NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARh10G02
Vector : pGCAP1

Lot# : 7674_B3Bd

Gene	PEX5L	
RefSeq_mRNA	NM_016559.3	9089 bp

● **Plasmid DNA purification**

Date : 23.02.15 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.02.16 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

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

Date : 23.02.16

DNA concentration (O.D.): 263 ng/ul

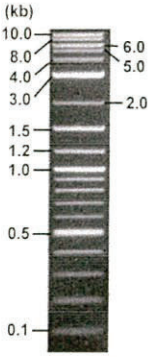
DNA	0.4 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.6 ul
Total	10 ul

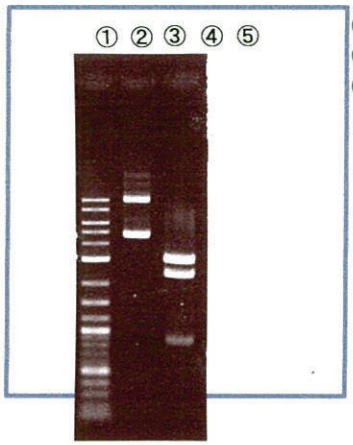
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.5, 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 : 2026/06/18

full sequence : ARh10G02hts01.seq

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

Date : 2026/07/23

DNA (263 ng/ul)	76 ul
10x TE	80 ul
dH_2O	644 ul
Total	800 ul

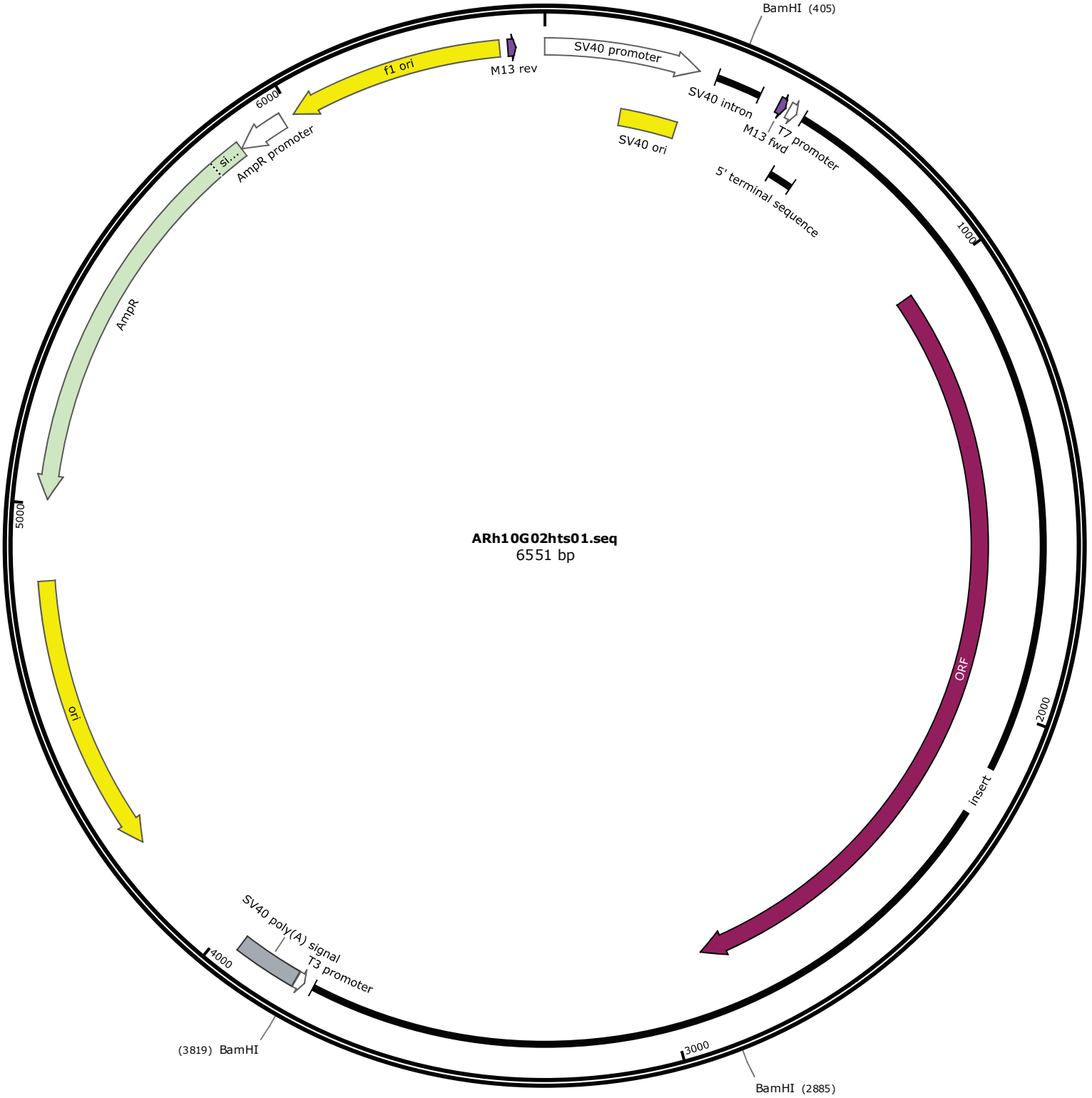
● **Shipping**

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '26.07.23 笹沼

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


BamHI (405)
SV40 promoter
f1 ori
M13 rev
SV40 intron
M13 fwd
T7 promoter
SV40 ori
5' terminal sequence
6000
1000
AmpR promoter
AmpR
5000
ARh10G02hts01.seq
6551 bp
ORF
2000
ori
insert
SV40 poly(A) signal
T3 promoter
4000
(3819) BamHI
3000
BamHI (2885)

BLAST Results

Questions/comments

Blast 2 sequences

Job title: ref|NM_016559|

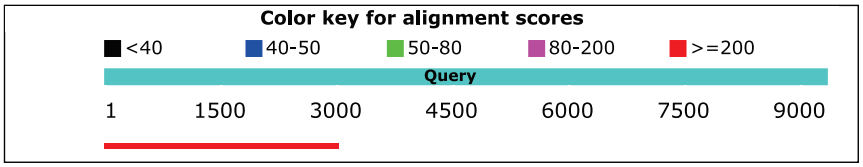
RID 372WJRNB114 (Expires on 06-19 14:09 pm)

Query ID	NM_016559.3	**Subject ID**	lcl|Query_3126139
Description	Homo sapiens peroxisomal biogenesis factor 5 like (PEX5L), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	9089	**Subject Length**	6551
		Program	BLASTN 2.17.0+

ARh10G02hts01.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	5500	5500	33%	0.0	100.00%	Query_3126139

Alignments

Sequence ID: Query_3126139 Length: 6551 Number of Matches: 1
Range 1: 676 to 3653

Score	Expect	Identities	Gaps	Strand	Frame
5500 bits(2978)	0.0()	2978/2978(100%)	0/2978(0%)	Plus/Plus	

Features:

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Query          1     AGGAAGCGAGAAAGAGTTCGGCGAAGAAGGAGTGAGTTCTAGAGACGCCCCGCGAGCAGG  60
