RIKEN_Clone_ID : IRAL034P20

Lot#: 7566_B5Hm

Vector : pOTB7

Gene	IRAK1	
Accession No.	BC014963.1	3337 bp
CDS		1902 bp

● Plasmid DNA purification

Date : 2025/08/21　　Culture : LB（25 ug/ml Chloramphenicol） 5 ml –> at 37 deg C over night

Date : 2025/08/22　　Purification : QIAGEN Miniprep kit –> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/08/22

DNA concentration（O.D.）: 355 ng/ul

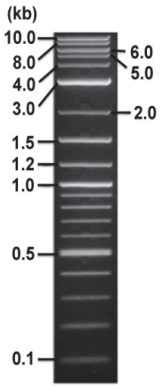
DNA	0.3 ul
Enzyme（BamHI + BglII ）	0.5 + 0.5 ul
Buffer H	1 ul
dH_2O	7.7 ul
Total	10 ul

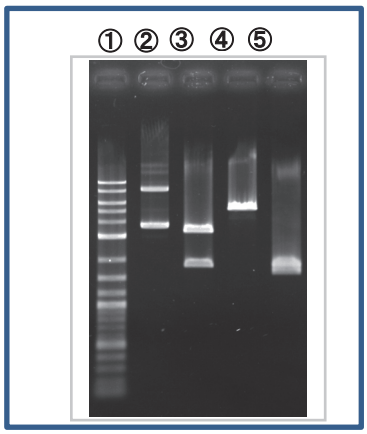
< Size of fragment expected from this clone >

BamHI	3.3 , 1.8 kb
BglII	5.1 kb
BamHI + BglII	1.6kb (Vector)　1.8, 1.7 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 : 2025/09/17

DNA (355 ng/ul)	82 ul
10x TE	116 ul
dH_2O	966 ul
Total	1,164 ul

● Confirmation of the sequence

Date : 2025/08/29

full sequence	IRAL034P20hts01.seq

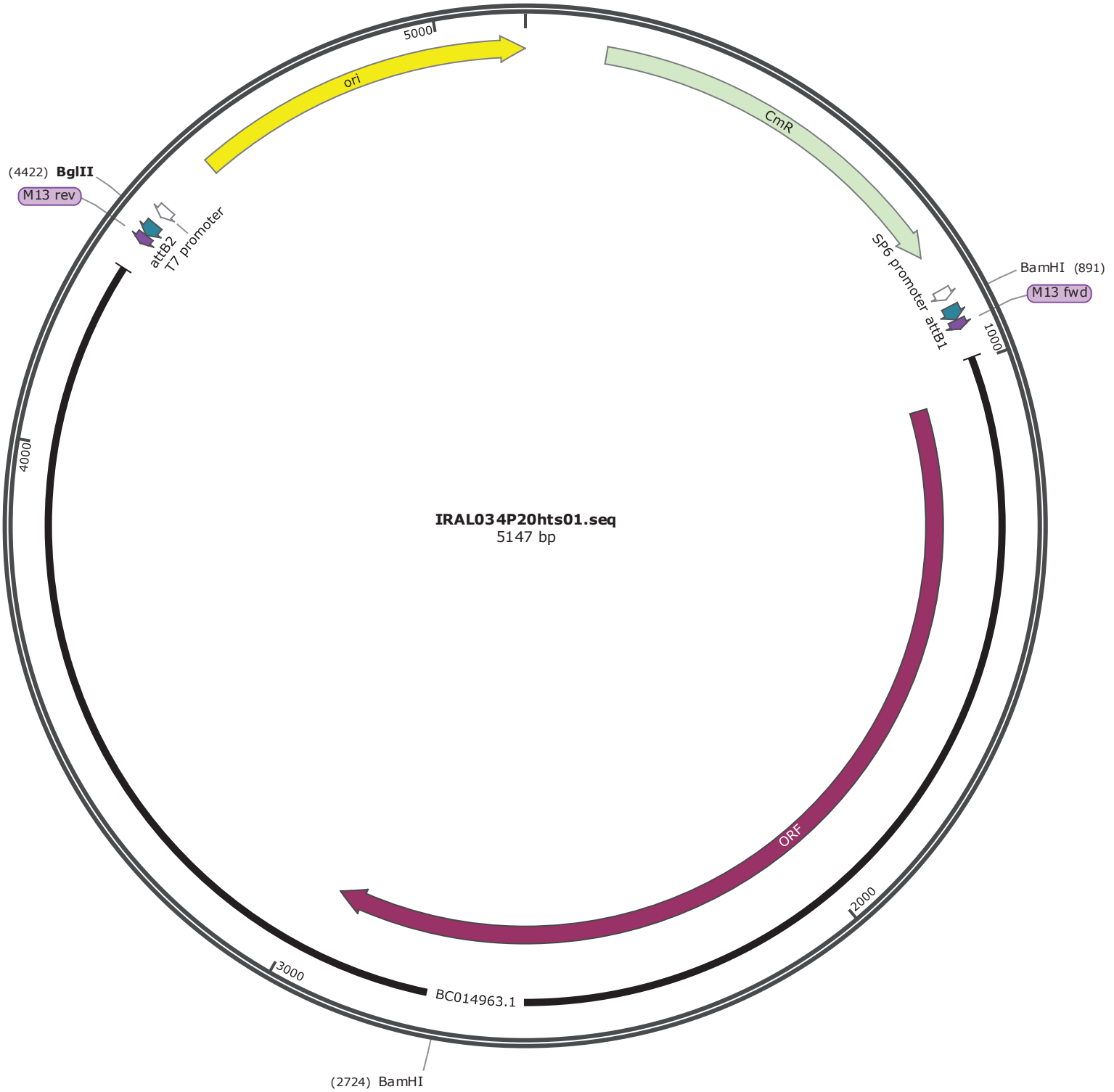
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ng/μl, Volume : μl

