RIKEN_Clone_ID : IRAK077G09

Lot#: 7566_B5K6

Vector : pBluescriptR

Gene	CDC25B	
Accession No.	BC051711.1	3608 bp
	CDS	1743 bp

● Plasmid DNA purification

Date : 2025/11/10　　Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C over night

Date : 2025/11/11　　Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2025/11/11

DNA concentration (O.D.): 387 ng/ul

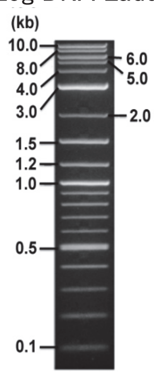
DNA	0.25 ul
Enzyme (EcoRI + BamHI)	0.5 + 0.5 ul
Buffer H	1 ul
dH_2O	7.75 ul
Total	10 ul

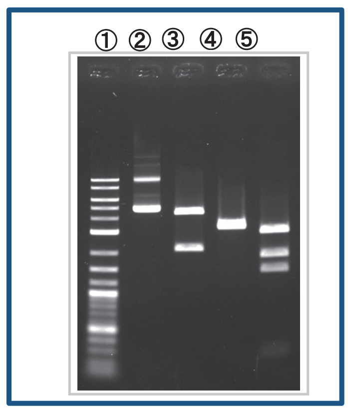
< Size of fragment expected from this clone >

EcoRI	4.4 , 2.2 kb
BamHI	3.4, 3.2 kb
EcoRI + BamHI	2.8kb (Vector)　1.9, 1.5, 0.3 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2−Log DNA Ladder (NEB#N3200L)





