NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBdS014I12

Lot# : 6608_B6Hk

Vector : pGCAP10

Gene	PSPC1	
RefSeq_mRNA	NM_001042414.4	2310 bp

● Plasmid DNA purification

Date : 2026/08/24

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

Date : 2026/08/25

Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2026/08/25

DNA concentration (O.D.): 318 ng/ul

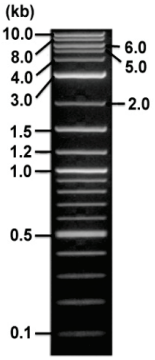
< Size of fragment expected from this clone >

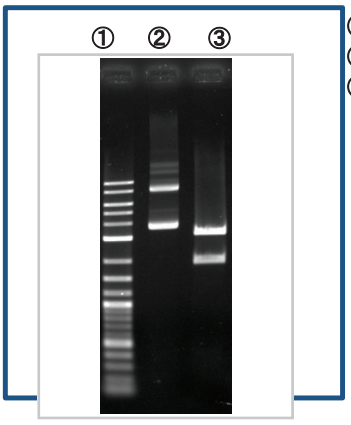
DNA	0.3	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.7	ul
Total	10	ul

BamHI 3.1kb (vector), 1.9 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 : 2026/08/28

full sequence	RBdS014I12hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/09/01

DNA (318 ng/ul)	84	ul
10x TE	107	ul
dH_2O	878	ul
Total	1,068	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


5000
(4602) BamHI
T3 promoter
SV40 poly(A) signal
ori
1000
AmpR
AmpR promoter
sign...
f1 ori
2000
M13 rev
SV40 promoter
SV40 ori
SV40 intron
M13 fwd
T7 promoter
3000
5' terminal sequence
ORF
insert
4000
RBdS014I12hts01.seq
5034 bp
(2705) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001354909:Homo sapiens paraspeckle component...

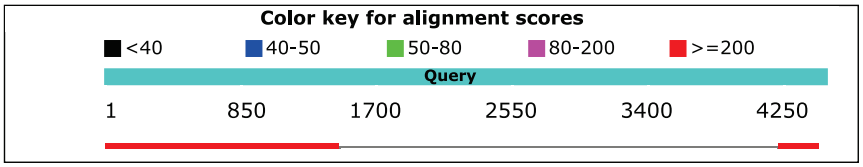
RID 91R0FEGW114 (Expires on 08-29 08:53 am)

Query ID	NM_001363660.2	**Subject ID**	lcl|Query_368149
Description	Homo sapiens paraspeckle component 1 (PSPC1), transcript variant 8, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	4418	**Subject Length**	5034
		Program	BLASTN 2.17.0+

RBdS014I12hts01.seq

Graphic Summary

Distribution of the top 2 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	2651	3087	38%	0.0	99.86%	Query_368149

Alignments

Sequence ID: Query_368149 Length: 5034 Number of Matches: 2
Range 1: 2865 to 4305

Score	Expect	Identities	Gaps	Strand	Frame
2651 bits(1435)	0.0()	1439/1441(99%)	0/1441(0%)	Plus/Plus	

