NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBdS015C05

Lot# : 6608_B5Bp

Vector : pGCAP10

Gene	DOHH	
RefSeq_mRNA	NM_001145165.2	1763 bp

● Plasmid DNA purification

Date : 2025/02/25 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2025/02/26 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/02/26

DNA concentration (O.D.): 349 ng/ul

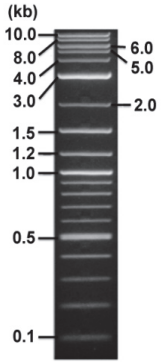
< Size of fragment expected from this clone >

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

BamHI 3.1kb (vector), 2.0 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 : 2025/02/27

full sequence	RBdS015C05hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/03/04

DNA (349 ng/ul)	80 ul
10x TE	112 ul
dH_2O	925 ul
Total	1,117 ul

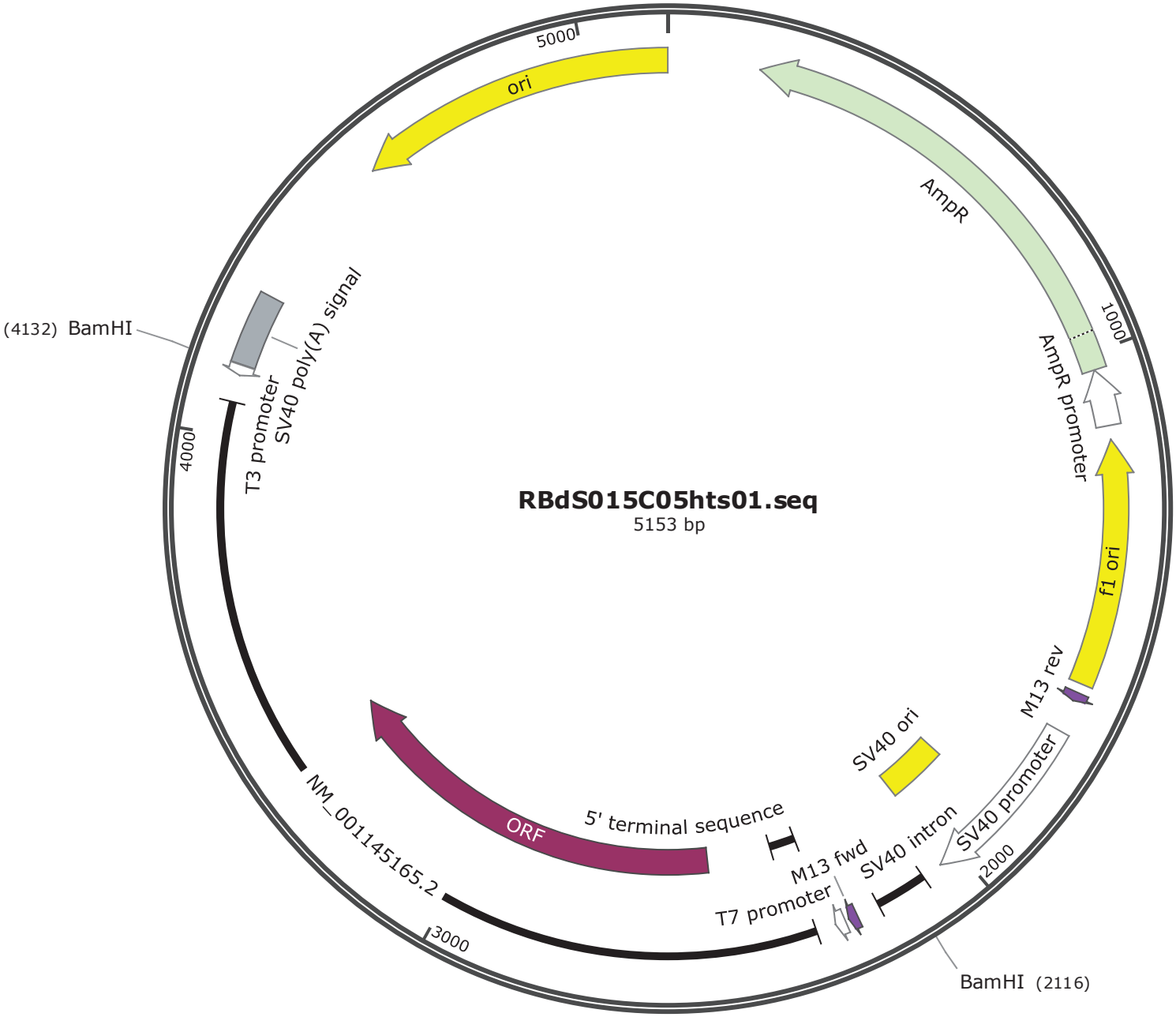
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '25.03.04 笹沼

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


RBdS015C05hts01.seq
5153 bp
5000
ori
AmpR
1000
AmpR promoter
f1 ori
M13 rev
SV40 ori
SV40 promoter
2000
SV40 intron
M13 fwd
T7 promoter
BamHI (2116)
3000
NM_001145165.2
5' terminal sequence
ORF
4000
T3 promoter
SV40 poly(A) signal
(4132) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

