RIKEN_Clone_ID : IRAL004D04

Lot#: 7566_B4Ji

Vector : pOTB7

Gene	HLA-E	
Accession No.	BC002578.2	1670 bp
	CDS	1077 bp

● Plasmid DNA purification

Date : 2024/10/24　　Culture : LB（25 ug/ml Chloramphenicol） 5 ml –> at 37 deg C over night

Date : 2024/10/25　　Purification : QIAGEN Miniprep kit –> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/10/25

DNA concentration（O.D.）: 202 ng/ul

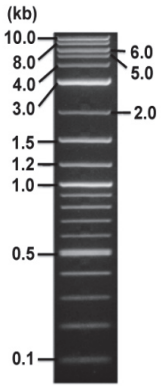
DNA	0.5 ul
Enzyme（BamHI + BglII ）	0.5 + 0.5 ul
Buffer H	1 ul
dH_2O	7.5 ul
Total	10 ul

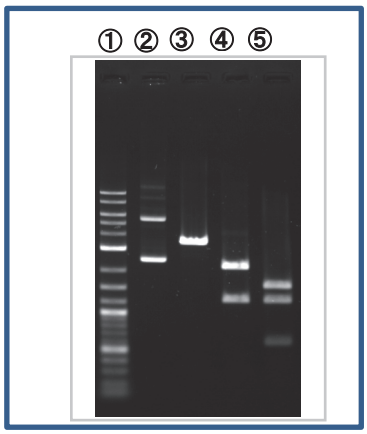
< Size of fragment expected from this clone >

BamHI	3.5 kb
BglII	2.2, 1.3 kb
BamHI + BglII	1.6kb (Vector)　1.3, 0.6 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 : 2024/11/01

DNA（202 ng/ul）	88 ul
10x TE	71 ul
dH_2O	552 ul
Total	711 ul

● Confirmation of the sequence

Date : 2024/10/31

full sequnece	IRAL004D04hts01.seq

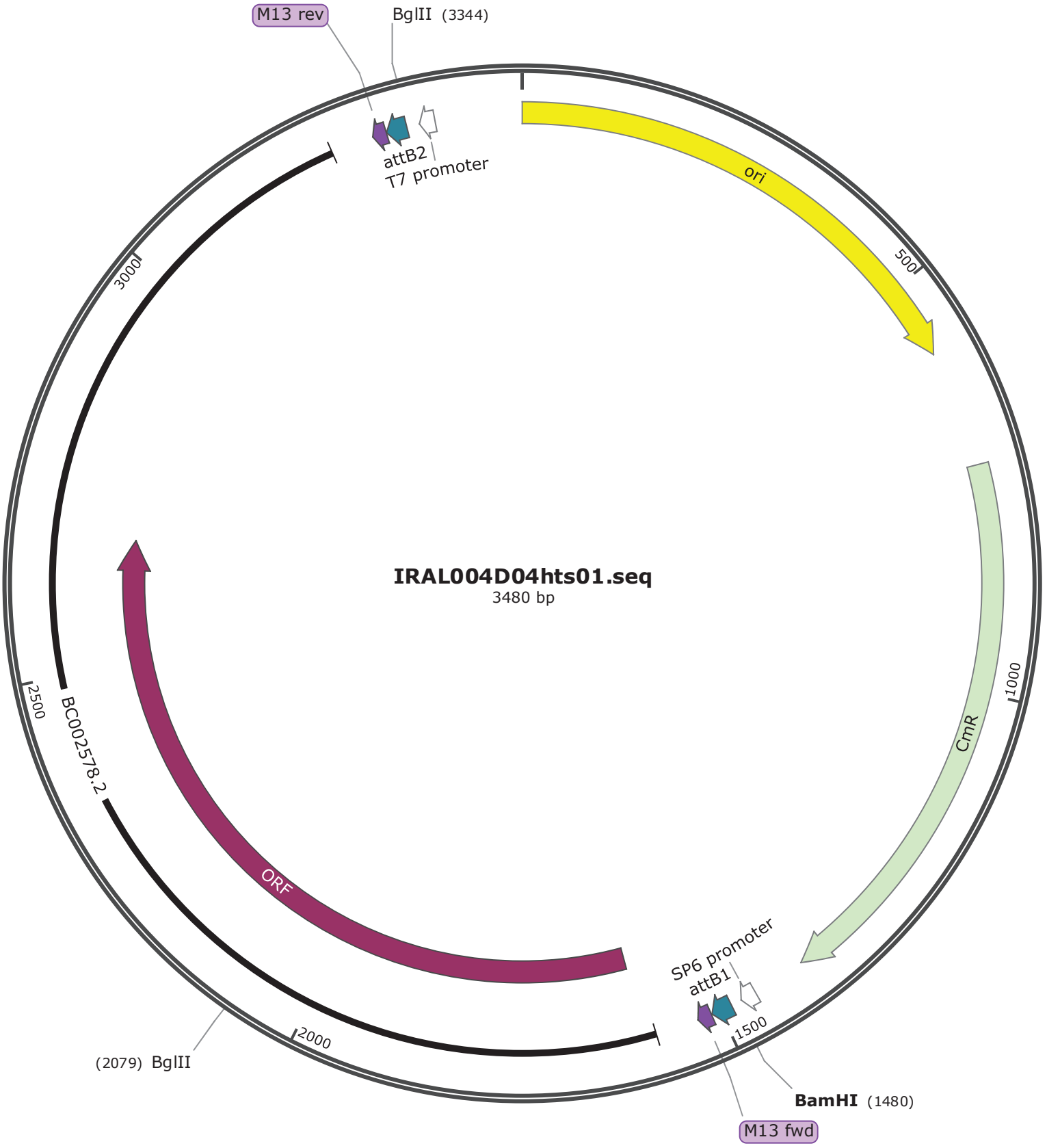
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ng/μl, Volume : μl