Features:

```
Query          6     TTTGAATGTGCAGCTGCAGCGGGCGTGAGTTGGGGGAGGACGGGTTGCCGACTCGCCTAC  65
Sbjct          2865  ..G.........................................................  2924

Query          66    CTAGCGGTCTCTTGATTGTCGATATTTTGTTGGCATAGGTTTATGTAGAGACGTATACAT  125
Sbjct          2925  ............................................................  2984

Query          126   ATATATAGACACACTGTCTATAAATCTAGGCCTGTATCCGGTGTCCGAGGCGAACTCAGT  185
Sbjct          2985  ..................T.........................................  3044

CDS:paraspeckle comp  1        M  M  L  R  G  N  L  K  Q  V  R  I  E  K  N  P  A  R  L
Query          186   AAGATGATGTTAAGAGGAAACCTGAAGCAAGTGCGCATTGAGAAAAACCCGGCCCGCCTT  245
Sbjct          3045  ............................................................  3104

CDS:paraspeckle comp  20       R  A  L  E  S  A  V  G  E  S  E  P  A  A  A  A  A  M  A  L
Query          246   CGCGCCCTGGAGTCCGCGGTGGGCGAGAGCGAGCCGGCGGCCGCGGCAGCCATGGCGCTC  305
Sbjct          3105  ............................................................  3164

CDS:paraspeckle comp  40       A  L  A  G  E  P  A  P  P  A  P  A  P  P  E  D  H  P  D  E
Query          306   GCTCTTGCCGGGGAGCCGGCACCGCCCGCGCCCGCGCCTCCAGAGGACCACCCGGACGAG  365
Sbjct          3165  ............................................................  3224
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CDS:paraspeckle comp  60    E  M  G  F  T  I  D  I  K  S  F  L  K  P  G  E  K  T  Y  T
Query                 366   GAGATGGGGTTCACTATCGACATCAAGAGTTTCCTCAAGCCGGGCGAGAAGACGTACACG  425
Sbjct                 3225  ............................................................  3284

CDS:paraspeckle comp  80    Q  R  C  R  L  F  V  G  N  L  P  T  D  I  T  E  E  D  F  K
Query                 426   CAGCGCTGCCGCCTCTTCGTGGGAAATCTGCCCACCGACATCACGGAGGAGGACTTCAAG  485
Sbjct                 3285  ............................................................  3344

CDS:paraspeckle comp  100   R  L  F  E  R  Y  G  E  P  S  E  V  F  I  N  R  D  R  G  F
Query                 486   AGGCTCTTCGAACGCTATGGCGAGCCCAGCGAAGTCTTCATCAACCGGGACCGTGGCTTC  545
Sbjct                 3345  ............................................................  3404

CDS:paraspeckle comp  120   G  F  I  R  L  E  S  R  T  L  A  E  I  A  K  A  E  L  D  G
Query                 546   GGCTTCATCCGCTTGGAATCCAGAACCCTGGCTGAAATTGCAAAAGCAGAGCTGGACGGC  605
Sbjct                 3405  ............................................................  3464

CDS:paraspeckle comp  140   T  I  L  K  S  R  P  L  R  I  R  F  A  T  H  G  A  A  L  T
Query                 606   ACCATTCTCAAGAGCAGACCTCTACGGATTCGCTTCGCTACACATGGAGCAGCCTTGACT  665
Sbjct                 3465  ............................................................  3524

CDS:paraspeckle comp  160   V  K  N  L  S  P  V  V  S  N  E  L  L  E  Q  A  F  S  Q  F
Query                 666   GTCAAGAACCTTTCTCCAGTTGTTTCCAATGAGCTGCTAGAGCAAGCATTTTCTCAGTTT  725
Sbjct                 3525  ............................................................  3584

CDS:paraspeckle comp  180   G  P  V  E  K  A  V  V  V  V  D  D  R  G  R  A  T  G  K  G
Query                 726   GGTCCAGTAGAGAAAGCTGTTGTGGTTGTGGATGATCCGCGGTAGAGCTACAGGAAAAGGT  785
Sbjct                 3585  ............................................................  3644

CDS:paraspeckle comp  200   F  V  E  F  A  A  K  P  P  A  R  K  A  L  E  R  C  G  D  G
Query                 786   TTTGTAGAGTTTGCAGCAAAACCTCCTGCACGAAAGGCTCTGGAAAGATGTGGTGATGGG  845
Sbjct                 3645  ............................................................  3704

