5-13

NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARe17F12
Vector : pKA1U5

UQCC3
Lot# : 7672_B3Bd

Gene	C11orf83	
RefSeq_mRNA	NM_001085372.3	1927 bp

● **Plasmid DNA purification**

Date : 23.03.14 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.15 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

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

Date : 23.03.15

DNA concentration (O.D.): 169 ng/ul

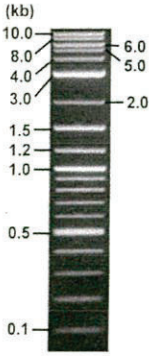
DNA	0.6 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.4 ul
Total	10 ul

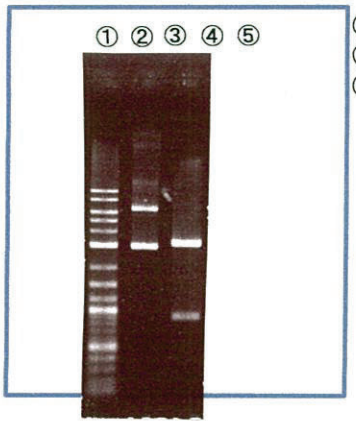
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 0.9 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder (NEB#N3200L)





①:Marker
②:uncut
③:BamHI

● **Confirmation of the** sequence

Date : 2026/06/16

full sequence : ARe17F12hts01.seq

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

Date : 2026/07/23

DNA (1699 ng/ul)	70 ul
10x TE	47 ul
dH_2O	356 ul
Total	473 ul

● **Shipping**

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY :

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http://dna.brc.riken.jp/index.html


(3559) BamHI
T3 promoter
SV40 poly(A) signal
3500
ori
500
insert
ORF
5' terminal sequence
3000
T7 promoter
M13 fwd
SV40 intron
(2707) BamHI
SV40 ori
SV40 promoter
2500
M13 rev
f1 ori
2000
AmpR promoter
signa...
1500
AmpR
1000
ARe17F12hts01.seq
3989 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001085372:Homo sapiens ubiquinol-cytochrome...

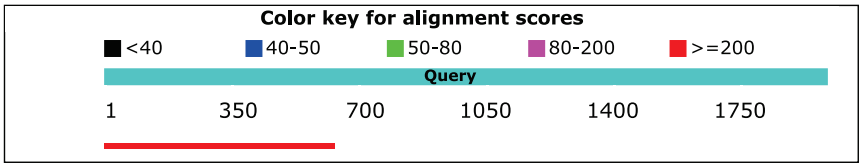
RID 3206R81X114 (Expires on 06-17 15:52 pm)

Query ID	NM_001085372.3	**Subject ID**	lcl|Query_8052427
Description	Homo sapiens ubiquinol-cytochrome c reductase complex assembly factor 3 (UQCC3), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	1927	**Subject Length**	3989
		Program	BLASTN 2.17.0+

ARe17F12hts01.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	1136	1136	32%	0.0	99.68%	Query_8052427

Alignments

Sequence ID: Query_8052427 Length: 3989 Number of Matches: 1
Range 1: 2878 to 3498

Score	Expect	Identities	Gaps	Strand	Frame
1136 bits(615)	0.0()	619/621(99%)	0/621(0%)	Plus/Plus	

Features:

```
Query          1     AGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGGAGCTCCCGTGGGCGCTCCGCTGGC  60
Sbjct          2878  ............................................................  2937

CDS:ubiquinol-cytoch 1                 M  D  S  L  R  K  M  L  I  S  V  A  M  L  G  A
Query          61    TGTGCAGGCGGCCATGGATTCCTTGCGGAAAATGCTGATCTCAGTCGCAATGCTGGGCGC  120
Sbjct          2938  ............................................................  2997

CDS:ubiquinol-cytoch 17    G  A  G  V  G  Y  A  L  L  V  I  V  T  P  G  E  R  R  K  Q
Query          121   AGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAGAGCGGCGGAAGCA  180
Sbjct          2998  ............................................................  3057

CDS:ubiquinol-cytoch 37    E  M  L  K  E  M  P  L  Q  D  P  R  S  R  E  E  A  A  R  T
Query          181   GGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAGGCGGCCAGGAC  240
Sbjct          3058  ............................................................  3117

CDS:ubiquinol-cytoch 57    Q  Q  L  L  L  A  T  L  Q  E  A  A  T  T  Q  E  N  V  A  W
Query          241   CCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAACGTGGCCTG  300
Sbjct          3118  ............................................................  3177

CDS:ubiquinol-cytoch 77    R  K  N  W  M  V  G  G  E  G  G  A  G  G  R  S  P
Query          301   GAGGAAGAACTGGATGGTTGGCGGCGAAGGCGGCGCCGGCGGGAGGTCACCGTGAGACCG  360
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Sbjct  3178  .....C.....A.....  3237

Query  361   GACTTGCCTCCGTGGGCGCCGGACCTTGGCTTGGGCGCAGGAATCCGAGGCAGCCTTTCT  420
Sbjct  3238  ............................................................  3297

Query  421   CCTTCGTGGGCCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGGTCC  480
Sbjct  3298  ............................................................  3357

Query  481   TGTGAGCTGCCGTCGGGTGAGCACGTTTCCCCCAAACCCTGGACTGACTGCTTTAAGGTC  540
Sbjct  3358  ............................................................  3417

Query  541   CGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAACTGAAAGAACCAATAAA  600
Sbjct  3418  ............................................................  3477

Query  601   ATCATGTTCCTCCACCCAGAA  621
Sbjct  3478  ....................  3498
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323 G>C (G84R)

338 G>A (G89S)

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