APPROVED BY :

検 '25.09.17 笹沼


5000
ori
CmR
(4422) BglII
M13 rev
attB2
T7 promoter
SP6 promoter
attB1
BamHI (891)
M13 fwd
1000
4000
IRAL034P20hts01.seq
5147 bp
ORF
2000
3000
BC014963.1
(2724) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

Job title: BC014963:Homo sapiens interleukin-1 receptor-associated...

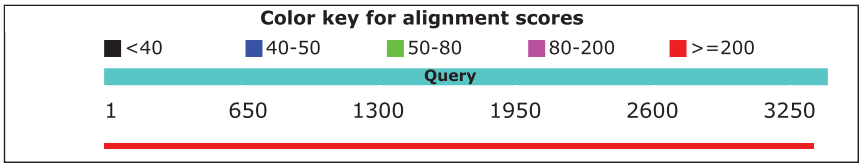
RID B2RA9XHF114 (Expires on 08-30 15:56 pm)

Query ID	BC014963.1	**Subject ID**	lcl|Query_7673899
Description	Homo sapiens interleukin-1 receptor-associated kinase 1, mRNA (cDNA clone MGC:23051 IMAGE:4906853), complete cds	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	3337	**Subject Length**	5147
		Program	BLASTN 2.17.0+

IRAL034P20hts01.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	6163	6163	100%	0.0	100.00%	Query_7673899

Alignments

Sequence ID: Query_7673899 Length: 5147 Number of Matches: 1
Range 1: 992 to 4328

Score	Expect	Identities	Gaps	Strand	Frame
6163 bits(3337)	0.0()	3337/3337(100%)	0/3337(0%)	Plus/Plus	

Features:

```
Query              1     cccaggcccgcgcccgccgcggccctgagaggccccggcaggtcccggcccggcggcggc  60
Sbjct              992   ............................................................  1051

CDS:Interleukin-1 re 1         M  A  G  G  P  G  P  G  E  P  A  A  P  G  A  Q  H  F  L
Query              61    agccatggccgggggccgggcccgggggagcccgcagcccccggcgcccAGCACTTCTT  120
Sbjct              1052  ............................................................  1111

CDS:Interleukin-1 re 20     Y  E  V  P  P  W  V  M  C  R  F  Y  K  V  M  D  A  L  E  P
Query              121   GTACGAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCC  180
Sbjct              1112  ............................................................  1171

CDS:Interleukin-1 re 40     A  D  W  C  Q  F  A  A  L  I  V  R  D  Q  T  E  L  R  L  C
Query              181   CGCCGACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTG  240
Sbjct              1172  ............................................................  1231

CDS:Interleukin-1 re 60     E  R  S  G  Q  R  T  A  S  V  L  W  P  W  I  N  R  N  A  R
Query              241   CGAGCGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCG  300
Sbjct              1232  ............................................................  1291

CDS:Interleukin-1 re 80     V  A  D  L  V  H  I  L  T  H  L  Q  L  L  R  A  R  D  I  I
Query              301   TGTGGCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCAT  360
Sbjct              1292  ............................................................  1351
```

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CDS:Interleukin-1 re  100    T  A  W  H  P  P  A  P  L  P  S  P  G  T  T  A  P  R  P  S
Query                 361    CACAGCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGAGGCCCAG  420
Sbjct                 1352   ............................................................  1411

CDS:Interleukin-1 re  120    S  I  P  A  P  A  E  A  E  A  W  S  P  R  K  L  P  S  S  A
Query                 421    CAGCATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAGTTGCCATCCTCAGC  480
Sbjct                 1412   ............................................................  1471

CDS:Interleukin-1 re  140    S  T  F  L  S  P  A  F  P  G  S  Q  T  H  S  G  P  E  L  G
Query                 481    CTCCACCTTCCTCTCCCCAGCTTTTCCAGGCTCCCAGACCCATTCAGGGCCTGAGCTCGG  540
Sbjct                 1472   ............................................................  1531

CDS:Interleukin-1 re  160    L  V  P  S  P  A  S  L  W  P  P  P  P  S  P  A  P  S  S  T
Query                 541    CCTGGTTCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGCCCCTTCTTCTAC  600
Sbjct                 1532   ............................................................  1591

CDS:Interleukin-1 re  180    K  P  G  P  E  S  S  V  S  L  L  Q  G  A  R  P  S  P  F  C
Query                 601    CAAGCCAGGCCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCTCTCCGTTTTG  660
Sbjct                 1592   ............................................................  1651

CDS:Interleukin-1 re  200    W  P  L  C  E  I  S  R  G  T  H  N  F  S  E  E  L  K  I  G
Query                 661    CTGGCCCCTCTGTGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGAGCTCAAGATCGG  720
Sbjct                 1652   ............................................................  1711