検 '24.11.01 笹沼

APPROVED BY :


M13 rev
BglII (3344)
attB2
T7 promoter
ori
500
1000
CmR
SP6 promoter
attB1
1500
BamHI (1480)
M13 fwd
2000
(2079) BglII
ORF
BC002578.2
2500
3000
IRAL004D04hts01.seq
3480 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: BC002578:Homo sapiens major histocompatibility...

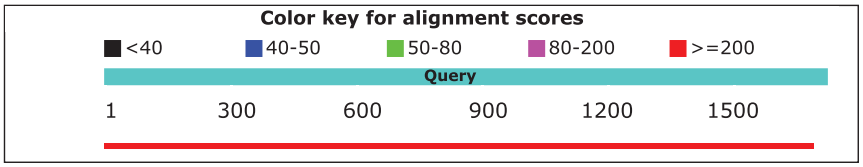
RID J6D7XWZ3114 (Expires on 11-01 15:42 pm)

Query ID	BC002578.2	**Subject ID**	lcl|Query_5708915
Description	Homo sapiens major histocompatibility complex, class I, E, mRNA (cDNA clone MGC:1408 IMAGE:3140835), complete cds	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	1670	**Subject Length**	3480
		Program	BLASTN 2.16.0+

IRAL004D04hts01.seq

Graphic Summary

Distribution of the top 3 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	3085	3194	100%	0.0	100.00%	Query_5708915

Alignments

Sequence ID: Query_5708915 Length: 3480 Number of Matches: 3
Range 1: 1581 to 3250

Score	Expect	Identities	Gaps	Strand	Frame
3085 bits(1670)	0.0()	1670/1670(100%)	0/1670(0%)	Plus/Plus	