①:Marker
②:uncut
③:EcoRI
④:BamHI
⑤:EcoRI + BamHI

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2025/11/18

DNA (387 ng/ul)	86 ul
10x TE	133 ul
dH_2O	1,112 ul
Total	1,331 ul

● Confirmation of the sequence

Date : 2025/11/17

full sequence	IRAK077G09hts01.seq

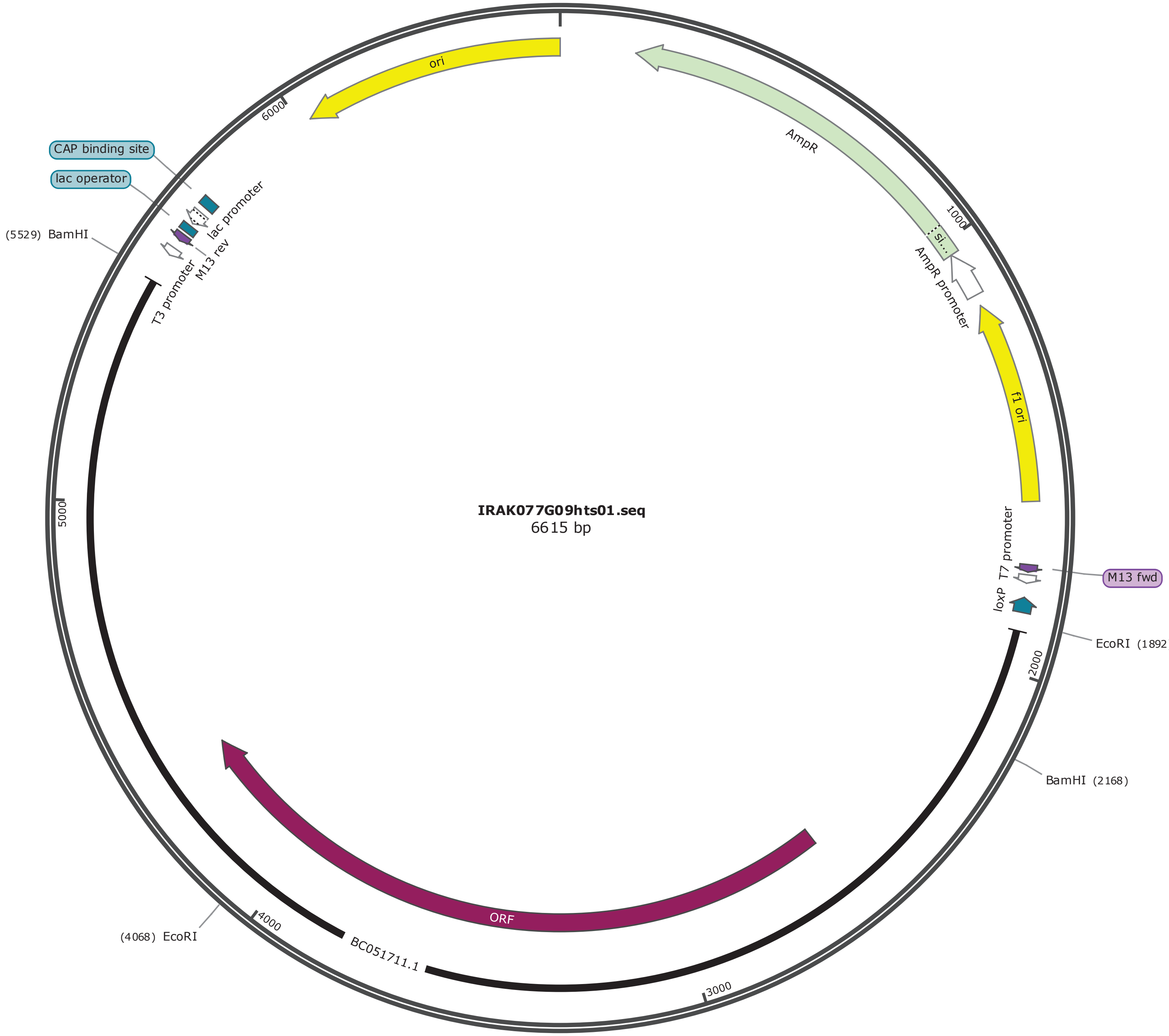
● Shipping

☑ Conc. : 25 ng/ μℓ, Volume : 40 μℓ

☐ Conc. : ___ng/ μℓ, Volume : μℓ

APPROVED BY : 検 '25.11.18 笹沼

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


IRAK077G09hts01.seq
6615 bp
ori
AmpR
AmpR promoter
f1 ori
T7 promoter
M13 fwd
loxP
EcoRI (1892)
BamHI (2168)
ORF
BC051711.1
(4068) EcoRI
T3 promoter
M13 rev
lac promoter
lac operator
CAP binding site
(5529) BamHI
1000
2000
3000
4000
5000
6000

BLAST ® » blastn suite-2sequences » RID-HNEFBG8P114

BLAST Results

Questions/comments

Blast 2 sequences

Job title: BC051711:Homo sapiens cell division cycle...

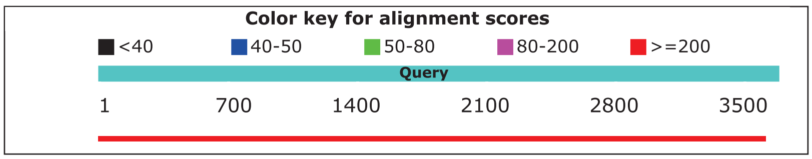
RID	HNEFBG8P114 (Expires on 11-18 13:00 pm)
Query ID	BC051711.1
Description	Homo sapiens cell division cycle 25 homolog B (S. pombe), mRNA (cDNA clone MGC:44614 IMAGE:5301205), complete cds
Molecule type	nucleic acid
Query Length	3608

Subject ID	lcl|Query_1526525
Description	None See details
Molecule type	dna
Subject Length	6615
Program	BLASTN 2.17.0+

IRAK077G09hts01.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	6663	6663	100%	0.0	100.00%	Query_1526525

Alignments

Sequence ID: Query_1526525 Length: 6615 Number of Matches: 1
Range 1: 1909 to 5516

Score	Expect	Identities	Gaps	Strand	Frame
6663 bits(3608)	0.0()	3608/3608(100%)	0/3608(0%)	Plus/Plus	

Features:

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Query  1     GCGGGACCTTGATTGAGTTAATGAACTTCACGCCTCAGCGTCCAGGTCTGTAAAATGGGG  60
Sbjct  1909  ............................................................  1968

Query  61    TGTCTAACGCAGACCGTACAGCCCAGCTGGGTTTAGCAAACTTCCGGGAGCCAGTTGGAG  120
Sbjct  1969  ............................................................  2028

Query  121   CCTCTCCCCATCCCTAGCGGTGATCCCAGGTGACGACATGCCGCGGGGGGTCCTGCGGAG  180
Sbjct  2029  ............................................................  2088

Query  181   GCCACCCTAGGGCGTTGCTGCTGCCTTTGGGAGTGTGGAGCTCCAAACCATGTCGCGAGA  240
Sbjct  2089  ............................................................  2148