CDS:Interleukin-1 re  220    E  G  G  F  G  C  V  Y  R  A  V  M  R  N  T  V  Y  A  V  K
Query                 721    GGAGGGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACGGTGTATGCTGTGAA  780
Sbjct                 1712   ............................................................  1771

CDS:Interleukin-1 re  240    R  L  K  E  N  A  D  L  E  W  T  A  V  K  Q  S  F  L  T  E
Query                 781    GAGGCTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCTGACCGA  840
Sbjct                 1772   ............................................................  1831

CDS:Interleukin-1 re  260    V  E  Q  L  S  R  F  R  H  P  N  I  V  D  F  A  G  Y  C  A
Query                 841    GGTGGAGCAGCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTTGCTGGCTACTGTGC  900
Sbjct                 1832   ............................................................  1891

CDS:Interleukin-1 re  280    Q  N  G  F  Y  C  L  V  Y  G  F  L  P  N  G  S  L  E  D  R
Query                 901    TCAGAACGGCTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGCTCCCTGGAGGACCG  960
Sbjct                 1892   ............................................................  1951

CDS:Interleukin-1 re  300    L  H  C  Q  T  Q  A  C  P  P  L  S  W  P  Q  R  L  D  I  L
Query                 961    TCTCCACTGCCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCT  1020
Sbjct                 1952   ............................................................  2011

CDS:Interleukin-1 re  320    L  G  T  A  R  A  I  Q  F  L  H  Q  D  S  P  S  L  I  H  G
Query                 1021   TCTGGGTACAGCCCGGGCAATTCAGTTTCTACATCAGGACAGCCCCAGCCTCATCCATGG  1080
Sbjct                 2012   ............................................................  2071

CDS:Interleukin-1 re  340    D  I  K  S  S  N  V  L  L  D  E  R  L  T  P  K  L  G  D  F
Query                 1081   AGACATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTT  1140
Sbjct                 2072   ............................................................  2131

CDS:Interleukin-1 re  360    G  L  A  R  F  S  R  F  A  G  S  S  P  S  Q  S  S  M  V  A
Query                 1141   TGGCCTGGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGC  1200
Sbjct                 2132   ............................................................  2191

