NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBdS081M01

Lot# : 6608_B6Go

Vector : pGCAP10

Gene	C20orf116	
RefSeq_mRNA	NM_023935.3	1303 bp

● Plasmid DNA purification

Date : 2026/07/27 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2026/07/28 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2026/07/28

DNA concentration (O.D.): 254 ng/ul

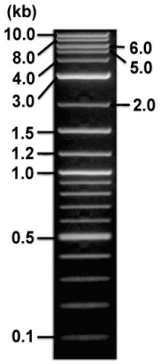
< Size of fragment expected from this clone >

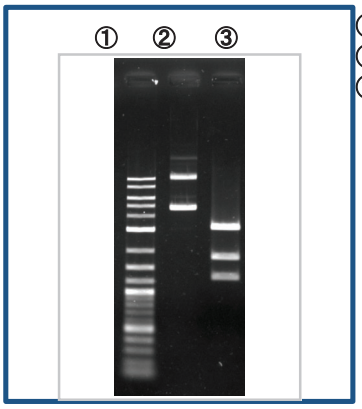
DNA	0.4 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.6 ul
Total	10 ul

BamHI 3.1kb (vector), 1.8, 1.3 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 : 2026/08/03

full sequence	RBdS081M01hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/08/04

DNA (254 ng/ul)	86 ul
10x TE	87 ul
dH_2O	700 ul
Total	874 ul

● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

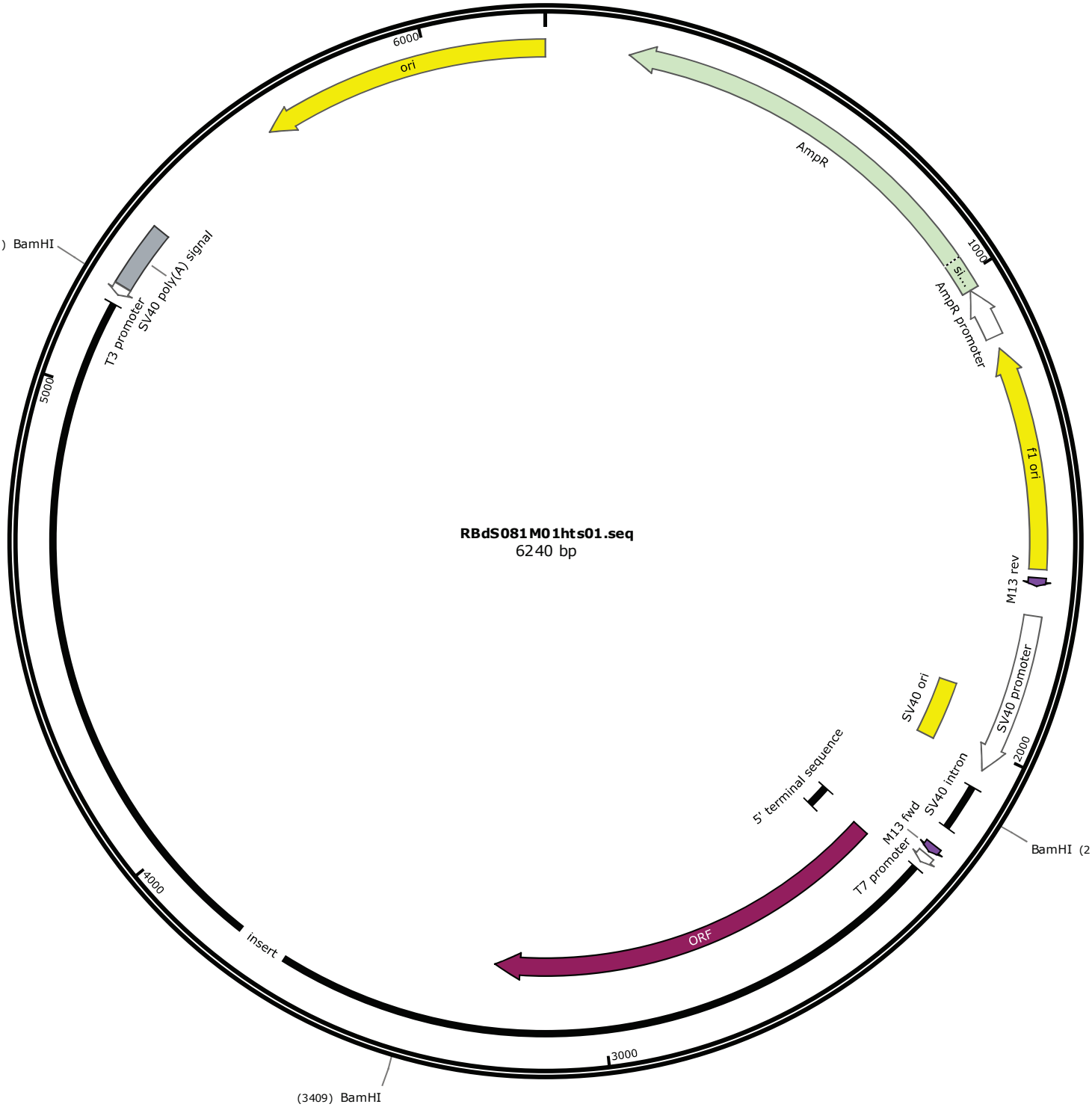
☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY :

検
'26.08.04
笹沼

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

1 つのフィーチャーが非表示です



BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_018359:Homo sapiens UFM1 specific peptidase...

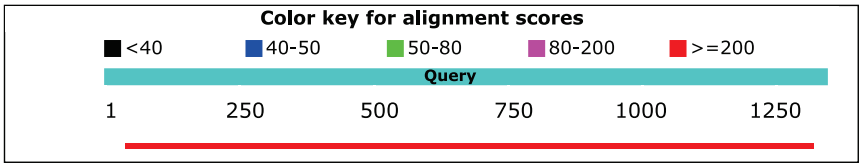
RID 6ZU2DX29114 (Expires on 08-04 09:01 am)

Query ID	NM_023935.3	**Subject ID**	lcl|Query_770173
Description	Homo sapiens DDRGK domain containing 1 (DDRGK1), mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	1303	**Subject Length**	6240
		Program	BLASTN 2.17.0+

RBdS081M01hts01.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	2333	2333	97%	0.0	100.00%	Query_770173

Alignments

Sequence ID: Query_770173 Length: 6240 Number of Matches: 1
Range 1: 2279 to 3541

Score	Expect	Identities	Gaps	Strand	Frame
2333 bits(1263)	0.0()	1263/1263(100%)	0/1263(0%)	Plus/Plus	