Query  241   GGCGGATTTTGGGAGGCCGGGATCCTCGCGCCAGGGGGATGTGCGAGGGTGTGGGATAAA  300
Sbjct  2149  ............................................................  2208

Query  301   TCTTAATTCCTCCGGCCCACCCAAAGCCTGGAAATCCAGCCTCCGCGCCTCTTGCCCTGC  360
Sbjct  2209  ............................................................  2268

Query  361   GGGCCCCGCCCTCAGTCCCGCCCTCATCTAACCCGCTACCCCATTGGTGGCGTCCGGCGG  420
Sbjct  2269  ............................................................  2328

Query  421   CGCGGCTGCTGTTATTTTTCGAATATATAAGGAGGTGGAAGTGGCAGCTGCAACTAGAGG  480
Sbjct  2329  ............................................................  2388
```

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Query                481   CTTCCCAGGCTGGTGCCTGAgcccggcgtccctcgccccccgccctccccgcatccctct  540
Sbjct                2389  ............................................................  2448

Query                541   cctccctcgcgcctggccctgtggctcttcctccctccctccttccccccccccccccAC  600
Sbjct                2449  ............................................................  2508

Query                601   CCCTCGCCCGCTGCCTCCCTCGGCCCAGCCAGCTGTGCCGGCGTTTGTTGGCTGCCCTGC  660
Sbjct                2509  ............................................................  2568

CDS:Cell division cy 1                                           M  E  V  P  Q  P  E
Query                661   GCCGGCCCTCCAGCCAGCCTTCTGCCGGCCCCGCCGCGATGGAGGTGCCCCAGCCGGAGC  720
Sbjct                2569  ............................................................  2628

CDS:Cell division cy 8     P  A  P  G  S  A  L  S  P  A  G  V  C  G  G  A  Q  R  P  G
Query                721   CCGCGCCAGGCTCGGCTCTCAGTCCAGCAGGCGTGTGCGGTGGCGCCCAGCGTCCGGGCC  780
Sbjct                2629  ............................................................  2688

CDS:Cell division cy 28    H  L  P  G  L  L  L  G  S  H  G  L  L  G  S  P  V  R  A  A
Query                781   ACCTCCCGGGCCTCCTGCTGGGATCTCATGGCCTCCTGGGGTCCCCGGTGCGGGCGGCCG  840
Sbjct                2689  ............................................................  2748

CDS:Cell division cy 48    A  S  S  P  V  T  T  L  T  Q  T  M  H  D  L  A  G  L  G  S
Query                841   CTTCCTCGCCGGTCACCACCCTCACCCAGACCATGCACGACCTCGCCGGGCTCGGCAGCG  900
Sbjct                2749  ............................................................  2808

CDS:Cell division cy 68    E  T  P  K  S  Q  V  G  T  L  L  F  R  S  R  S  R  L  T  H
Query                901   AAACCCCAAAGAGTCAGGTAGGGACCCTGCTCTTCCGCAGCCGCAGCCGCCTGACGCACC  960
Sbjct                2809  ............................................................  2868

CDS:Cell division cy 88    L  S  L  S  R  R  A  S  E  S  S  L  S  S  E  S  S  E  S  S
Query                961   TATCCCTGTCTCGACGGGCATCCGAATCCTCCCTGTCGTCTGAATCCTCCGAATCTTCTG  1020
Sbjct                2869  ............................................................  2928

CDS:Cell division cy 108   D  A  G  L  C  M  D  S  P  S  P  M  D  P  H  M  A  E  Q  T
Query                1021  ATGCAGGTCTCTGCATGGATTCCCCCAGCCCTATGGACCCCCACATGGCGGAGCAGACGT  1080
Sbjct                2929  ............................................................  2988

CDS:Cell division cy 128   F  E  Q  A  I  Q  A  A  S  R  I  I  R  N  E  Q  F  A  I  R
Query                1081  TTGAACAGGCCATCCAGGCAGCCAGCCGGATCATTCGAAACGAGCAGTTTGCCATCAGAC  1140
Sbjct                2989  ............................................................  3048

CDS:Cell division cy 148   R  F  Q  S  M  P  V  R  L  L  G  H  S  P  V  L  R  N  I  T
Query                1141  GCTTCCAGTCTATGCCGGTGAGGCTGCTGGGCCACAGCCCCGTGCTTCGGAACATCACCA  1200
Sbjct                3049  ............................................................  3108

CDS:Cell division cy 168   N  S  Q  A  P  D  G  R  R  K  S  E  A  G  S  G  A  A  S  S
Query                1201  ACTCCCAGGCGCCCGACGGCCGGAGGAAGAGCGAGGCGGGCAGTGGAGCTGCCAGCAGCT  1260
Sbjct                3109  ............................................................  3168

CDS:Cell division cy 188   S  G  E  D  K  E  N  D  G  F  V  F  K  M  P  W  K  P  T  H
Query                1261  CTGGGGAAGACAAGGAGAATGATGGATTTGTCTTCAAGATGCCATGGAAGCCCACACATC  1320
Sbjct                3169  ............................................................  3228

CDS:Cell division cy 208   P  S  S  T  H  A  L  A  E  W  A  S  R  R  E  A  F  A  Q  R
Query                1321  CCAGCTCCACCCATGCTCTGGCAGAGTGGGCCAGCCGCAGGGAAGCCTTTGCCCAGAGAC  1380