Features:

```
CDS:Major histocompa  1                    M  V  D  G  T  L  L  L  L  L  S  E  A  L  A
Query                 1    CAGAGGCTGGGATCATGGTAGATGGAACCCTCCTTTTACTCCTCTCGGAGGCCCTGGCCC  60
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1581 CAGAGGCTGGGATCATGGTAGATGGAACCCTCCTTTTACTCCTCTCGGAGGCCCTGGCCC 1640

CDS:Major histocompa  16   L  T  Q  T  W  A  G  S  H  S  L  K  Y  F  H  T  S  V  S  R
Query                 61   TTACCCAGACCTGGGCGGGCTCCCACTCCTTGAAGTATTTCCACACTTCCGTGTCCCGGC  120
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1641 TTACCCAGACCTGGGCGGGCTCCCACTCCTTGAAGTATTTCCACACTTCCGTGTCCCGGC 1700

CDS:Major histocompa  36   P  G  R  G  E  P  R  F  I  S  V  G  Y  V  D  D  T  Q  F  V
Query                 121  CCGGCCGCGGGGAGCCCCGCTTCATCTCTGTGGGCTACGTGGACGACACCCAGTTCGTGC  180
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1701 CCGGCCGCGGGGAGCCCCGCTTCATCTCTGTGGGCTACGTGGACGACACCCAGTTCGTGC 1760

CDS:Major histocompa  56   R  F  D  N  D  A  A  S  P  R  M  V  P  R  A  P  W  M  E  Q
Query                 181  GCTTCGACAACGACGCCGCGAGTCCGAGGATGGTGCCGCGGGCGCCGTGGATGGAGCAGG  240
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1761 GCTTCGACAACGACGCCGCGAGTCCGAGGATGGTGCCGCGGGCGCCGTGGATGGAGCAGG 1820

CDS:Major histocompa  76   E  G  S  E  Y  W  D  R  E  T  R  S  A  R  D  T  A  Q  I  F
Query                 241  AGGGGTCAGAGTATTGGGACCGGGAGACACGGAGCGCCAGGGACACCGCACAGATTTTCC  300
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Sbjct                1821  AGGGGTCAGAGTATTGGGACCGGGAGACACGGAGCGCCAGGGACACCGCACAGATTTTCC  1880

CDS:Major histocompa   96  R  V  N  L  R  T  L  R  G  Y  Y  N  Q  S  E  A  G  S  H  T
Query                 301  GAGTGAACCTGCGGACGCTGCGCGGCTACTACAATCAGAGCGAGGCCGGGTCTCACACCC  360
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                1881  GAGTGAACCTGCGGACGCTGCGCGGCTACTACAATCAGAGCGAGGCCGGGTCTCACACCC  1940

CDS:Major histocompa  116  L  Q  W  M  H  G  C  E  L  G  P  D  R  R  F  L  R  G  Y  E
Query                 361  TGCAGTGGATGCATGGCTGCGAGCTGGGGCCCGACAGGCGCTTCCTCCGCGGGTATGAAC  420
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                1941  TGCAGTGGATGCATGGCTGCGAGCTGGGGCCCGACAGGCGCTTCCTCCGCGGGTATGAAC  2000

CDS:Major histocompa  136  Q  F  A  Y  D  G  K  D  Y  L  T  L  N  E  D  L  R  S  W  T
Query                 421  AGTTCGCCTACGACGGCAAGGATTATCTCACCCTGAATGAGGACCTGCGCTCCTGGACCG  480
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2001  AGTTCGCCTACGACGGCAAGGATTATCTCACCCTGAATGAGGACCTGCGCTCCTGGACCG  2060

CDS:Major histocompa  156  A  V  D  T  A  A  Q  I  S  E  Q  K  S  N  D  A  S  E  A  E
Query                 481  CGGTGGACACGGCGGCTCAGATCTCCGAGCAAAAGTCAAATGATGCCTCTGAGGCGGAGC  540
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2061  CGGTGGACACGGCGGCTCAGATCTCCGAGCAAAAGTCAAATGATGCCTCTGAGGCGGAGC  2120

CDS:Major histocompa  176  H  Q  R  A  Y  L  E  D  T  C  V  E  W  L  H  K  Y  L  E  K
Query                 541  ACCAGAGAGCCTACCTGGAAGACACATGCGTGGAGTGGCTCCACAAATACCTGGAGAAGG  600
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2121  ACCAGAGAGCCTACCTGGAAGACACATGCGTGGAGTGGCTCCACAAATACCTGGAGAAGG  2180

CDS:Major histocompa  196  G  K  E  T  L  L  H  L  E  P  P  K  T  H  V  T  H  H  P  I
Query                 601  GGAAGGAGACGCTGCTTCACCTGGAGCCCCCAAAGACACACGTGACTCACCACCCCATCT  660
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2181  GGAAGGAGACGCTGCTTCACCTGGAGCCCCCAAAGACACACGTGACTCACCACCCCATCT  2240

CDS:Major histocompa  216  S  D  H  E  A  T  L  R  C  W  A  L  G  F  Y  P  A  E  I  T
Query                 661  CTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACAC  720
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2241  CTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACAC  2300

CDS:Major histocompa  236  L  T  W  Q  Q  D  G  E  G  H  T  Q  D  T  E  L  V  E  T  R
Query                 721  TGACCTGGCAGCAGGATGGGGAGGGCCATACCCAGGACACGGAGCTCGTGGAGACCAGGC  780
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2301  TGACCTGGCAGCAGGATGGGGAGGGCCATACCCAGGACACGGAGCTCGTGGAGACCAGGC  2360

CDS:Major histocompa  256  P  A  G  D  G  T  F  Q  K  W  A  A  V  V  V  P  S  G  E  E
Query                 781  CTGCAGGGGATGGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTTCTGGAGAGGAGC  840
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2361  CTGCAGGGGATGGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTTCTGGAGAGGAGC  2420

CDS:Major histocompa  276  Q  R  Y  T  C  H  V  Q  H  E  G  L  P  E  P  V  T  L  R  W
Query                 841  AGAGATACACGTGCCATGTGCAGCATGAGGGGCTACCCGAGCCCGTCACCCTGAGATGGA  900
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2421  AGAGATACACGTGCCATGTGCAGCATGAGGGGCTACCCGAGCCCGTCACCCTGAGATGGA  2480

CDS:Major histocompa  296  K  P  A  S  Q  P  T  I  P  I  V  G  I  I  A  G  L  V  L  L
Query                 901  AGCCGGCTTCCCAGCCCACCATCCCCATCGTGGGCATCATTGCTGGCCTGGTTCTCCTTG  960
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2481  AGCCGGCTTCCCAGCCCACCATCCCCATCGTGGGCATCATTGCTGGCCTGGTTCTCCTTG  2540

CDS:Major histocompa  316  G  S  V  V  S  G  A  V  V  A  A  V  I  W  R  K  K  S  S  G
Query                 961  GATCTGTGGTCTCTGGAGCTGTGGTTGCTGCTGTGATATGGAGGAAGAAGAGCTCAGGTG  1020
```