Sbjct          676   ............................................................  735

Query          61    ACCCGCGCCTGCAGGAGAGCCTGGCCGACCCGGCTCCTCGCCTTCTCTGCGCGCTCTCCC  120
Sbjct          736   ............................................................  795

Query          121   GCGTCCGCTTTCAGCACCCCGAGCGGAGAACAGTTCCCGGCAGCCCGCAGCGCTGCCGAG  180
Sbjct          796   ............................................................  855

Query          181   TGGCCGCCGGCCGGCCGAGTACCCGGAGCTCCAGGGGGCTCAGGAGCACCCTCTGAGAAC  240
Sbjct          856   ............................................................  915

Query          241   CCGCTGTGCACCCACCTTTTCCCCTCTTTTGGTGGGCAAGTAAGCACGGGGGAAAAGCAT  300
Sbjct          916   ............................................................  975

CDS:PEX5-related pro 1                                       M  Y  Q  G  H  M  Q
Query          301   CCGGTGGCCTCAGGGAGCCCTGAAGAAACCGAAGCAGAATGTACCAGGGACACATGCAGA  360
Sbjct          976   ............................................................  1035

CDS:PEX5-related pro 8     K  S  K  E  Q  G  Y  G  K  L  S  S  D  E  D  L  E  I  I  V
Query          361   AAAGTAAAGAACAAGGATATGGAAAACTAAGCAGTGATGAAGACCTCGAAATAATTGTTG  420
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Sbjct                1036  ..........................................................  1095

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Query                 421  ATCAAAAGCAGGGAAAAGGCTCTAGGGCGGCAGATAAGGCTGTTGCCATGGTGATGAAGG  480
Sbjct                1096  ..........................................................  1155

CDS:PEX5-related pro   48  E  I  P  R  E  E  S  A  E  E  K  P  L  L  T  M  T  S  Q  L
Query                 481  AGATACCGAGGGAGGAGTCTGCTGAAGAAAAGCCCCTCCTTACTATGACATCACAGCTGG  540
Sbjct                1156  ..........................................................  1215

CDS:PEX5-related pro   68  V  N  E  Q  Q  E  S  R  P  L  L  S  P  S  I  D  D  F  L  C
Query                 541  TGAATGAGCAACAAGAAAGCAGACCCCTCCTGAGTCCCTCCATCGATGACTTTCTCTGTG  600
Sbjct                1216  ..........................................................  1275