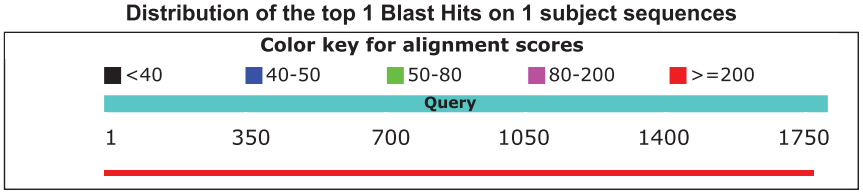
Job title: NM_001145165:Homo sapiens deoxyhypusine hydroxylase...

RID W06AG5GM114 (Expires on 02-28 14:50 pm)

Query ID	NM_001145165.2	**Subject ID**	lcl|Query_1227891
Description	Homo sapiens deoxyhypusine hydroxylase (DOHH), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	1763	**Subject Length**	5153
		Program	BLASTN 2.16.1+

RBdS015C05hts01.seq

Graphic Summary



Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	3256	3256	100%	0.0	100.00%	Query_1227891

Alignments

Sequence ID: Query_1227891 Length: 5153 Number of Matches: 1
Range 1: 2300 to 4062

Score	Expect	Identities	Gaps	Strand	Frame
3256 bits(1763)	0.0()	1763/1763(100%)	0/1763(0%)	Plus/Plus	

Features:

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Query          1     GAGAAAATGGCGGCCCCCAGACCGCACTGCGGGCGTCGCGGCAGGTGAAGCGGTGGTGGC  60
Sbjct          2300  ............................................................  2359

Query          61    AGAGGCGCCTGCGGTTACTGGCCGGGCCGACGGGTCCTGAGTCTCCAGAGCTCGGTTCTT  120
Sbjct          2360  ............................................................  2419

Query          121   ACATCCCCGCGTCCCCAGGTTTAGCCTGAGCAGGGTTGTGGAAGGCCGGGACCCATTGAC  180
Sbjct          2420  ............................................................  2479

CDS:deoxyhypusine hy 1           M  V  T  E  Q  E  V  D  A  I  G  Q  T  L  V  D  P  K
Query          181   AGCACGATGGTGACGGAGCAGGAGGTGGATGCCATCGGGCAGACGCTGGTGGACCCCAAG  240
Sbjct          2480  ............................................................  2539

CDS:deoxyhypusine hy 19    Q  P  L  Q  A  R  F  R  A  L  F  T  L  R  G  L  G  G  P  G
Query          241   CAGCCCCTGCAGGCCCGCTTCCGGGCGCTGTTCACGCTGCGTGGGCTCGGCGGCCCAGGC  300
Sbjct          2540  ............................................................  2599

CDS:deoxyhypusine hy 39    A  I  A  W  I  S  Q  A  F  D  D  D  S  A  L  L  K  H  E  L
Query          301   GCCATTGCATGGATCAGCCAGGCCTTCGATGACGATTCCGCCCTGCTCAAGCACGAGCTG  360
Sbjct          2600  ............................................................  2659

CDS:deoxyhypusine hy 59    A  Y  C  L  G  Q  M  Q  D  A  R  A  I  P  M  L  V  D  V  L
Query          361   GCCTACTGCCTGGGCCAGATGCAGGATGCCCGCGCCATCCCCATGCTGGTGGACGTGCTG  420
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Sbjct                 2660  ..........................................................  2719

CDS:deoxyhypusine hy  79     Q  D  T  R  Q  E  P  M  V  R  H  E  A  G  E  A  L  G  A  I
Query                 421   CAAGACACCCGTCAGGAGCCCATGGTGCGCCATGAGGCAGGGGAGGCCCTGGGGGCCATC  480
Sbjct                 2720  ..........................................................  2779

CDS:deoxyhypusine hy  99     G  D  P  E  V  L  E  I  L  K  Q  Y  S  S  D  P  V  I  E  V
Query                 481   GGGGACCCGGAAGTTCTGGAGATCCTGAAGCAGTATTCCTCGGACCCCGTCATCGAGGTG  540
Sbjct                 2780  ..........................................................  2839

CDS:deoxyhypusine hy  119    A  E  T  C  Q  L  A  V  R  R  L  E  W  L  Q  Q  H  G  G  E
Query                 541   GCCGAGACCTGCCAGCTGGCCGTGCGCAGGCTGGAGTGGCTGCAGCAGCACGGCGGGGAG  600
Sbjct                 2840  ..........................................................  2899

CDS:deoxyhypusine hy  139    P  A  A  G  P  Y  L  S  V  D  P  A  P  P  A  E  E  R  D  V
Query                 601   CCGGCGGCGGGACCCTACCTCTCCGTGGACCCTGCCCCGCCGGCTGAGGAGCGTGACGTG  660
Sbjct                 2900  ..........................................................  2959