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                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2541  GATCTGTGGTCTCTGGAGCTGTGGTTGCTGCTGTGATATGGAGGAAGAAGAGCTCAGGTG  2600

CDS:Major histocompa  336  G  K  G  G  S  Y  S  K  A  E  W  S  D  S  A  Q  G  S  E  S
Query                1021  GAAAAGGAGGGAGCTACTCTAAGGCTGAGTGGAGCGACAGTGCCCAGGGGTCTGAGTCTC  1080
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2601  GAAAAGGAGGGAGCTACTCTAAGGCTGAGTGGAGCGACAGTGCCCAGGGGTCTGAGTCTC  2660

CDS:Major histocompa  356  H  S  L
Query                1081  ACAGCTTGTAAAGCCTGAGACAGCTGCCTTGTGTGCGACTGAGATGCACAGCTGCCTTGT  1140
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2661  ACAGCTTGTAAAGCCTGAGACAGCTGCCTTGTGTGCGACTGAGATGCACAGCTGCCTTGT  2720

Query                1141  GTGCGACTGAGATGCAGGATTTCCTCACGCCTCCCCTATGTGTCTTAGGGGACTCTGGCT  1200
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2721  GTGCGACTGAGATGCAGGATTTCCTCACGCCTCCCCTATGTGTCTTAGGGGACTCTGGCT  2780

Query                1201  TCTCTTTTTGCAAGGGCCTCTGAATCTGTCTGTGTCCCTGTTAGCACAATGTGAGGAGGT  1260
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2781  TCTCTTTTTGCAAGGGCCTCTGAATCTGTCTGTGTCCCTGTTAGCACAATGTGAGGAGGT  2840

Query                1261  AGAGAAACAGTCCACCTCTGTGTCTACCATGACCCCCTTCCTCACACTGACCTGTGTTCC  1320
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2841  AGAGAAACAGTCCACCTCTGTGTCTACCATGACCCCCTTCCTCACACTGACCTGTGTTCC  2900

Query                1321  TTCCCTGTTCTCTTTTCTATTAAAAATAAGAACCTGGGCAGAGTGCGGCAGCTCATGCCT  1380
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2901  TTCCCTGTTCTCTTTTCTATTAAAAATAAGAACCTGGGCAGAGTGCGGCAGCTCATGCCT  2960

Query                1381  GTAATCCCAGCACTTAGGGAGGCCGAGGAGGGCAGATCACGAGGTCAGGAGATCGAAACC  1440
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                2961  GTAATCCCAGCACTTAGGGAGGCCGAGGAGGGCAGATCACGAGGTCAGGAGATCGAAACC  3020