CDS:paraspeckle comp  220   A  F  L  L  T  T  T  P  R  P  V  I  V  E  P  M  E  Q  F  D
Query                 846   GCATTCTTGCTAACAACGACCCCTCGTCCAGTCATTGTGGAACCCATGGAGCAGTTTGAT  905
Sbjct                 3705  ............................................................  3764

CDS:paraspeckle comp  240   D  E  D  G  L  P  E  K  L  M  Q  K  T  Q  Q  Y  H  K  E  R
Query                 906   GATGAAGATGGCTTGCCAGAGAAGCTGATGCAGAAAACTCAACAATATCATAAGGAAAGA  965
Sbjct                 3765  ............................................................  3824

CDS:paraspeckle comp  260   E  Q  P  P  R  F  A  Q  P  G  T  F  F  F  E  Y  A  S  R  W
Query                 966   GAACAACCACCACGTTTTGCTCAACCTGGGACATTTGAATTTGAGTATGCATCTCGATGG  1025
Sbjct                 3825  ............................................................  3884

CDS:paraspeckle comp  280   K  A  L  D  E  M  E  K  Q  Q  R  E  Q  V  D  R  N  I  R  E
Query                 1026  AAGGCTCTTGATGAAATGGAAAAGCAGCAGCGTGAGCAGGTTGATAGAAACATCAGAGAA  1085
Sbjct                 3885  ............................................................  3944

CDS:paraspeckle comp  300   A  K  E  K  L  E  A  E  M  E  A  A  R  H  E  H  Q  L  M  L
Query                 1086  GCCAAAGAGAAACTGGAGGCAGAAATGGAAGCAGCTAGGCATGAACACCAATTAATGCTA  1145
Sbjct                 3945  ............................................................  4004

CDS:paraspeckle comp  320   M  R  Q  D  L  M  R  R  Q  E  E  L  R  R  L  E  E  L  R  N
Query                 1146  ATGAGGCAAGATCTAATGAGGCGTCAAGAAGAACTCAGACGCTTGGAAGAACTCAGAAAC  1205
Sbjct                 4005  ............................................................  4064

CDS:paraspeckle comp  340   Q  E  L  Q  K  R  K  Q  I  Q  L  R  H  E  E  E  H  R  R  R
Query                 1206  CAAGAGTTGCAAAAACGGAAGCAAATACAACTAAGACATGAAGAGGAGCATCGGCGGCGT  1265
Sbjct                 4065  ............................................................  4124
```

```
CDS:paraspeckle comp  360   E  E  E  M  I  R  H  R  E  Q  E  E  L  R  R  Q  Q  E  G  F
Query                 1266  GAGGAAGAAATGATCCGACACAGAGAACAGGAGGAACTGAGGCGACAGCAAGAGGGCTTT  1325
Sbjct                 4125  ............................................................  4184

CDS:paraspeckle comp  380   K  P  N  Y  M  E  N  G  D  K  R  K  C  G
Query                 1326  AAGCCAAACTACATGGAAAATGGTGATAAAAGAAAATGTGGCTGAAGTTACCCGAAGTTC  1385
Sbjct                 4185  ............................................................  4244

Query                 1386  AGCTTGCAGTGTAATTCAGAAGAGTTAAGACCAGAAGTACTGGAATCATACTTCCTTTCA  1445
Sbjct                 4245  ............................................................  4304

Query                 1446  G  1446
Sbjct                 4305  .  4305
```

Range 2: 4303 to 4538

Score	Expect	Identities	Gaps	Strand	Frame
436 bits(236)	7e-125()	236/236(100%)	0/236(0%)	Plus/Plus	

Features:

```
Query  4183  CAGTCTTGCCACTTGCCTAGTGAGGCTTTTCCGAACCTGGAAGGAGACGTCTAGAAATCC  4242
Sbjct  4303  ............................................................  4362

Query  4243  CAACTTTGCTGTGTAAGGACCATTAGCTGCAAGTCAGTGGAAGTCTATAGAAAGCAGTGT  4302
Sbjct  4363  ............................................................  4422

Query  4303  GAATTCCATAGTGGTCTTGACTTCTTAGCAAGGATTTGGGATAAGTCTAAAACTTCAGAC  4362
Sbjct  4423  ............................................................  4482

Query  4363  TTAAAGCTTTGAAGCATGTTAACTGCATGAAATATTAAACATTTCGAACTTCTTTA  4418
Sbjct  4483  ........................................................  4538
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