CDS:PEX5-related pro   88  E  T  K  S  E  A  I  A  R  P  V  T  S  N  T  A  V  L  T  T
Query                 601  AAACCAAATCGGAAGCAATAGCAAGGCCAGTAACATCCAATACAGCTGTATTGACCACTG  660
Sbjct                1276  ..........................................................  1335

CDS:PEX5-related pro  108  G  L  D  L  L  D  L  S  E  P  V  S  Q  T  Q  T  K  A  K  K
Query                 661  GCTTAGATCTCCTCGACCTGAGTGAACCAGTCTCTCAAACCCAAACCAAAGCCAAGAAGT  720
Sbjct                1336  ..........................................................  1395

CDS:PEX5-related pro  128  S  E  P  S  S  K  T  S  S  L  K  K  K  A  D  G  S  D  L  I
Query                 721  CAGAGCCCTCATCAAAAACCTCATCCCTCAAGAAAAAGGCCGATGGATCTGACCTCATCA  780
Sbjct                1396  ..........................................................  1455

CDS:PEX5-related pro  148  S  T  D  A  E  Q  R  G  Q  P  L  R  V  P  E  T  S  S  L  D
Query                 781  GCACGGATGCTGAGCAGAGAGGCCAGCCTCTCAGAGTCCCGGAGACTTCATCCTTAGATC  840
Sbjct                1456  ..........................................................  1515

CDS:PEX5-related pro  168  L  D  I  Q  T  Q  L  E  K  W  D  D  V  K  F  H  G  D  R  N
Query                 841  TAGACATTCAAACACAACTGGAAAAATGGGACGATGTTAAGTTTCATGGAGATCGAAATA  900
Sbjct                1516  ..........................................................  1575

CDS:PEX5-related pro  188  T  K  G  H  P  M  A  E  R  K  S  S  S  S  R  T  G  S  K  E
Query                 901  CCAAGGGACATCCAATGGCAGAGAGAAAATCATCCTCATCTAGAACTGGATCAAAAGAGC  960
Sbjct                1576  ..........................................................  1635

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Query                 961  TCTTATGGTCCTCAGAACACAGATCTCAACCAGAACTGAGTGGTGGAAAAAGCGCCCTCA 1020
Sbjct                1636  ..........................................................  1695

CDS:PEX5-related pro  228  N  S  E  S  A  S  E  L  E  L  V  A  P  T  Q  A  R  L  T  K
Query                1021  ACTCTGAGTCGGCTTCAGAATTGGAATTAGTGGCTCCGACTCAGGCTCGACTGACCAAAG 1080
Sbjct                1696  ..........................................................  1755

CDS:PEX5-related pro  248  E  H  R  W  G  S  A  L  L  S  R  N  H  S  L  E  E  E  F  E
Query                1081  AACATCGCTGGGGAAGCGCATTACTTTCTAGAAACCACTCCTTAGAAGAAGAGTTTGAAA 1140
Sbjct                1756  ..........................................................  1815

CDS:PEX5-related pro  268  R  A  K  A  A  V  E  S  D  T  E  F  W  D  K  M  Q  A  E  W
Query                1141  GGGCAAAAGCAGCAGTGGAGTCAGATACAGAGTTTTGGGATAAGATGCAAGCAGAATGGG 1200
Sbjct                1816  ..........................................................  1875

CDS:PEX5-related pro  288  E  E  M  A  R  R  N  W  I  S  E  N  Q  E  A  Q  N  Q  V  T
Query                1201  AAGAAATGGCTCGGAGGAACTGGATATCTGAGAACCAAGAAGCCCAGAACCAAGTAACCA 1260
Sbjct                1876  ..........................................................  1935

CDS:PEX5-related pro  308  I  S  A  S  E  K  G  Y  Y  F  H  T  E  N  P  F  K  D  W  P


Query                1261  TCTCGGCTAGTGAGAAGGGATATTACTTTCACACTGAAAACCCCTTCAAGGACTGGCCTG 1320
Sbjct                1936  ..........................................................  1995

CDS:PEX5-related pro  328  G  A  F  E  E  G  L  K  R  L  K  E  G  D  L  P  V  T  I  L
Query                1321  GAGCATTTGAAGAAGGCTTAAAAAGGCTGAAGGAAGGGGATCTGCCAGTCACCATCCTGT 1380
Sbjct                1996  ..........................................................  2055

CDS:PEX5-related pro  348  F  M  E  A  A  I  L  Q  D  P  G  D  A  E  A  W  Q  F  L  G
Query                1381  TCATGGAAGCAGCAATTCTTCAGGACCCTGGAGATGCAGAGGCATGGCAGTTCCTCGGGA 1440
Sbjct                2056  ..........................................................  2115

