NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : RBdS177F15

Lot# : 6608_B6Do

Vector : pGCAP10

Gene	DLG3	
RefSeq_mRNA	NM_020730.3	5090 bp

● Plasmid DNA purification

Date : 2026/04/27

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

Date : 2026/04/28

Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2026/04/28

DNA concentration (O.D.): 310 ng/ul

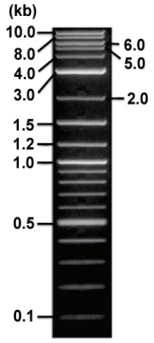
DNA	0.35 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.65 ul
Total	10 ul

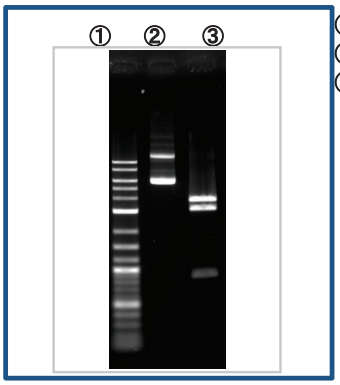
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 3.8, 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 : 2026/05/07

full sequence	RBdS177F15hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/05/12

DNA (310 ng/ul)	82 ul
10x TE	102 ul
dH_2O	833 ul
Total	1,017 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


(7362) BamHI
ori
T3 promoter
SV40 poly(A) signal
7000
1000
AmpR
AmpR promoter
6000
RBdS177F15hts01.seq
7794 bp
f1 ori
2000
M13 rev
SV40 ori
SV40 promoter
5' terminal sequence
M13 fwd
SV40 intron
T7 promoter
BamHI (2705)
insert
5000
3000
ORF
4000
BamHI (3577)

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001166278:Homo sapiens discs large MAGUK...

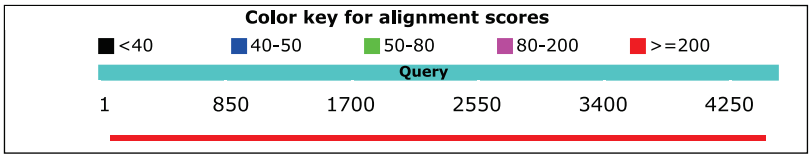
RID ZSA0KJMJ114 (Expires on 05-08 13:50 pm)

Query ID	NM_001166278.2	**Subject ID**	lcl|Query_1089853
Description	Homo sapiens discs large MAGUK scaffold protein 3 (DLG3), transcript variant 3, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	4453	**Subject Length**	7794
		Program	BLASTN 2.17.0+

RBdS177F15hts01.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	8069	8069	98%	0.0	100.00%	Query_1089853

Alignments

Sequence ID: Query_1089853 Length: 7794 Number of Matches: 1
Range 1: 2927 to 7295

Score	Expect	Identities	Gaps	Strand	Frame
8069 bits(4369)	0.0()	4369/4369(100%)	0/4369(0%)	Plus/Plus	

