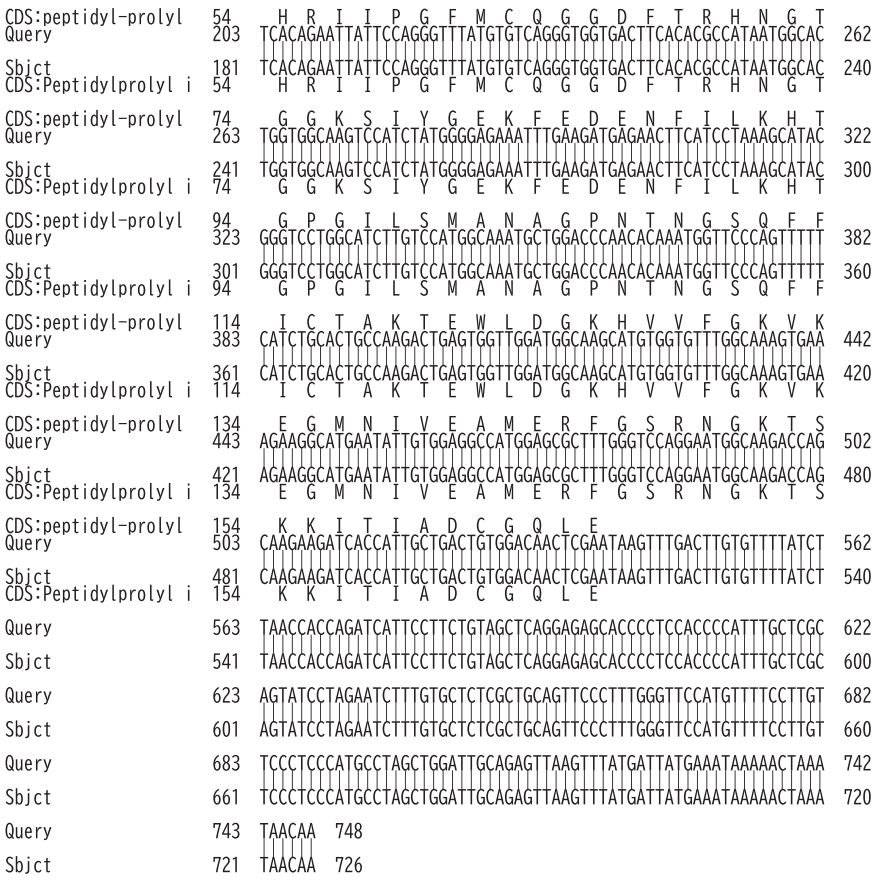
Score	Expect	Identities	Gaps	Strand	Frame
1341 bits(726)	0.0()	726/726(100%)	0/726(0%)	Plus/Plus	

Features:

```
CDS:peptidyl-prolyl   1                          M  V  N  P  T  V  F  F  D  I  A  V  D
Query                 23   GGAAAACCGTGTACTATTAGCCATGGTCAACCCCACCGTGTTCTTCGACATTGCCGTCGA  82
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1    GGAAAACCGTGTACTATTAGCCATGGTCAACCCCACCGTGTTCTTCGACATTGCCGTCGA  60
CDS:Peptidylprolyl i  1                          M  V  N  P  T  V  F  F  D  I  A  V  D

CDS:peptidyl-prolyl   14     G  E  P  L  G  R  V  S  F  E  L  F  A  D  K  V  P  K  T  A
Query                 83   CGGCGAGCCCTTGGGCCGCGTCTCCTTTGAGCTGTTTGCAGACAAGGTCCCAAAGACAGC  142
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 61   CGGCGAGCCCTTGGGCCGCGTCTCCTTTGAGCTGTTTGCAGACAAGGTCCCAAAGACAGC  120
CDS:Peptidylprolyl i  14     G  E  P  L  G  R  V  S  F  E  L  F  A  D  K  V  P  K  T  A

CDS:peptidyl-prolyl   34     E  N  F  R  A  L  S  T  G  E  K  G  F  G  Y  K  G  S  C  F
Query                 143  AGAAAATTTTCGTGCTCTGAGCACTGGAGAGAAAGGATTTGGTTATAAGGGTTCCTGCTT  202
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 121  AGAAAATTTTCGTGCTCTGAGCACTGGAGAGAAAGGATTTGGTTATAAGGGTTCCTGCTT  180
CDS:Peptidylprolyl i  34     E  N  F  R  A  L  S  T  G  E  K  G  F  G  Y  K  G  S  C  F
```



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