CDS:Interleukin-1 re  380    R  T  Q  T  V  R  G  T  L  A  Y  L  P  E  E  Y  I  K  T  G
Query                 1201   CCGGACACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAGTACATCAAGACGGG  1260
Sbjct                 2192   ............................................................  2251
```

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CDS:Interleukin-1 re  400    R  L  A  V  D  T  D  T  F  S  F  G  V  V  V  L  E  T  L  A
Query                 1261   AAGGCTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTGGC  1320
Sbjct                 2252   ............................................................  2311

CDS:Interleukin-1 re  420    G  Q  R  A  V  K  T  H  G  A  R  T  K  Y  L  V  Y  E  R  L
Query                 1321   TGGTCAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGGTGTACGAGAGGCT  1380
Sbjct                 2312   ............................................................  2371

CDS:Interleukin-1 re  440    E  K  L  Q  A  V  V  A  G  V  P  G  H  L  E  A  A  S  C  I
Query                 1381   AGAGAAGCTGCAGGCAGTGGTGGCGGGGGTGCCCGGGCATTTGGAGGCCGCCAGCTGCAT  1440
Sbjct                 2372   ............................................................  2431

CDS:Interleukin-1 re  460    P  P  S  P  Q  E  N  S  Y  V  S  S  T  G  R  A  H  S  G  A
Query                 1441   CCCCCCTTCCCCGCAGGAGAACTCCTACGTGTCCAGCACTGGCAGAGCCCACAGTGGGGC  1500
Sbjct                 2432   ............................................................  2491

CDS:Interleukin-1 re  480    A  P  W  Q  P  L  A  A  P  S  G  A  S  A  Q  A  A  E  Q  L
Query                 1501   TGCTCCATGGCAGCCCCTGGCAGCGCCATCAGGAGCCAGTGCCCAGGCAGCAGAGCAGCT  1560
Sbjct                 2492   ............................................................  2551

CDS:Interleukin-1 re  500    Q  R  G  P  N  Q  P  V  E  S  D  E  S  L  G  G  L  S  A  A
Query                 1561   GCAGAGAGGCCCCAACCAGCCCGTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGCTGC  1620
Sbjct                 2552   ............................................................  2611

CDS:Interleukin-1 re  520    L  R  S  W  H  L  T  P  S  C  P  L  D  P  A  P  L  R  E  A
Query                 1621   CCTGCGCTCCTGGCACTTGACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGAGGC  1680
Sbjct                 2612   ............................................................  2671

CDS:Interleukin-1 re  540    G  C  P  Q  G  D  T  A  G  E  S  S  W  G  S  G  P  G  S  R
Query                 1681   CGGCTGTCCTCAGGGGGACACGGCAGGAGAATCGAGCTGGGGGAGTGGCCCAGGATCCCG  1740
Sbjct                 2672   ............................................................  2731

CDS:Interleukin-1 re  560    P  T  A  V  E  G  L  A  L  G  S  S  A  S  S  S  S  E  P  P
Query                 1741   GCCCACAGCCGTGGAAGGACTGGCCCTTGGCAGCTCTGCATCATCGTCGTCAGAGCCACC  1800
Sbjct                 2732   ............................................................  2791

CDS:Interleukin-1 re  580    Q  I  I  I  N  P  A  R  Q  K  M  V  Q  K  L  A  L  Y  E  D
Query                 1801   GCAGATTATCATCAACCCTGCCCGACAGAAGATGGTCCAGAAGCTGGCCCTGTACGAGGA  1860
Sbjct                 2792   ............................................................  2851

CDS:Interleukin-1 re  600    G  A  L  D  S  L  Q  L  L  S  S  S  S  L  P  G  L  G  L  E
Query                 1861   TGGGGCCCTGGACAGCCTGCAGCTGCTGTCGTCCAGCTCCCTCCCAGGCTTGGGCCTGGA  1920
Sbjct                 2852   ............................................................  2911

CDS:Interleukin-1 re  620    Q  D  R  Q  G  P  E  E  S  D  E  F  Q  S
Query                 1921   ACAGGACAGGCAGGGGCCCGAAGAAAGTGATGAATTTCAGAGCTGATGTGTTCACCTGGG  1980
Sbjct                 2912   ............................................................  2971

Query                 1981   CAGATCCCCCAAATCCGGAAGTCAAAGTTCTCATGGTCAGAAGTTCTCATGGTGCACGAG  2040
Sbjct                 2972   ............................................................  3031

Query                 2041   TCCTCAGCACTCTGCCGGCAGTGGGGGTGGGGGCCCATGCCCGCGGGGGAGAGAAGGAGG  2100
Sbjct                 3032   ............................................................  3091

Query                 2101   TGGCCCTGCTGTTCTAGGCTCTGTGGGCATAGGCAGGCAGAGTGGAACCCTGCCTCCATG  2160
Sbjct                 3092   ............................................................  3151

Query                 2161   CCAGCATCTGGGGGCAAGGAAGGCTGGCATCATCCAGTGAGGAGGCTGGCGCATGTTGGG  2220
```

```
Sbjct  3152 ..................................................  3211

Query  2221 AGGCTGCTGGCTGCACAGACCCGTGAGGGGAGGAGAGGGGCTGCTGTGCAGGGGTGTGGA  2280
Sbjct  3212 ..................................................  3271

Query  2281 GTAGGGAGCTGGCTCCCCTGAGAGCCATGCAGGGCGTCTGCAGCCCAGGCCTCTGGCAGC  2340
Sbjct  3272 ..................................................  3331

Query  2341 AGCTCTTTGCCCATCTCTTTGGACAGTGGCCACCCTGCACAATGGGGCCGACGAGGCCTA  2400
Sbjct  3332 ..................................................  3391

Query  2401 GGGCCCTCCTACCTGCTTACAATTTGGAAAAGTGTGGCCGGGTGCGGTGGCTCACGCCTG  2460
Sbjct  3392 ..................................................  3451

Query  2461 TAATCCCAGCACTTTGGGAGGCCAAGGCAGGAGGATCGCTGGAGCCCAGTAGGTCAAGAC  2520
Sbjct  3452 ..................................................  3511

Query  2521 CAGCCAGGGCAACATGATGAGACCCTGTCTCTGCCAAAAAATTTTTTAAACTATTAGCCT  2580
Sbjct  3512 ..................................................  3571

Query  2581 GGCGTGGTAGCGCACGCCTGTGGTCCCAGCTGCTGGGGAGGCTGAAGTAGGAGGATCATT  2640
Sbjct  3572 ..................................................  3631

Query  2641 TATGCTTGGGAGGTCGAGGCTGCAGTGAGTCATGATTGTATGACTGCACTCCAGCCTGGG  2700
Sbjct  3632 ..................................................  3691

Query  2701 TGACAGAGCAAGACCCTGTTTCAAAAAGAAAAACCCTGGGAAAAGTGAAGTATGGCTGTA  2760
Sbjct  3692 ..................................................  3751

Query  2761 AGTCTCATGGTTCAGTCCTAGCAAGAAGCGAGAATTCTGAGATCCTCCAGAAAGTCGAGC  2820
Sbjct  3752 ..................................................  3811

Query  2821 AGCACCCACCTCCAACCTCGGGCCAGTGTCTTCAGGCTTTACTGGGGACCTGCGAGCTGG  2880
Sbjct  3812 ..................................................  3871

Query  2881 CCTAATGTGGTGGCCTGCAAGCCAGGCCATCCCTGGGCGCCACAGACGAGCTCCGAGCCA  2940
Sbjct  3872 ..................................................  3931

Query  2941 GGTCAGGCTTCGGAGGCCACAAGCTCAGCCTCAGGCCCAGGCACTGATTGTGGCAGAGGG  3000
Sbjct  3932 ..................................................  3991

Query  3001 GCCACTACCCAAGGTCTAGCTAGGCCCAAGACCTAGTTACCCAGACAGTGAGAAGCCCCT  3060
Sbjct  3992 ..................................................  4051

Query  3061 GGAAGGCAGAAAAGTTGGGAGCATGGCAGACAGGGAAGGGAAACATTTTCAGGGAAAAGA  3120
Sbjct  4052 ..................................................  4111

Query  3121 CATGTATCACATGTCTTCAGAAGCAAGTCAGGTTTCATGTAACCGAGTGTCCTCTTGCGT  3180
Sbjct  4112 ..................................................  4171

Query  3181 GTCCAAAAGTAGCCCAGGGCTGTAGCACAGGCTTCACAGTGATTTTGTGTTCAGCCGTGA  3240
Sbjct  4172 ..................................................  4231

Query  3241 GTCACACTACATGCCCCCGTGAAGCTGGGCATTGGTGACGTCCAGGTTGTCCTTGAGTAA  3300
Sbjct  4232 ..................................................  4291

Query  3301 TAAAAACGTATGTTGCAATaaaaaaaaaaaaaaaaaa  3337
Sbjct  4292 ....................................  4328
```



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BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001025243:Homo sapiens interleukin 1 receptor...