Sbjct                3229  ............................................................  3288

CDS:Cell division cy 228   P  S  S  A  P  D  L  M  C  L  S  P  D  R  K  M  E  V  E  E
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Query                1381  CCAGCTCGGCCCCCGACCTGATGTGTCTCAGTCCTGACCGGAAGATGGAAGTGGAGGAGC  1440
Sbjct                3289  ............................................................  3348

CDS:Cell division cy 248   L  S  P  L  A  L  G  R  F  S  L  T  P  A  E  G  D  T  E  E
Query                1441  TCAGCCCCCTGGCCCTAGGTCGCTTCTCTCTGACCCCTGCAGAGGGGGATACTGAGGAAG  1500
Sbjct                3349  ............................................................  3408

CDS:Cell division cy 268   D  D  G  F  V  D  I  L  E  S  D  L  K  D  D  D  A  V  P  P
Query                1501  ATGATGGATTTGTGGACATCCTAGAGAGTGACTTAAAGGATGATGATGCAGTTCCCCCAG  1560
Sbjct                3409  ............................................................  3468

CDS:Cell division cy 288   G  M  E  S  L  I  S  A  P  L  V  K  T  L  E  K  E  E  E  K
Query                1561  GCATGGAGAGTCTCATTAGTGCCCCACTGGTCAAGACCTTGGAAAAGGAAGAGGAAAAGG  1620
Sbjct                3469  ............................................................  3528

CDS:Cell division cy 308   D  L  V  M  Y  S  K  C  Q  R  L  F  R  S  P  S  M  P  C  S
Query                1621  ACCTCGTCATGTACAGCAAGTGCCAGCGGCTCTTCCGCTCTCCGTCCATGCCCTGCAGCG  1680
Sbjct                3529  ............................................................  3588

CDS:Cell division cy 328   V  I  R  P  I  L  K  R  L  E  R  P  Q  D  R  D  T  P  V  Q
Query                1681  TGATCCGGCCCATCCTCAAGAGGCTGGAGCGGCCCCAGGACAGGGACACGCCCGTGCAGA  1740
Sbjct                3589  ............................................................  3648

CDS:Cell division cy 348   N  K  R  R  R  S  V  T  P  P  E  E  Q  Q  E  A  E  E  P  K
Query                1741  ATAAGCGGAGGCGGAGCGTGACCCCTCCTGAGGAGCAGCAGGAGGCTGAGGAACCTAAAG  1800
Sbjct                3649  ............................................................  3708

CDS:Cell division cy 368   A  R  V  L  R  S  K  S  L  C  H  D  E  I  E  N  L  L  D  S
Query                1801  CCCGCGTCCTCCGCTCAAAATCACTGTGTCACGATGAGATCGAGAACCTCCTGGACAGTG  1860
Sbjct                3709  ............................................................  3768

CDS:Cell division cy 388   D  H  R  E  L  I  G  D  Y  S  K  A  F  L  L  Q  T  V  D  G
Query                1861  ACCACCGAGAGCTGATTGGAGATTACTCTAAGGCCTTCCTCCTACAGACAGTAGACGGAA  1920
Sbjct                3769  ............................................................  3828

CDS:Cell division cy 408   K  H  Q  D  L  K  Y  I  S  P  E  T  M  V  A  L  L  T  G  K
Query                1921  AGCACCAAGACCTCAAGTACATCTCACCAGAAACGATGGTGGCCCTATTGACGGGCAAGT  1980
Sbjct                3829  ............................................................  3888

CDS:Cell division cy 428   F  S  N  I  V  D  K  F  V  I  V  D  C  R  Y  P  Y  E  Y  E
Query                1981  TCAGCAACATCGTGGATAAGTTTGTGATTGTAGACTGCAGATACCCCTATGAATATGAAG  2040
Sbjct                3889  ............................................................  3948

CDS:Cell division cy 448   G  G  H  I  K  T  A  V  N  L  P  L  E  R  D  A  E  S  F  L
Query                2041  GCGGGCACATCAAGACTGCGGTGAACTTGCCCCTGGAACGCGACGCCGAGAGCTTCCTAC  2100
Sbjct                3949  ............................................................  4008

CDS:Cell division cy 468   L  K  S  P  I  A  P  C  S  L  D  K  R  V  I  L  I  F  H  C
Query                2101  TGAAGAGCCCCATCGCGCCCTGTAGCCTGGACAAGAGAGTCATCCTCATTTTCCACTGTG  2160
Sbjct                4009  ............................................................  4068

CDS:Cell division cy 488   E  F  S  S  E  R  G  P  R  M  C  R  F  I  R  E  R  D  R  A
Query                2161  AATTCTCATCTGAGCGTGGGCCCCGCATGTGCCGTTTCATCAGGGAACGAGACCGTGCTG  2220
Sbjct                4069  ............................................................  4128

CDS:Cell division cy 508   V  N  D  Y  P  S  L  Y  Y  P  E  M  Y  I  L  K  G  G  Y  K
Query                2221  TCAACGACTACCCCAGCCTCTACTACCCTGAGATGTATATCCTGAAAGGCGGCTACAAGG  2280
Sbjct                4129  ............................................................  4188
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CDS:Cell division cy  528   E  F  F  P  Q  H  P  N  F  C  E  P  Q  D  Y  R  P  M  N  H