CDS:deoxyhypusine hy  159    G  R  L  R  E  A  L  L  D  E  S  R  P  L  F  E  R  Y  R  A
Query                 661   GGGCGCCTGCGGGAGGCGCTGCTGGATGAGTCCCGGCCGCTCTTCGAGCGATACCGCGCC  720
Sbjct                 2960  ..........................................................  3019

CDS:deoxyhypusine hy  179    M  F  A  L  R  N  A  G  G  E  E  A  A  L  A  L  A  E  G  L
Query                 721   ATGTTCGCCCTGCGCAACGCGGGAGGCGAGGAGGCCGCCCTGGCGCTGGCCGAGGGTCTG  780
Sbjct                 3020  ..........................................................  3079

CDS:deoxyhypusine hy  199    H  C  G  S  A  L  F  R  H  E  V  G  Y  V  L  G  Q  L  Q  H
Query                 781   CACTGTGGGAGCGCCCTCTTCCGCCACGAGGTCGGCTACGTCCTGGGACAGCTGCAGCAC  840
Sbjct                 3080  ..........................................................  3139

CDS:deoxyhypusine hy  219    E  A  A  V  P  Q  L  A  A  A  L  A  R  C  T  E  N  P  M  V
Query                 841   GAGGCGGCGGTGCCCCAGCTGGCGGCCGCCCTGGCCCGATGCACCGAGAACCCCATGGTG  900
Sbjct                 3140  ..........................................................  3199

CDS:deoxyhypusine hy  239    R  H  E  C  A  E  A  L  G  A  I  A  R  P  A  C  L  A  A  L
Query                 901   CGGCACGAGTGCGCGGAGGCCCTGGGCGCCATTGCCCGGCCCGCCTGCCTGGCCGCGCTG  960
Sbjct                 3200  ..........................................................  3259

CDS:deoxyhypusine hy  259    Q  A  H  A  D  D  P  E  R  V  V  R  E  S  C  E  V  A  L  D
Query                 961   CAGGCTCACGCGGACGACCCAGAGCGCGTGGTGCGTGAGAGCTGCGAGGTGGCTCTGGAC  1020
Sbjct                 3260  ..........................................................  3319

CDS:deoxyhypusine hy  279    M  Y  E  H  E  T  G  R  A  F  Q  Y  A  D  G  L  E  Q  L  R
Query                 1021  ATGTATGAGCACGAGACCGGGCGGGCCTTCCAGTACGCGGACGGCCTGGAGCAGCTGCGC  1080
Sbjct                 3320  ..........................................................  3379

CDS:deoxyhypusine hy  299    G  A  P  S
Query                 1081  GGGGCCCCCTCCTAGGGCCCCACCCTCACCCGGAGCTCCCGGAGGACTCTTGAGGGCCGC  1140
Sbjct                 3380  ..........................................................  3439

Query                 1141  TCCTCCCCCGCAGAGCTTTGGCGTCTAAACCGGGTGTGTGTAAATCGGTGTCATCGCTTG  1200
Sbjct                 3440  ..........................................................  3499

Query                 1201  TGTCTTGCTGGGCGCATGGTTGCTGTCCCCCTCCTCCGTCTGGGACCGAGGAGCTGCCGT  1260
Sbjct                 3500  ..........................................................  3559

Query                 1261  TGTGCTGTGACTCCCTGAGTCCCCTGACTGCTCCTCGGGGCCTGGCGCAGGGCTGTAGCG  1320
Sbjct                 3560  ..........................................................  3619

Query                 1321  TGGAAGTTTCCAGGCTTGGGGTGGGACTCTGCGGGAGGCTCTGGGATGCCCGGCTcagga  1380
Sbjct                 3620  ..........................................................  3679

Query                 1381  caggggaggattgcgagggaagccaggggaggatcgcgagggaagccaggggaggatcgc  1440
Sbjct                 3680  ..........................................................  3739

Query                 1441  gagggaagccaggggaggatcgcgagggaagccaggggaggatcgcgagggaagccaagg  1500
Sbjct                 3740  ..........................................................  3799

Query                 1501  gaggatcgcgaggggagccaggggaggatcgcgagggaagccaggggCAGAGCTGGGGCT  1560
Sbjct                 3800  ..........................................................  3859

Query                 1561  CTGGGAAGAGGCTGACGTTATGGTGGCTTCAGCTTCACTAGGAATGGGACACAGGGTCTG  1620
Sbjct                 3860  ..........................................................  3919

Query                 1621  GGGGCCTCTGACTCCCCCACCCCGAGGCCTGGGTAGGGACAGGGTGGTGGTCCCTGAGTG  1680
Sbjct                 3920  ..........................................................  3979

Query                 1681  GGTCAGGTAGGGCACAGGGGCCAGGGAGGGACAAGCAGACCTCAGAGCGCTGCCCAGATG  1740
Sbjct                 3980  ..........................................................  4039

Query                 1741  GAATATTAAATTATTTTTGCCAA  1763
Sbjct                 4040  .......................  4062
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