Features:

```
CDS:disks large homo  1                                                M  M  N  S
Query                 85    CAGAATACAGTCGCTTTGAATCGAAGATACATGACTTACGAGAACAAATGATGAACAGCA  144
Sbjct                 2927  ............................................................  2986

CDS:disks large homo  5     S  M  S  S  G  S  G  S  L  R  T  S  E  K  R  S  L  Y  V  R
Query                 145   GCATGAGCTCTGGGTCTGGGTCCCTCCGAACAAGTGAAAAGAGGTCCTTGTATGTCAGGG  204
Sbjct                 2987  ............................................................  3046

CDS:disks large homo  25    A  L  F  D  Y  D  R  T  R  D  S  C  L  P  S  Q  G  L  S  F
Query                 205   CCCTGTTTGATTATGATCGGACTCGGGACAGCTGCCTGCCAAGCCAGGGGCTCAGCTTCT  264
Sbjct                 3047  ............................................................  3106

CDS:disks large homo  45    S  Y  G  D  I  L  H  V  I  N  A  S  D  D  E  W  W  Q  A  R
Query                 265   CTTATGGTGACATTCTGCATGTCATTAATGCCTCTGATGATGAGTGGTGGCAGGCAAGGC  324
Sbjct                 3107  ............................................................  3166

CDS:disks large homo  65    L  V  T  P  H  G  E  S  E  Q  I  G  V  I  P  S  K  K  R  V
Query                 325   TGGTGACCCCACACGGAGAAAGTGAGCAGATCGGTGTGATCCCCAGTAAGAAGAGGGTGG  384
Sbjct                 3167  ............................................................  3226

CDS:disks large homo  85    E  K  K  E  R  A  R  L  K  T  V  K  F  H  A  R  T  G  M  I
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Query                385  AAAAGAAAGAAAGAGCTCGATTGAAAACTGTGAAGTTCCATGCCAGGACGGGGATGATTG  444
Sbjct               3227  ............................................................  3286

CDS:disks large homo 105  E  S  N  R  S  I  K  T  K  R  K  K  S  F  R  L  S  R  K  F
Query                445  AGTCTAACAGGTCGATCAAAACGAAACGTAAAAAGAGTTTCCGCCTCTCTCGAAAGTTTC  504
Sbjct               3287  ............................................................  3346

CDS:disks large homo 125  P  F  Y  K  S  K  E  N  M  A  Q  E  S  S  I  Q  E  Q  G  V
Query                505  CATTTTACAAGAGCAAAGAAAACATGGCCCAGGAGAGCAGCATACAGGAACAGGGAGTGA  564
Sbjct               3347  ............................................................  3406

CDS:disks large homo 145  T  S  N  T  S  D  S  E  S  S  S  K  G  Q  E  D  A  I  L  S
Query                565  CATCCAACACCAGTGACAGCGAAAGCAGTTCCAAAGGACAAGAGGATGCTATTTTGTCAT  624
Sbjct               3407  ............................................................  3466

CDS:disks large homo 165  Y  E  P  V  T  R  Q  E  I  H  Y  A  R  P  V  I  I  L  G  P
Query                625  ATGAGCCAGTGACACGGCAAGAAATTCACTATGCAAGGCCTGTGATCATCCTGGGCCCAA  684
Sbjct               3467  ............................................................  3526

CDS:disks large homo 185  M  K  D  R  V  N  D  D  L  I  S  E  F  P  H  K  F  G  S  C
Query                685  TGAAGGACCGAGTCAATGATGACCTGATCTCCGAATTTCCACATAAATTTGGATCCTGTG  744
Sbjct               3527  ............................................................  3586

CDS:disks large homo 205  V  P  H  T  T  R  P  R  R  D  N  E  V  D  G  Q  D  Y  H  F
Query                745  TGCCACATACTACCCGGCCTCGACGTGATAATGAGGTGGATGGACAAGACTACCACTTTG  804
Sbjct               3587  ............................................................  3646

CDS:disks large homo 225  V  V  S  R  F  Q  M  E  K  D  I  Q  D  N  K  F  I  E  A  G
Query                805  TGGTGTCCCGAGAACAAATGGAGAAAGATATTCAGGACAACAAGTTCATCGAGGCGGGCC  864
Sbjct               3647  ............................................................  3706

CDS:disks large homo 245  Q  F  N  D  N  L  Y  G  T  S  I  Q  S  V  R  A  V  A  E  R
Query                865  AATTTAATGATAACCTCTATGGGACCAGCATCCAGTCAGTGCGGGCAGTTGCAGAGAGGG  924
Sbjct               3707  ............................................................  3766

CDS:disks large homo 265  G  K  H  C  I  L  D  V  S  G  N  A  I  K  R  L  Q  Q  A  Q
Query                925  GCAAGCACTGCATCTTAGATGTTTCCGGCAATGCTATCAAGAGACTGCAGCAAGCACAAC  984
Sbjct               3767  ............................................................  3826

CDS:disks large homo 285  L  Y  P  I  A  I  F  I  K  P  K  S  I  E  A  L  M  E  M  N
Query                985  TTTACCCCATTGCCATTTTCATCAAGCCCAAGTCCATTGAAGCCCTTATGGAAATGAACC  1044
Sbjct               3827  ............................................................  3886

CDS:disks large homo 305  R  R  Q  T  Y  E  Q  A  N  K  I  Y  D  K  A  M  K  L  E  Q