Query                 2281  AGTTCTTCCCTCAGCACCCGAACTTCTGTGAACCCCAGGACTACCGGCCCATGAACCACG  2340
Sbjct                 4189  ............................................................  4248

CDS:Cell division cy  548   E  A  F  K  D  E  L  K  T  F  R  L  K  T  R  S  W  A  G  E
Query                 2341  AGGCCTTCAAGGATGAGCTAAAGACCTTCCGCCTCAAGACTCGCAGCTGGGCTGGGGAGC  2400
Sbjct                 4249  ............................................................  4308

CDS:Cell division cy  568   R  S  R  R  E  L  C  S  R  L  Q  D  Q
Query                 2401  GGAGCCGGCGGGAGCTCTGTAGCCGGCTGCAGGACCAGTGAGGGGCCTGCGCCAGTCCTG  2460
Sbjct                 4309  ............................................................  4368

Query                 2461  CTACCTCCCTTGCCTTTCGAGGCCTGAAGCCAGCTGCCCTATGGGCCTGCCGGGCTGAGG  2520
Sbjct                 4369  ............................................................  4428

Query                 2521  GCCTGCTGGAGGCCTCAGGTGCTGTCCATGGGAAAGATGGTGTGGGTGTCCTGCCTGTCT  2580
Sbjct                 4429  ............................................................  4488

Query                 2581  GCCCCAGCCCAGATTCCCCTGTGTCATCCCATCATTTTCCATATCCTGGTGCCCCCCACC  2640
Sbjct                 4489  ............................................................  4548

Query                 2641  CCTGGAAGAGCCCAGTCTGTTGAGTTAGTTAAGTTGGGTTAATACCAGCTTAAAGGCAGT  2700
Sbjct                 4549  ............................................................  4608

Query                 2701  ATTTTGTGTCCTCCAGGAGCTTCTTGTTTCCTTGTTAGGGTTAACCCTTCATCTTCCTGT  2760
Sbjct                 4609  ............................................................  4668

Query                 2761  GTCCTGAAACGCTCCTTTGTGTGTGTGTCAGCTGAGGCTGGGGGAGAGCCGTGGTCCCTG  2820
Sbjct                 4669  ............................................................  4728

Query                 2821  AGGATGGGTCAGAGCTAAACTCCTTCCTGGCCTGAGAGTCAGCTCTCTGCCCTGTGTACT  2880
Sbjct                 4729  ............................................................  4788

Query                 2881  TCCCGGGCCAGGGCTGCCCCTAATCTCTGTAGGAACCGTGGTATGTCTGCCATGTTGCCC  2940
Sbjct                 4789  ............................................................  4848

Query                 2941  CTTTCTCTTTTCCCCTTTCCTGTCCAACCATACGAGCACCTCCAGCCTGAACAGAAGCTC  3000
Sbjct                 4849  ............................................................  4908

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Sbjct                 4909  ............................................................  4968

Query                 3061  CAGGACACTTCCGTAGACTGTTTAGGTTCCCCTGTCAAATATCAGTTACCCACTCGGTCC  3120
Sbjct                 4969  ............................................................  5028

Query                 3121  CAGTTTTGTTGCCCCAGAAAGGGATGTTATTATCCTTGGGGGCTCCCAGGGCAAGGGTTA  3180
Sbjct                 5029  ............................................................  5088

Query                 3181  AGGCCTGAATCATGAGCCTGCTGGAAGCCCAGCCCCTACTGCTGTGAACCCTGGGGCCTG  3240
Sbjct                 5089  ............................................................  5148

Query                 3241  ACTGCTCAGAACTTGCTGCTGTCTTGTTGCggatggatggaaggttggatggatgggtgg  3300
Sbjct                 5149  ............................................................  5208

Query                 3301  atggccgtggatggccgtggatgCGCAGTGCCTTGCATACCCAAACCAGGTGGGAGCGTT  3360
Sbjct                 5209  ............................................................  5268

Query                 3361  TTGTTGAGCATGACAGCCTGCAGCAGGAATATATGTGTGCCTATTTGTGTGGACAAAAAT  3420
Sbjct                 5269  ............................................................  5328
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```
Query                 3421  ATTTACACTTAGGGTTTGGAGCTATTCAAGAGGAAATGTCACAGAAGCAGCTAAACCAAG  3480
Sbjct                 5329  ............................................................  5388

Query                 3481  GACTGAGCACCCTCTGGATTCTGAATCTCAAGATGGGGGCAGGGCTGTGCTTGAAGGCCC  3540
Sbjct                 5389  ............................................................  5448

Query                 3541  TGCTGAGTCATCTGTTAGGGCCTTGGTTCAATAAAGCACTGAGCAAGTTGAGaaaaaaaa  3600
Sbjct                 5449  ............................................................  5508

Query                 3601  aaaaaaaa  3608
Sbjct                 5509  ........  5516
```