Query                1441  ATCCTGGCTAACACGGTGAAACCCCGTCTCTACTaaaaaatacaaaaaaTTAGCTGGGCG  1500
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                3021  ATCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAAATACAAAAAATTAGCTGGGCG  3080

Query                1501  CAGAGGCACGGGCCTGTAGTCCCAGCTACTCAGGAGGCGGAGGCAGGAGAATGGCGTCAA  1560
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                3081  CAGAGGCACGGGCCTGTAGTCCCAGCTACTCAGGAGGCGGAGGCAGGAGAATGGCGTCAA  3140

Query                1561  CCCGGGAGGCGGAGGTTGCAGTGAGCCAGGATTGTGCGACTGCACTCCAGCCTGGGTGAC  1620
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                3141  CCCGGGAGGCGGAGGTTGCAGTGAGCCAGGATTGTGCGACTGCACTCCAGCCTGGGTGAC  3200

Query                1621  AGGGTGAAACGCCATCTCaaaaaataaaaattaaaaaaaaaaaaaaaaaa  1670
                           ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                3201  AGGGTGAAACGCCATCTCAAAAAATAAAAATTAAAAAAAAAAAAAAAAAA  3250
```

Range 2: 2680 to 2708

Score	Expect	Identities	Gaps	Strand	Frame
54.7 bits(29)	2e-10()	29/29(100%)	0/29(0%)	Plus/Plus	

Features:

BLAST Results

Questions/comments

Blast 2 sequences

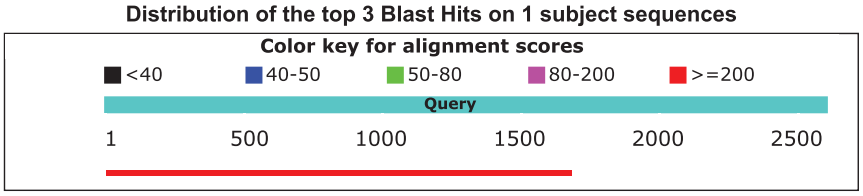
Job title: NM_005516:Homo sapiens major histocompatibility...

RID HKRPTSCW114 (Expires on 10-25 13:44 pm)

Query ID NM_005516.6
Description Homo sapiens major histocompatibility complex, class I, E (HLA-E), mRNA
Molecule type nucleic acid
Query Length 2548

Subject ID BC002578.2
Description Homo sapiens major histocompatibility complex, class I, E, mRNA (cDNA clone MGC:1408 IMAGE:3140835), complete cds
See details
Molecule type nucleic acid
Subject Length 1670
Program BLASTN 2.16.0+

Graphic Summary



Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Homo sapiens major histocompatibility complex, class I, E, mRNA (cDNA clone MGC:1408 IMAGE:3140835), complete cds	3055	3164	65%	0.0	99.76%	BC002578.2

Alignments

Homo sapiens major histocompatibility complex, class I, E, mRNA (cDNA clone MGC:1408 IMAGE:3140835), complete cds
Sequence ID: **BC002578.2** Length: 1670 Number of Matches: 3
Range 1: 1 to 1666

Score	Expect	Identities	Gaps	Strand	Frame
3055 bits(1654)	0.0()	1662/1666(99%)	0/1666(0%)	Plus/Plus	

Features:

```
CDS:HLA class I hist  1                   M  V  D  G  T  L  L  L  L  L  S  E  A  L  A
Query                 10  CAGAGGCTGGGATCATGGTAGATGGAACCCTCCTTTTACTCCTCTCGGAGGCCCTGGCCC  69
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1   CAGAGGCTGGGATCATGGTAGATGGAACCCTCCTTTTACTCCTCTCGGAGGCCCTGGCCC  60
CDS:Major histocompa  1                   M  V  D  G  T  L  L  L  L  L  S  E  A  L  A

CDS:HLA class I hist  16  L  T  Q  T  W  A  G  S  H  S  L  K  Y  F  H  T  S  V  S  R
Query                 70  TTACCCAGACCTGGGCGGGCTCCCACTCCTTGAAGTATTTCCACACTTCCGTGTCCCGGC  129
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 61  TTACCCAGACCTGGGCGGGCTCCCACTCCTTGAAGTATTTCCACACTTCCGTGTCCCGGC  120
CDS:Major histocompa  16  L  T  Q  T  W  A  G  S  H  S  L  K  Y  F  H  T  S  V  S  R