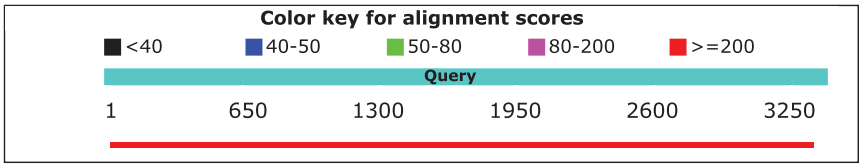
RID B2R0P6UM114 (Expires on 08-30 15:51 pm)

Query ID NM_001025243.2
Description Homo sapiens interleukin 1 receptor associated kinase 1 (IRAK1), transcript variant 3, mRNA
Molecule type nucleic acid
Query Length 3344

Subject ID BC014963.1
Description Homo sapiens interleukin-1 receptor-associated kinase 1, mRNA (cDNA clone MGC:23051 IMAGE:4906853), complete cds
See details
Molecule type nucleic acid
Subject Length 3337
Program BLASTN 2.17.0+

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 interleukin-1 receptor-associated kinase 1, mRNA (cDNA clone MGC:23051 IMAGE:4906853), complete cds	6111	6111	99%	0.0	99.91%	BC014963.1

Alignments

Homo sapiens interleukin-1 receptor-associated kinase 1, mRNA (cDNA clone MGC:23051 IMAGE:4906853), complete cds
Sequence ID: **BC014963.1** Length: 3337 Number of Matches: 1
Range 1: 1 to 3318

Score	Expect	Identities	Gaps	Strand	Frame
6111 bits(3309)	0.0()	3315/3318(99%)	0/3318(0%)	Plus/Plus	