Features:

```
CDS:DDRGK domain-con  1                    M  V  A  P  V  W  Y  L  V  A  A  A  L  L  V
Query                 41   ACTGAGGCCCTCGTCATGGTGGCGCCTGTGTGGTACTTGGTAGCGGCGGCTCTGCTAGTC  100
Sbjct                 2279 ............................................................  2338

CDS:DDRGK domain-con  16    G  F  I  L  F  L  T  R  S  R  G  R  A  A  S  A  G  Q  E  P
Query                 101  GGCTTTATCCTCTTCCTGACTCGCAGCCGGGGCCGGGCGGCATCAGCCGGCCAAGAGCCA  160
Sbjct                 2339 ............................................................  2398

CDS:DDRGK domain-con  36    L  H  N  E  E  L  A  G  A  G  R  V  A  Q  P  G  P  L  E  P
Query                 161  CTGCACAATGAGGAGCTGGCAGGAGCAGGCCGGGTGGCCCAGCCTGGGCCCCTGGAGCCT  220
Sbjct                 2399 ............................................................  2458

CDS:DDRGK domain-con  56    E  E  P  R  A  G  G  R  P  R  R  R  R  D  L  G  S  R  L  Q
Query                 221  GAGGAGCCGAGAGCTGGAGGCAGGCCTCGGCGCCGGAGGGACCTGGGCAGCCGCCTACAG  280
Sbjct                 2459 ............................................................  2518

CDS:DDRGK domain-con  76    A  Q  R  R  A  Q  R  V  A  W  A  E  A  D  E  N  E  E  E  A
Query                 281  GCCCAGCGTCGAGCCCAGCGGGTGGCCTGGGCAGAAGCAGATGAGAACGAGGAGGAAGCT  340
Sbjct                 2519 ............................................................  2578

CDS:DDRGK domain-con  96     V  I  L  A  Q  E  E  E  G  V  E  K  P  A  E  T  H  L  S  G
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Query                341   GTCATCCTAGCCCAGGAGGAGGAAGGTGTCGAGAAGCCAGCGGAAACTCACCTGTCGGGG  400
Sbjct                2579  ............................................................  2638

CDS:DDRGK domain-con 116    K  I  G  A  K  K  L  R  K  L  E  E  K  Q  A  R  K  A  Q  R
Query                401   AAAATTGGAGCTAAGAAACTGCGGAAGCTGGAGGAGAAACAAGCGCGAAAGGCCCAGCGT  460
Sbjct                2639  ............................................................  2698

CDS:DDRGK domain-con 136    E  A  E  E  A  E  R  E  E  R  K  R  L  E  S  Q  R  E  A  E
Query                461   GAGGCAGAGGAGGCTGAACGTGAGGAGCGGAAACGACTCGAGTCCCAGCGCGAAGCTgag  520
Sbjct                2699  ............................................................  2758

CDS:DDRGK domain-con 156    W  K  K  E  E  E  R  L  R  L  E  E  E  Q  K  E  E  E  E  R
Query                521   tggaagaaggaggaggagcggcttcgcctggaggaggagcagaaggaggaggaggagagg  580
Sbjct                2759  ............................................................  2818

CDS:DDRGK domain-con 176    K  A  R  E  E  Q  A  Q  R  E  H  E  E  Y  L  K  L  K  E  A
Query                581   aaggcccgcgaggagcaggcccagcgggagcatgaggagTACCTGAAACTGAAGGAGGCC  640
Sbjct                2819  ............................................................  2878

CDS:DDRGK domain-con 196    F  V  V  E  E  E  G  V  G  E  T  M  T  E  E  Q  S  Q  S  F
Query                641   TTTGTGGTGGAGGAGGAAGGCGTAGGAGAGACCATGACTGAGGAACAGTCCCAGAGCTTC  700
Sbjct                2879  ............................................................  2938

CDS:DDRGK domain-con 216    L  T  E  F  I  N  Y  I  K  Q  S  K  V  V  L  L  E  D  L  A
Query                701   CTGACAGAGTTCATCAACTACATCAAGCAGTCCAAGGTTGTGCTCTTGGAAGACCTGGCT  760
Sbjct                2939  ............................................................  2998

CDS:DDRGK domain-con 236    S  Q  V  G  L  R  T  Q  D  T  I  N  R  I  Q  D  L  L  A  E
Query                761   TCCCAGGTGGGCCTACGCACTCAGGACACCATAAATCGCATCCAGGACCTGCTGGCTGAG  820
Sbjct                2999  ............................................................  3058

CDS:DDRGK domain-con 256    G  T  I  T  G  V  I  D  D  R  G  K  F  I  Y  I  T  P  E  E
Query                821   GGGACTATAACAGGTGTGATTGACGACCGGGGCAAGTTCATCTACATAACCCCAGAGGAA  880
Sbjct                3059  ............................................................  3118

CDS:DDRGK domain-con 276    L  A  A  V  A  N  F  I  R  Q  R  G  R  V  S  I  A  E  L  A
Query                881   CTGGCCGCCGTGGCCAACTTCATCCGACAGCGGGGCCGGGTGTCCATCGCCGAGCTTGCC  940
Sbjct                3119  ............................................................  3178

CDS:DDRGK domain-con 296    Q  A  S  N  S  L  I  A  W  G  R  E  S  P  A  Q  A  P  A
Query                941   CAAGCCAGCAACTCCCTCATCGCCTGGGGCCGGGAGTCCCCTGCCCAAGCCCCAGCCTGA  1000
Sbjct                3179  ............................................................  3238

Query                1001  CCCCAGTCCTTCCCTCTTGGACTCAGAGTTGGTGTGGCCTACCTGGCTATACATCTTCAT  1060
Sbjct                3239  ............................................................  3298

Query                1061  CCCTCCCCACCATCCTGGGGAAGTGATGGTGTGGCCAGGCAGTTATAGATTAAAGGCCTG  1120
Sbjct                3299  ............................................................  3358

Query                1121  TGAGTACTGCTGAGCTTGGTGTGGCTTGGTGTGGCAGAAGGCCTGGCCTAGGATCCTAGA  1180
Sbjct                3359  ............................................................  3418

Query                1181  TAAGCAGGTGAAATTTAGGCTTCAGAATATATCCGAGAGGTGGGGAGGGTCCCTTGGAAG  1240
Sbjct                3419  ............................................................  3478

Query                1241  CTGGTGAAGTCCTGTTCTTATTATGAATCCATTCATTCAAGAAAATAGCCTGTTGCACAT  1300
Sbjct                3479  ............................................................  3538

Query                1301  TTA  1303

Sbjct                3539  ...  3541
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