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BLAST ® » blastn suite-2sequences » RID-GRT0VD03114

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_021873:Homo sapiens cell division cycle...

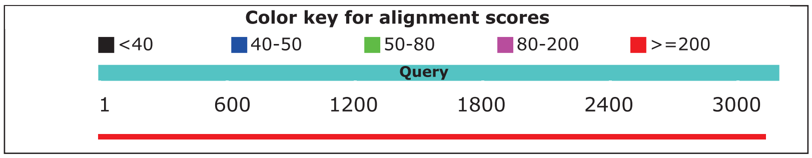
RID GRT0VD03114 (Expires on 11-07 06:56 am)

Query ID NM_021873.4
Description Homo sapiens cell division cycle 25B (CDC25B), transcript variant 1, mRNA
Molecule type nucleic acid
Query Length 3119

Subject ID BC051711.1
Description Homo sapiens cell division cycle 25 homolog B (S. pombe), mRNA (cDNA clone MGC:44614 IMAGE:5301205), complete cds
See details
Molecule type nucleic acid
Subject Length 3608
Program BLASTN 2.17.0+

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
Homo sapiens cell division cycle 25 homolog B (S. pombe), mRNA (cDNA clone MGC:44614 IMAGE:5301205), complete cds	5733	5733	100%	0.0	99.84%	**BC051711.1**

Alignments

Homo sapiens cell division cycle 25 homolog B (S. pombe), mRNA (cDNA clone MGC:44614 IMAGE:5301205), complete cds
Sequence ID: **BC051711.1** Length: 3608 Number of Matches: 1
Range 1: 476 to 3595

Score	Expect	Identities	Gaps	Strand	Frame
5733 bits(3104)	0.0()	3116/3121(99%)	3/3121(0%)	Plus/Plus	