Features:

```
Query              27   cccaggcccgcgcccgccgcggccctgagaggccccggcaggtcccggcccggcggcggc  86
Sbjct              1    ............................................................  60

CDS:interleukin-1 re  1        M  A  G  G  P  G  P  G  E  P  A  A  P  G  A  Q  H  F  L
Query              87   agccatggccgggggccgggcccgggggagcccgcagcccccggcgcccAGCACTTCTT  146
Sbjct              61   ..........................................................  120
CDS:Interleukin-1 re  1        M  A  G  G  P  G  P  G  E  P  A  A  P  G  A  Q  H  F  L

CDS:interleukin-1 re  20     Y  E  V  P  P  W  V  M  C  R  F  Y  K  V  M  D  A  L  E  P
Query              147  GTACGAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCC  206
Sbjct              121  ..........................................................  180
CDS:Interleukin-1 re  20     Y  E  V  P  P  W  V  M  C  R  F  Y  K  V  M  D  A  L  E  P

CDS:interleukin-1 re  40     A  D  W  C  Q  F  A  A  L  I  V  R  D  Q  T  E  L  R  L  C
Query              207  CGCCGACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTG  266
Sbjct              181  ..........................................................  240
CDS:Interleukin-1 re  40     A  D  W  C  Q  F  A  A  L  I  V  R  D  Q  T  E  L  R  L  C
```

```
CDS:interleukin-1 re  60    E  R  S  G  Q  R  T  A  S  V  L  W  P  W  I  N  R  N  A  R
Query                 267   CGAGCGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCG  326
Sbjct                 241   ..............................................................  300
CDS:interleukin-1 re  60    E  R  S  G  Q  R  T  A  S  V  L  W  P  W  I  N  R  N  A  R

CDS:interleukin-1 re  80    V  A  D  L  V  H  I  L  T  H  L  Q  L  L  R  A  R  D  I  I
Query                 327   TGTGGCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCAT  386
Sbjct                 301   ..............................................................  360
CDS:interleukin-1 re  80    V  A  D  L  V  H  I  L  T  H  L  Q  L  L  R  A  R  D  I  I

CDS:interleukin-1 re  100   T  A  W  H  P  P  A  P  L  P  S  P  G  T  T  A  P  R  P  S
Query                 387   CACAGCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGAGGCCCAG  446
Sbjct                 361   ..............................................................  420
CDS:interleukin-1 re  100   T  A  W  H  P  P  A  P  L  P  S  P  G  T  T  A  P  R  P  S

CDS:interleukin-1 re  120   S  I  P  A  P  A  E  A  E  A  W  S  P  R  K  L  P  S  S  A
Query                 447   CAGCATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAGTTGCCATCCTCAGC  506
Sbjct                 421   ..............................................................  480
CDS:interleukin-1 re  120   S  I  P  A  P  A  E  A  E  A  W  S  P  R  K  L  P  S  S  A

CDS:interleukin-1 re  140   S  T  F  L  S  P  A  F  P  G  S  Q  T  H  S  G  P  E  L  G
Query                 507   CTCCACCTTCCTCTCCCCAGCTTTTCCAGGCTCCCAGACCCATTCAGGGCCTGAGCTCGG  566
Sbjct                 481   ..............................................................  540
CDS:interleukin-1 re  140   S  T  F  L  S  P  A  F  P  G  S  Q  T  H  S  G  P  E  L  G

CDS:interleukin-1 re  160   L  V  P  S  P  A  S  L  W  P  P  P  P  S  P  A  P  S  S  T
Query                 567   CCTGGTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGCCCCTTCTTCTAC  626
Sbjct                 541   ....T.........................................................  600
CDS:interleukin-1 re  160   L  V  P  S  P  A  S  L  W  P  P  P  P  S  P  A  P  S  S  T

CDS:interleukin-1 re  180   K  P  G  P  E  S  S  V  S  L  L  Q  G  A  R  P  F  P  F  C
Query                 627   CAAGCCAGGCCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCTTTCCGTTTTG  686
Sbjct                 601   ..............................C...............................  660
CDS:interleukin-1 re  180   K  P  G  P  E  S  S  V  S  L  L  Q  G  A  R  P  S  P  F  C

CDS:interleukin-1 re  200   W  P  L  C  E  I  S  R  G  T  H  N  F  S  E  E  L  K  I  G
Query                 687   CTGGCCCCTCTGTGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGAGCTCAAGATCGG  746
Sbjct                 661   ..............................................................  720
CDS:interleukin-1 re  200   W  P  L  C  E  I  S  R  G  T  H  N  F  S  E  E  L  K  I  G

CDS:interleukin-1 re  220   E  G  G  F  G  C  V  Y  R  A  V  M  R  N  T  V  Y  A  V  K
Query                 747   GGAGGGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACGGTGTATGCTGTGAA  806
Sbjct                 721   ..............................................................  780
CDS:interleukin-1 re  220   E  G  G  F  G  C  V  Y  R  A  V  M  R  N  T  V  Y  A  V  K

CDS:interleukin-1 re  240   R  L  K  E  N  A  D  L  E  W  T  A  V  K  Q  S  F  L  T  E
Query                 807   GAGGCTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCTGACCGA  866
Sbjct                 781   ..............................................................  840
CDS:interleukin-1 re  240   R  L  K  E  N  A  D  L  E  W  T  A  V  K  Q  S  F  L  T  E

CDS:interleukin-1 re  260   V  E  Q  L  S  R  F  R  H  P  N  I  V  D  F  A  G  Y  C  A
Query                 867   GGTGGAGCAGCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTTGCTGGCTACTGTGC  926
Sbjct                 841   ..............................................................  900
CDS:interleukin-1 re  260   V  E  Q  L  S  R  F  R  H  P  N  I  V  D  F  A  G  Y  C  A

CDS:interleukin-1 re  280   Q  N  G  F  Y  C  L  V  Y  G  F  L  P  N  G  S  L  E  D  R
Query                 927   TCAGAACGGCTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGCTCCCTGGAGGACCG  986
Sbjct                 901   ..............................................................  960
CDS:interleukin-1 re  280   Q  N  G  F  Y  C  L  V  Y  G  F  L  P  N  G  S  L  E  D  R
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573 C>T

677 T>C (F196S)

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CDS:interleukin-1 re  300   L  H  C  Q  T  Q  A  C  P  P  L  S  W  P  Q  R  L  D  I  L
Query                 987   TCTCCACTGCCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCT  1046
Sbjct                 961   ..............................................................  1020
CDS:interleukin-1 re  300   L  H  C  Q  T  Q  A  C  P  P  L  S  W  P  Q  R  L  D  I  L

CDS:interleukin-1 re  320   L  G  T  A  R  A  I  Q  F  L  H  Q  D  S  P  S  L  I  H  G
Query                 1047  TCTGGGTACAGCCCGGGCAATTCAGTTTCTACATCAGGACAGCCCCAGCCTCATCCATGG  1106
Sbjct                 1021  ..............................................................  1080
CDS:interleukin-1 re  320   L  G  T  A  R  A  I  Q  F  L  H  Q  D  S  P  S  L  I  H  G

CDS:interleukin-1 re  340   D  I  K  S  S  N  V  L  L  D  E  R  L  T  P  K  L  G  D  F
Query                 1107  AGACATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTT  1166
Sbjct                 1081  ..............................................................  1140
CDS:interleukin-1 re  340   D  I  K  S  S  N  V  L  L  D  E  R  L  T  P  K  L  G  D  F

CDS:interleukin-1 re  360   G  L  A  R  F  S  R  F  A  G  S  S  P  S  Q  S  S  M  V  A
Query                 1167  TGGCCTGGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGC  1226
Sbjct                 1141  ..............................................................  1200
CDS:interleukin-1 re  360   G  L  A  R  F  S  R  F  A  G  S  S  P  S  Q  S  S  M  V  A

CDS:interleukin-1 re  380   R  T  Q  T  V  R  G  T  L  A  Y  L  P  E  E  Y  I  K  T  G
Query                 1227  CCGGACACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCCGAGGAGTACATCAAGACGGG  1286
Sbjct                 1201  ..............................................................  1260
CDS:interleukin-1 re  380   R  T  Q  T  V  R  G  T  L  A  Y  L  P  E  E  Y  I  K  T  G

CDS:interleukin-1 re  400   R  L  A  V  D  T  D  T  F  S  F  G  V  V  V  L  E  T  L  A
Query                 1287  AAGGCTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTGGC  1346
Sbjct                 1261  ..............................................................  1320
CDS:interleukin-1 re  400   R  L  A  V  D  T  D  T  F  S  F  G  V  V  V  L  E  T  L  A

CDS:interleukin-1 re  420   G  Q  R  A  V  K  T  H  G  A  R  T  K  Y  L  V  Y  E  R  L
Query                 1347  TGGTCAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGGTGTACGAGAGGCT  1406
Sbjct                 1321  ..............................................................  1380
CDS:interleukin-1 re  420   G  Q  R  A  V  K  T  H  G  A  R  T  K  Y  L  V  Y  E  R  L

CDS:interleukin-1 re  440   E  K  L  Q  A  V  V  A  G  V  P  G  H  S  E  A  A  S  C  I
Query                 1407  AGAGAAGCTGCAGGCAGTGGTGGCGGGGGTGCCCGGGCATTCGGAGGCCGCCAGCTGCAT  1466
Sbjct                 1381  ..............................T...............................  1440
CDS:interleukin-1 re  440   E  K  L  Q  A  V  V  A  G  V  P  G  H  L  E  A  A  S  C  I

CDS:interleukin-1 re  460   P  P  S  P  Q  E  N  S  Y  V  S  S  T  G  R  A  H  S  G  A
Query                 1467  CCCCCCTTCCCCGCAGGAGAACTCCTACGTGTCCAGCACTGGCAGAGCCCACAGTGGGGC  1526
Sbjct                 1441  ..............................................................  1500
CDS:interleukin-1 re  460   P  P  S  P  Q  E  N  S  Y  V  S  S  T  G  R  A  H  S  G  A

CDS:interleukin-1 re  480   A  P  W  Q  P  L  A  A  P  S  G  A  S  A  Q  A  A  E  Q  L
Query                 1527  TGCTCCATGGCAGCCCCTGGCAGCGCCATCAGGAGCCAGTGCCCAGGCAGCAGAGCAGCT  1586
Sbjct                 1501  ..............................................................  1560
CDS:interleukin-1 re  480   A  P  W  Q  P  L  A  A  P  S  G  A  S  A  Q  A  A  E  Q  L

CDS:interleukin-1 re  500   Q  R  G  P  N  Q  P  V  E  S  D  E  S  L  G  G  L  S  A  A
Query                 1587  GCAGAGAGGCCCCAACCAGCCCGTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGCTGC  1646
Sbjct                 1561  ..............................................................  1620
CDS:interleukin-1 re  500   Q  R  G  P  N  Q  P  V  E  S  D  E  S  L  G  G  L  S  A  A

CDS:interleukin-1 re  520   L  R  S  W  H  L  T  P  S  C  P  L  D  P  A  P  L  R  E  A
Query                 1647  CCTGCGCTCCTGGCACTTGACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGAGGC  1706
Sbjct                 1621  ..............................................................  1680
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1448 C>T (S453L)

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CDS:Interleukin-1 re  520    L  R  S  W  H  L  T  P  S  C  P  L  D  P  A  P  L  R  E  A

CDS:interleukin-1 re  540    G  C  P  Q  G  D  T  A  G  E  S  S  W  G  S  G  P  G  S  R
Query                 1707   CGGCTGTCCTCAGGGGGACACGGCAGGAGAATCGAGCTGGGGGAGTGGCCCAGGATCCCG  1766
Sbjct                 1681   ............................................................  1740
CDS:Interleukin-1 re  540    G  C  P  Q  G  D  T  A  G  E  S  S  W  G  S  G  P  G  S  R

CDS:interleukin-1 re  560    P  T  A  V  E  G  L  A  L  G  S  S  A  S  S  S  S  E  P  P
Query                 1767   GCCCACAGCCGTGGAAGGACTGGCCCTTGGCAGCTCTGCATCATCGTCGTCAGAGCCACC  1826
Sbjct                 1741   ............................................................  1800