CDS:HLA class I hist  36  P  G  R  G  E  P  R  F  I  S  V  G  Y  V  D  D  T  Q  F  V
Query                 130 CCGGCCGCGGGGAGCCCCGCTTCATCTCTGTGGGCTACGTGGACGACACCCAGTTCGTGC  189
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 121 CCGGCCGCGGGGAGCCCCGCTTCATCTCTGTGGGCTACGTGGACGACACCCAGTTCGTGC  180
CDS:Major histocompa  36  P  G  R  G  E  P  R  F  I  S  V  G  Y  V  D  D  T  Q  F  V
```

```
CDS:HLA class I hist  56   R  F  D  N  D  A  A  S  P  R  M  V  P  R  A  P  W  M  E  Q
Query                 190  GCTTCGACAACGACGCCGCGAGTCCGAGGATGGTGCCGCGGGCGCCGTGGATGGAGCAGG  249
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 181  GCTTCGACAACGACGCCGCGAGTCCGAGGATGGTGCCGCGGGCGCCGTGGATGGAGCAGG  240
CDS:Major histocompa  56   R  F  D  N  D  A  A  S  P  R  M  V  P  R  A  P  W  M  E  Q

CDS:HLA class I hist  76   E  G  S  E  Y  W  D  R  E  T  R  S  A  R  D  T  A  Q  I  F
Query                 250  AGGGGTCAGAGTATTGGGACCGGGAGACACGGAGCGCCAGGGACACCGCACAGATTTTCC  309
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 241  AGGGGTCAGAGTATTGGGACCGGGAGACACGGAGCGCCAGGGACACCGCACAGATTTTCC  300
CDS:Major histocompa  76   E  G  S  E  Y  W  D  R  E  T  R  S  A  R  D  T  A  Q  I  F

CDS:HLA class I hist  96   R  V  N  L  R  T  L  R  G  Y  Y  N  Q  S  E  A  G  S  H  T
Query                 310  GAGTGAATCTGCGGACGCTGCGCGGCTACTACAATCAGAGCGAGGCCGGGTCTCACACCC  369
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 301  GAGTGAACCTGCGGACGCTGCGCGGCTACTACAATCAGAGCGAGGCCGGGTCTCACACCC  360
CDS:Major histocompa  96   R  V  N  L  R  T  L  R  G  Y  Y  N  Q  S  E  A  G  S  H  T

CDS:HLA class I hist  116  L  Q  W  M  H  G  C  E  L  G  P  D  G  R  F  L  R  G  Y  E
Query                 370  TGCAGTGGATGCATGGCTGCGAGCTGGGGCCCGACGGGCGCTTCCTCCGCGGGTATGAAC  429
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 361  TGCAGTGGATGCATGGCTGCGAGCTGGGGCCCGACAGGCGCTTCCTCCGCGGGTATGAAC  420
CDS:Major histocompa  116  L  Q  W  M  H  G  C  E  L  G  P  D  R  R  F  L  R  G  Y  E

CDS:HLA class I hist  136  Q  F  A  Y  D  G  K  D  Y  L  T  L  N  E  D  L  R  S  W  T
Query                 430  AGTTCGCCTACGACGGCAAGGATTATCTCACCCTGAATGAGGACCTGCGCTCCTGGACCG  489
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 421  AGTTCGCCTACGACGGCAAGGATTATCTCACCCTGAATGAGGACCTGCGCTCCTGGACCG  480
CDS:Major histocompa  136  Q  F  A  Y  D  G  K  D  Y  L  T  L  N  E  D  L  R  S  W  T

CDS:HLA class I hist  156  A  V  D  T  A  A  Q  I  S  E  Q  K  S  N  D  A  S  E  A  E
Query                 490  CGGTGGACACGGCGGCTCAGATCTCCGAGCAAAAGTCAAATGATGCCTCTGAGGCGGAGC  549
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 481  CGGTGGACACGGCGGCTCAGATCTCCGAGCAAAAGTCAAATGATGCCTCTGAGGCGGAGC  540
CDS:Major histocompa  156  A  V  D  T  A  A  Q  I  S  E  Q  K  S  N  D  A  S  E  A  E

CDS:HLA class I hist  176  H  Q  R  A  Y  L  E  D  T  C  V  E  W  L  H  K  Y  L  E  K
Query                 550  ACCAGAGAGCCTACCTGGAAGACACATGCGTGGAGTGGCTCCACAAATACCTGGAGAAGG  609
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 541  ACCAGAGAGCCTACCTGGAAGACACATGCGTGGAGTGGCTCCACAAATACCTGGAGAAGG  600
CDS:Major histocompa  176  H  Q  R  A  Y  L  E  D  T  C  V  E  W  L  H  K  Y  L  E  K