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Query                1441  TAACCCAGGCGGAGAATGAAAATGAACAAGCAGCTATTGTCGCCCTCCAGAGGTGCTTAG 1500
Sbjct                2116  ..........................................................  2175

CDS:PEX5-related pro  388  E  L  Q  P  N  N  L  K  A  L  M  A  L  A  V  S  Y  T  N  T
Query                1501  AATTACAGCCCAACAACTTAAAAGCTTTGATGGCCTTGGCTGTGAGTTATACTAACACTG 1560
Sbjct                2176  ..........................................................  2235

CDS:PEX5-related pro  408  G  H  Q  Q  D  A  C  D  A  L  K  N  W  I  K  Q  N  P  K  Y
Query                1561  GCCATCAGCAGGATGCCTGTGACGCTCTGAAGAATTGGATTAAGCAAAATCCAAAGTACA 1620
Sbjct                2236  ..........................................................  2295

CDS:PEX5-related pro  428  K  Y  L  V  K  S  K  K  G  S  P  G  L  T  R  R  M  S  K  S
Query                1621  AATACCTTGTGAAAAGCAAGAAGGGATCTCCAGGCCTCACCCGGCGGATGTCTAAGTCCC 1680
Sbjct                2296  ..........................................................  2355

CDS:PEX5-related pro  448  P  V  D  S  S  V  L  E  G  V  K  E  L  Y  L  E  A  A  H  Q
Query                1681  CAGTTGATAGCTCTGTTCTGGAAGGGGTGAAGGAATTATATCTGGAAGCTGCCCACCAAA 1740
Sbjct                2356  ..........................................................  2415

CDS:PEX5-related pro  468  N  G  D  M  I  D  P  D  L  Q  T  G  L  G  V  L  F  H  L  S
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Sbjct                2416  ..........................................................  2475

CDS:PEX5-related pro  488  G  E  F  N  R  A  I  D  A  F  N  A  A  L  T  V  R  P  E  D
Query                1801  GAGAATTTAATAGAGCAATAGATGCATTTAACGCTGCCTTAACTGTTCGGCCAGAGGACT 1860
Sbjct                2476  ..........................................................  2535

CDS:PEX5-related pro  508  Y  S  L  W  N  R  L  G  A  T  L  A  N  G  D  R  S  E  E  A
Query                1861  ATTCACTATGGAACCGCCTCGGGGCGACCTTGGCGAACGGAGACCGCAGCGAGGAAGCCG 1920
Sbjct                2536  ..........................................................  2595

CDS:PEX5-related pro  528  V  E  A  Y  T  R  A  L  E  I  Q  P  G  F  I  R  S  R  Y  N
Query                1921  TGGAGGCCTATACGCGAGCACTGGAGATTCAGCCAGGATTCATCCGGTCCAGATACAACC 1980
Sbjct                2596  ..........................................................  2655

CDS:PEX5-related pro  548  L  G  I  S  C  I  N  L  G  A  Y  R  E  A  V  S  N  F  L  T
Query                1981  TAGGAATAAGCTGCATCAACCTGGGCGCCTACAGAGAAGCGGTCAGCAATTTTCTCACTG 2040
Sbjct                2656  ..........................................................  2715

CDS:PEX5-related pro  568  A  L  S  L  Q  R  K  S  R  N  Q  Q  Q  V  P  H  P  A  I  S
Query                2041  CCCTCAGTTTGCAAAGAAAGAGCAGGAATCAGCAGCAAGTTCCTCATCCTGCAATCTCTG 2100
Sbjct                2716  ..........................................................  2775

CDS:PEX5-related pro  588  G  N  I  W  A  A  L  R  I  A  L  S  L  M  D  Q  P  E  L  F
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Sbjct                2776  ..........................................................  2835
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Sbjct                2836  ............................................................  2895

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Sbjct                2896  ............................................................  2955

Query                2281  ACTATTTTATTATGAATTTCAAAAGGATAAATCAAATATTCAAAAGGCCATGGTCATATA  2340
Sbjct                2956  ............................................................  3015

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Sbjct                3016  ............................................................  3075

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Sbjct                3076  ............................................................  3135

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Sbjct                3196  ............................................................  3255

Query                2581  TGGGAAACATGGAAAAAGCACTGCCTCAGATTGGGAAATTCTGACTGTTTCTGAACTGTC  2640
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Sbjct                3436  ............................................................  3495

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Sbjct                3556  ............................................................  3615

Query                2941  ACTAGATCAACGGACCAAATAAACAATTCCTGAAGACA  2978
Sbjct                3616  .....................................  3653
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