Query                1045 GAAGGCAGACATATGAACAAGCAAATAAGATCTATGACAAAGCCATGAAACTGGAGCAGG  1104
Sbjct               3887  ............................................................  3946

CDS:disks large homo 325  E  F  G  E  Y  F  T  A  I  V  Q  G  D  S  L  E  E  I  Y  N
Query                1105 AATTTGGAGAGTACTTTACAGCCATTGTACAGGGTGACTCACTGGAAGAGATTTATAACA  1164
Sbjct               3947  ............................................................  4006

CDS:disks large homo 345  K  I  K  Q  I  I  E  D  Q  S  G  H  Y  I  W  V  P  S  P  E
Query                1165 AAATCAAACAAATCATTGAGGACCAGTCTGGGCACTACATTTGGGTCCCATCCCCTGAAA  1224
Sbjct               4007  ............................................................  4066

CDS:disks large homo 365  K  L
Query                1225 AACTCTGAAGAATCCCCTCCAACCATTCTCTTGTGAACAGAAGAAATCAAGTCCCTCTTC  1284
Sbjct               4067  ............................................................  4126

Query                1285 CCTCCTCCCTCTTCATTCCTGTCCCCATGGGGAGAACAAATGCTACTGTTCTTGTCCCCT  1344
Sbjct               4127  ............................................................  4186

Query                1345 TTTTTAGATATGTCaaaaaaaaTTAAGTTTTCTAGTCCTGTTCttttttttttttttaagt  1404
Sbjct               4187  ............................................................  4246

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Sbjct               4307  ............................................................  4366

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Sbjct               4367  ............................................................  4426

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Sbjct               4427  ............................................................  4486

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Sbjct               4487  ............................................................  4546

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Query                1825 TTAGAAAATCTATGGAGACTTCATCAATGGTACTATGTTATTAGAGAAATGCTTTAATTT  1884
Sbjct               4667  ............................................................  4726

Query                1885 TCATATTCCAATCAGATGGCATCTTCTATCCCAGCTGGTTGGGAAGGGATTGAAGATGGT  1944
Sbjct               4727  ............................................................  4786

Query                1945 AGCAAGTGCTGCACTAAGGGCACTCGCATTTGGTCATTCTCTTGAGAGCTAGGAGGGGTC  2004
Sbjct               4787  ............................................................  4846

Query                2005 AGCCTGAGGCCGGAGAGGAAGGGCTTTTGCCTGGGGTGAGAGGGTGAGAGACTTGACCTG  2064
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Sbjct               4907  ............................................................  4966

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Sbjct               4967  ............................................................  5026

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Sbjct               5027  ............................................................  5086

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Sbjct               5267  ............................................................  5326
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Query  2485  TGCCTTCCAGTTCTGTGCTGGGATGGCGGGACAGCACTTGGCTTGCTTGGCCAGCTGCGT  2544
Sbjct  5327  ............................................................  5386

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Sbjct  5387  ............................................................  5446

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Sbjct  5447  ............................................................  5506

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Sbjct  5867  ............................................................  5926

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Sbjct  6467  ............................................................  6526

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Sbjct  7007  ............................................................  7066

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Sbjct  7067  ............................................................  7126

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Query  4405  AACCTTATGGTCTACCCATGAATAAATAAAATATTTGTTCAAGCACAAA  4453
Sbjct  7247  ................................................  7295
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