CDS:HLA class I hist  196  G  K  E  T  L  L  H  L  E  P  P  K  T  H  V  T  H  H  P  I
Query                 610  GGAAGGAGACGCTGCTTCACCTGGAGCCCCCAAAGACACACGTGACTCACCACCCCATCT  669
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 601  GGAAGGAGACGCTGCTTCACCTGGAGCCCCCAAAGACACACGTGACTCACCACCCCATCT  660
CDS:Major histocompa  196  G  K  E  T  L  L  H  L  E  P  P  K  T  H  V  T  H  H  P  I

CDS:HLA class I hist  216  S  D  H  E  A  T  L  R  C  W  A  L  G  F  Y  P  A  E  I  T
Query                 670  CTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACAC  729
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 661  CTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACAC  720
CDS:Major histocompa  216  S  D  H  E  A  T  L  R  C  W  A  L  G  F  Y  P  A  E  I  T

CDS:HLA class I hist  236  L  T  W  Q  Q  D  G  E  G  H  T  Q  D  T  E  L  V  E  T  R
Query                 730  TGACCTGGCAGCAGGATGGGGAGGGCCATACCCAGGACACGGAGCTCGTGGAGACCAGGC  789
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 721  TGACCTGGCAGCAGGATGGGGAGGGCCATACCCAGGACACGGAGCTCGTGGAGACCAGGC  780
CDS:Major histocompa  236  L  T  W  Q  Q  D  G  E  G  H  T  Q  D  T  E  L  V  E  T  R
```

317 T>C

405 G>A (G128R)

```
CDS:HLA class I hist  256  P  A  G  D  G  T  F  Q  K  W  A  A  V  V  V  P  S  G  E  E
Query                 790  CTGCAGGGGATGGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTTCTGGAGAGGAGC  849
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 781  CTGCAGGGGATGGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTTCTGGAGAGGAGC  840
CDS:Major histocompa  256  P  A  G  D  G  T  F  Q  K  W  A  A  V  V  V  P  S  G  E  E

CDS:HLA class I hist  276  Q  R  Y  T  C  H  V  Q  H  E  G  L  P  E  P  V  T  L  R  W
Query                 850  AGAGATACACGTGCCATGTGCAGCATGAGGGGCTACCCGAGCCCGTCACCCTGAGATGGA  909
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 841  AGAGATACACGTGCCATGTGCAGCATGAGGGGCTACCCGAGCCCGTCACCCTGAGATGGA  900
CDS:Major histocompa  276  Q  R  Y  T  C  H  V  Q  H  E  G  L  P  E  P  V  T  L  R  W

CDS:HLA class I hist  296  K  P  A  S  Q  P  T  I  P  I  V  G  I  I  A  G  L  V  L  L
Query                 910  AGCCGGCTTCCCAGCCCACCATCCCCATCGTGGGCATCATTGCTGGCCTGGTTCTCCTTG  969
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 901  AGCCGGCTTCCCAGCCCACCATCCCCATCGTGGGCATCATTGCTGGCCTGGTTCTCCTTG  960
CDS:Major histocompa  296  K  P  A  S  Q  P  T  I  P  I  V  G  I  I  A  G  L  V  L  L

CDS:HLA class I hist  316  G  S  V  V  S  G  A  V  V  A  A  V  I  W  R  K  K  S  S  G
Query                 970  GATCTGTGGTCTCTGGAGCTGTGGTTGCTGCTGTGATATGGAGGAAGAAGAGCTCAGGTG  1029
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 961  GATCTGTGGTCTCTGGAGCTGTGGTTGCTGCTGTGATATGGAGGAAGAAGAGCTCAGGTG  1020
CDS:Major histocompa  316  G  S  V  V  S  G  A  V  V  A  A  V  I  W  R  K  K  S  S  G

CDS:HLA class I hist  336  G  K  G  G  S  Y  S  K  A  E  W  S  D  S  A  Q  G  S  E  S
Query                 1030 GAAAAGGAGGGAGCTACTCTAAGGCTGAGTGGAGCGACAGTGCCCAGGGGTCTGAGTCTC  1089
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1021 GAAAAGGAGGGAGCTACTCTAAGGCTGAGTGGAGCGACAGTGCCCAGGGGTCTGAGTCTC  1080
CDS:Major histocompa  336  G  K  G  G  S  Y  S  K  A  E  W  S  D  S  A  Q  G  S  E  S