Features:

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Query                 1    AGAGGCTTCCCTGGCTGGTGCCTGAgcccggcgtccctcgccccccgccctccccgcatc  60
Sbjct                 476  ...........A................................................  535

Query                 61   cctctcctccctcgcgcctggccctgtggctcttcctccctccctcctt--ccccccccc  118
Sbjct                 536  .................................................CC.........  595

Query                 119  cccACCCCTCGCCCGCTGCCTCCCTCGGCCCAGCCAGCTGTGCCGGCGTTTGTTGGCTGC  178
Sbjct                 596  ............................................................  655

CDS:M-phase inducer   1                                                 M  E  V  P  Q
Query                 179  CCTGCGCCCGGCCCTCCAGCCAGCCTTCTGCCGGCCCCGCCGCGATGGAGGTGCCCCAGC  238
Sbjct                 656  ......-.....................................................  714
CDS:Cell division cy  1                                                 M  E  V  P  Q

CDS:M-phase inducer   6    P  E  P  A  P  G  S  A  L  S  P  A  G  V  C  G  G  A  Q  R
Query                 239  CGGAGCCCGCGCCAGGCTCGGCTCTCAGTCCAGCAGGCGTGTGCGGTGGCGCCCAGCGTC  298
Sbjct                 715  ............................................................  774
```

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CDS:Cell division cy  6     P  E  P  A  P  G  S  A  L  S  P  A  G  V  C  G  G  A  Q  R

CDS:M-phase inducer   26    P  G  H  L  P  G  L  L  L  G  S  H  G  L  L  G  S  P  V  R
Query                 299   CGGGCCACCTCCCGGGCCTCCTGCTGGGATCTCATGGCCTCCTGGGGTCCCCGGTGCGGG  358
Sbjct                 775   ............................................................  834
CDS:Cell division cy  26    P  G  H  L  P  G  L  L  L  G  S  H  G  L  L  G  S  P  V  R

CDS:M-phase inducer   46    A  A  A  S  S  P  V  T  T  L  T  Q  T  M  H  D  L  A  G  L
Query                 359   CGGCCGCTTCCTCGCCGGTCACCACCCTCACCCAGACCATGCACGACCTCGCCGGGCTCG  418
Sbjct                 835   ............................................................  894
CDS:Cell division cy  46    A  A  A  S  S  P  V  T  T  L  T  Q  T  M  H  D  L  A  G  L

CDS:M-phase inducer   66    G  S  E  T  P  K  S  Q  V  G  T  L  L  F  R  S  R  S  R  L
Query                 419   GCAGCGAAACCCCAAAGAGTCAGGTAGGGACCCTGCTCTTCCGCAGCCGCAGCCGCCTGA  478
Sbjct                 895   ............................................................  954
CDS:Cell division cy  66    G  S  E  T  P  K  S  Q  V  G  T  L  L  F  R  S  R  S  R  L

CDS:M-phase inducer   86    T  H  L  S  L  S  R  R  A  S  E  S  S  L  S  S  E  S  S  E
Query                 479   CGCACCTATCCCTGTCTCGACGGGCATCCGAATCCTCCCTGTCGTCTGAATCCTCCGAAT  538
Sbjct                 955   ............................................................  1014
CDS:Cell division cy  86    T  H  L  S  L  S  R  R  A  S  E  S  S  L  S  S  E  S  S  E

CDS:M-phase inducer   106   S  S  D  A  G  L  C  M  D  S  P  S  P  M  D  P  H  M  A  E
Query                 539   CTTCTGATGCAGGTCTCTGCATGGATTCCCCCAGCCCTATGGACCCCCACATGGCGGAGC  598
Sbjct                 1015  ............................................................  1074
CDS:Cell division cy  106   S  S  D  A  G  L  C  M  D  S  P  S  P  M  D  P  H  M  A  E

CDS:M-phase inducer   126   Q  T  F  E  Q  A  I  Q  A  A  S  R  I  I  R  N  E  Q  F  A
Query                 599   AGACGTTTGAACAGGCCATCCAGGCAGCCAGCCGGATCATTCGAAACGAGCAGTTTGCCA  658
Sbjct                 1075  ............................................................  1134