CDS:Interleukin-1 re  560    P  T  A  V  E  G  L  A  L  G  S  S  A  S  S  S  S  E  P  P

CDS:interleukin-1 re  580    Q  I  I  I  N  P  A  R  Q  K  M  V  Q  K  L  A  L  Y  E  D
Query                 1827   GCAGATTATCATCAACCCTGCCCGACAGAAGATGGTCCAGAAGCTGGCCCTGTACGAGGA  1886
Sbjct                 1801   ............................................................  1860
CDS:Interleukin-1 re  580    Q  I  I  I  N  P  A  R  Q  K  M  V  Q  K  L  A  L  Y  E  D

CDS:interleukin-1 re  600    G  A  L  D  S  L  Q  L  L  S  S  S  S  L  P  G  L  G  L  E
Query                 1887   TGGGGCCCTGGACAGCCTGCAGCTGCTGTCGTCCAGCTCCCTCCCAGGCTTGGGCCTGGA  1946
Sbjct                 1861   ............................................................  1920
CDS:Interleukin-1 re  600    G  A  L  D  S  L  Q  L  L  S  S  S  S  L  P  G  L  G  L  E

CDS:interleukin-1 re  620    Q  D  R  Q  G  P  E  E  S  D  E  F  Q  S
Query                 1947   ACAGGACAGGCAGGGGCCCGAAGAAAGTGATGAATTTCAGAGCTGATGTGTTCACCTGGG  2006
Sbjct                 1921   ............................................................  1980
CDS:Interleukin-1 re  620    Q  D  R  Q  G  P  E  E  S  D  E  F  Q  S

Query                 2007   CAGATCCCCCAAATCCGGAAGTCAAAGTTCTCATGGTCAGAAGTTCTCATGGTGCACGAG  2066
Sbjct                 1981   ............................................................  2040

Query                 2067   TCCTCAGCACTCTGCCGGCAGTGGGGGTGGGGGCCCATGCCCGCGGGGGAGAGAAGGAGG  2126
Sbjct                 2041   ............................................................  2100

Query                 2127   TGGCCCTGCTGTTCTAGGCTCTGTGGGCATAGGCAGGCAGAGTGGAACCCTGCCTCCATG  2186
Sbjct                 2101   ............................................................  2160

Query                 2187   CCAGCATCTGGGGGCAAGGAAGGCTGGCATCATCCAGTGAGGAGGCTGGCGCATGTTGGG  2246
Sbjct                 2161   ............................................................  2220

Query                 2247   AGGCTGCTGGCTGCACAGACCCGTGAGGGGAGGAGAGGGGCTGCTGTGCAGGGGTGTGGA  2306
Sbjct                 2221   ............................................................  2280

Query                 2307   GTAGGGAGCTGGCTCCCCTGAGAGCCATGCAGGGCGTCTGCAGCCCAGGCCTCTGGCAGC  2366
Sbjct                 2281   ............................................................  2340

Query                 2367   AGCTCTTTGCCCATCTCTTTGGACAGTGGCCACCCTGCACAATGGGGCCGACGAGGCCTA  2426
Sbjct                 2341   ............................................................  2400

Query                 2427   GGGCCCTCCTACCTGCTTACAATTTGGAAAAGTGTGGCCGGGTGCGGTGGCTCACGCCTG  2486
Sbjct                 2401   ............................................................  2460

Query                 2487   TAATCCCAGCACTTTGGGAGGCCAAGGCAGGAGGATCGCTGGAGCCCAGTAGGTCAAGAC  2546
Sbjct                 2461   ............................................................  2520

Query                 2547   CAGCCAGGGCAACATGATGAGACCCTGTCTCTGCCAAAAAATTTTTTAAACTATTAGCCT  2606
Sbjct                 2521   ............................................................  2580

Query                 2607   GGCGTGGTAGCGCACGCCTGTGGTCCCAGCTGCTGGGGAGGCTGAAGTAGGAGGATCATT  2666
Sbjct                 2581   ............................................................  2640

Query                 2667   TATGCTTGGGAGGTCGAGGCTGCAGTGAGTCATGATTGTATGACTGCACTCCAGCCTGGG  2726
Sbjct                 2641   ............................................................  2700

Query                 2727   TGACAGAGCAAGACCCTGTTTCAAAAAGAAAAACCCTGGGAAAAGTGAAGTATGGCTGTA  2786
Sbjct                 2701   ............................................................  2760

Query                 2787   AGTCTCATGGTTCAGTCCTAGCAAGAAGCGAGAATTCTGAGATCCTCCAGAAAGTCGAGC  2846
Sbjct                 2761   ............................................................  2820

Query                 2847   AGCACCCACCTCCAACCTCGGGCCAGTGTCTTCAGGCTTTACTGGGGACCTGCGAGCTGG  2906
Sbjct                 2821   ............................................................  2880

Query                 2907   CCTAATGTGGTGGCCTGCAAGCCAGGCCATCCCTGGGCGCCACAGACGAGCTCCGAGCCA  2966
Sbjct                 2881   ............................................................  2940

Query                 2967   GGTCAGGCTTCGGAGGCCACAAGCTCAGCCTCAGGCCCAGGCACTGATTGTGGCAGAGGG  3026
Sbjct                 2941   ............................................................  3000

Query                 3027   GCCACTACCCAAGGTCTAGCTAGGCCCAAGACCTAGTTACCCAGACAGTGAGAAGCCCCT  3086
Sbjct                 3001   ............................................................  3060

Query                 3087   GGAAGGCAGAAAAGTTGGGAGCATGGCAGACAGGGAAGGGAAACATTTTCAGGGAAAAGA  3146
Sbjct                 3061   ............................................................  3120

Query                 3147   CATGTATCACATGTCTTCAGAAGCAAGTCAGGTTTCATGTAACCGAGTGTCCTCTTGCGT  3206
Sbjct                 3121   ............................................................  3180

Query                 3207   GTCCAAAAGTAGCCCAGGGCTGTAGCACAGGCTTCACAGTGATTTTGTGTTCAGCCGTGA  3266
Sbjct                 3181   ............................................................  3240

Query                 3267   GTCACACTACATGCCCCCGTGAAGCTGGGCATTGGTGACGTCCAGGTTGTCCTTGAGTAA  3326
Sbjct                 3241   ............................................................  3300

Query                 3327   TAAAAACGTATGTTGCAA  3344
Sbjct                 3301   ..................  3318
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