CDS:HLA class I hist  356  H  S  L
Query                 1090 ACAGCTTGTAAAGCCTGAGACAGCTGCCTTGTGTGCGACTGAGATGCACAGCTGCCTTGT  1149
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1081 ACAGCTTGTAAAGCCTGAGACAGCTGCCTTGTGTGCGACTGAGATGCACAGCTGCCTTGT  1140
CDS:Major histocompa  356  H  S  L

Query                 1150 GTGCGACTGAGATGCAGGATTTCCTCACGCCTCCCCTATGTGTCTTAGGGGACTCTGGCT  1209
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1141 GTGCGACTGAGATGCAGGATTTCCTCACGCCTCCCCTATGTGTCTTAGGGGACTCTGGCT  1200

Query                 1210 TCTCTTTTTGCAAGGGCCTCTGAATCTGTCTGTGTCCCTGTTAGCACAATGTGAGGAGGT  1269
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1201 TCTCTTTTTGCAAGGGCCTCTGAATCTGTCTGTGTCCCTGTTAGCACAATGTGAGGAGGT  1260

Query                 1270 AGAGAAACAGTCCACCTCTGTGTCTACCATGACCCCCTTCCTCACACTGACCTGTGTTCC  1329
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1261 AGAGAAACAGTCCACCTCTGTGTCTACCATGACCCCCTTCCTCACACTGACCTGTGTTCC  1320

Query                 1330 TTCCCTGTTCTCTTTTCTATTAAAAATAAGAACCTGGGCAGAGTGCGGCAGCTCATGCCT  1389
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1321 TTCCCTGTTCTCTTTTCTATTAAAAATAAGAACCTGGGCAGAGTGCGGCAGCTCATGCCT  1380

Query                 1390 GTAATCCCAGCACTTAGGGAGGCCGAGGAGGGCAGATCACGAGGTCAGGAGATCGAAACC  1449
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 1381 GTAATCCCAGCACTTAGGGAGGCCGAGGAGGGCAGATCACGAGGTCAGGAGATCGAAACC  1440

Query                 1450 ATCCTGGCTAACACGGTGAAACCCCGTCTCTACTaaaaaatacaaaaaaTTAGCTGGGCG  1509
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct  1441  ATCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAAATACAAAAAATTAGCTGGGCG  1500
Query  1510  CAGAGGCACGGGCCTGTAGTCCCAGCTACTCAGGAGGCGGAGGCAGGAGAATGGCGTCAA  1569
Sbjct  1501  CAGAGGCACGGGCCTGTAGTCCCAGCTACTCAGGAGGCGGAGGCAGGAGAATGGCGTCAA  1560
Query  1570  CCCGGGAGGCGGAGGTTGCAGTGAGCCAGGATTGTGCGACTGCACTCCAGCCTGGGTGAC  1629
Sbjct  1561  CCCGGGAGGCGGAGGTTGCAGTGAGCCAGGATTGTGCGACTGCACTCCAGCCTGGGTGAC  1620
Query  1630  AGGGTGAAACGCCATCTCaaaaaataaaaattgaaaaataaaaaaa  1675
Sbjct  1621  AGGGTGAAACGCCATCTCAAAAAATAAAAATTAAAAAAAAAAAAAA  1666
```

Range 2: 1100 to 1128

Score	Expect	Identities	Gaps	Strand	Frame
54.7 bits(29)	1e-10()	29/29(100%)	0/29(0%)	Plus/Plus	

Features:

```
Query  1137  ACAGCTGCCTTGTGTGCGACTGAGATGCA  1165
Sbjct  1100  ACAGCTGCCTTGTGTGCGACTGAGATGCA  1128
```

Range 3: 1128 to 1156

Score	Expect	Identities	Gaps	Strand	Frame
54.7 bits(29)	1e-10()	29/29(100%)	0/29(0%)	Plus/Plus	

Features:

```
Query  1109  ACAGCTGCCTTGTGTGCGACTGAGATGCA  1137
Sbjct  1128  ACAGCTGCCTTGTGTGCGACTGAGATGCA  1156
```

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