CDS:Cell division cy  126   Q  T  F  E  Q  A  I  Q  A  A  S  R  I  I  R  N  E  Q  F  A

CDS:M-phase inducer   146   I  R  R  F  Q  S  M  P  V  R  L  L  G  H  S  P  V  L  R  N
Query                 659   TCAGACGCTTCCAGTCTATGCCGGTGAGGCTGCTGGGCCACAGCCCCGTGCTTCGGAACA  718
Sbjct                 1135  ............................................................  1194
CDS:Cell division cy  146   I  R  R  F  Q  S  M  P  V  R  L  L  G  H  S  P  V  L  R  N

CDS:M-phase inducer   166   I  T  N  S  Q  A  P  D  G  R  R  K  S  E  A  G  S  G  A  A
Query                 719   TCACCAACTCCCAGGCGCCCGACGGCCGGAGGAAGAGCGAGGCGGGCAGTGGAGCTGCCA  778
Sbjct                 1195  ............................................................  1254
CDS:Cell division cy  166   I  T  N  S  Q  A  P  D  G  R  R  K  S  E  A  G  S  G  A  A

CDS:M-phase inducer   186   S  S  S  G  E  D  K  E  N  D  G  F  V  F  K  M  P  W  K  P
Query                 779   GCAGCTCTGGGGAAGACAAGGAGAATGATGGATTTGTCTTCAAGATGCCATGGAAGCCCA  838
Sbjct                 1255  ............................................................  1314
CDS:Cell division cy  186   S  S  S  G  E  D  K  E  N  D  G  F  V  F  K  M  P  W  K  P

CDS:M-phase inducer   206   T  H  P  S  S  T  H  A  L  A  E  W  A  S  R  R  E  A  F  A
Query                 839   CACATCCCAGCTCCACCCATGCTCTGGCAGAGTGGGCCAGCCGCAGGGAAGCCTTTGCCC  898
Sbjct                 1315  ............................................................  1374
CDS:Cell division cy  206   T  H  P  S  S  T  H  A  L  A  E  W  A  S  R  R  E  A  F  A

CDS:M-phase inducer   226   Q  R  P  S  S  A  P  D  L  M  C  L  S  P  D  R  K  M  E  V
Query                 899   AGAGACCCAGCTCGGCCCCCGACCTGATGTGTCTCAGTCCTGACCGGAAGATGGAAGTGG  958
Sbjct                 1375  ............................................................  1434
CDS:Cell division cy  226   Q  R  P  S  S  A  P  D  L  M  C  L  S  P  D  R  K  M  E  V

CDS:M-phase inducer   246   E  E  L  S  P  L  A  L  G  R  F  S  L  T  P  A  E  G  D  T
Query                 959   AGGAGCTCAGCCCCCTGGCCCTAGGTCGCTTCTCTCTGACCCCTGCAGAGGGGGATACTG  1018
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Sbjct                 1435  ............................................................  1494
CDS:Cell division cy  246   E  E  L  S  P  L  A  L  G  R  F  S  L  T  P  A  E  G  D  T

CDS:M-phase inducer   266   E  E  D  D  G  F  V  D  I  L  E  S  D  L  K  D  D  D  A  V
Query                 1019  AGGAAGATGATGGATTTGTGGACATCCTAGAGAGTGACTTAAAGGATGATGATGCAGTTC  1078
Sbjct                 1495  ............................................................  1554
CDS:Cell division cy  266   E  E  D  D  G  F  V  D  I  L  E  S  D  L  K  D  D  D  A  V

CDS:M-phase inducer   286   P  P  G  M  E  S  L  I  S  A  P  L  V  K  T  L  E  K  E  E
Query                 1079  CCCCAGGCATGGAGAGTCTCATTAGTGCCCCACTGGTCAAGACCTTGGAAAAGGAAGAGG  1138
Sbjct                 1555  ............................................................  1614
CDS:Cell division cy  286   P  P  G  M  E  S  L  I  S  A  P  L  V  K  T  L  E  K  E  E

CDS:M-phase inducer   306   E  K  D  L  V  M  Y  S  K  C  Q  R  L  F  R  S  P  S  M  P
Query                 1139  AAAAGGACCTCGTCATGTACAGCAAGTGCCAGCGGCTCTTCCGCTCTCCGTCCATGCCCT  1198
Sbjct                 1615  ............................................................  1674
CDS:Cell division cy  306   E  K  D  L  V  M  Y  S  K  C  Q  R  L  F  R  S  P  S  M  P

CDS:M-phase inducer   326   C  S  V  I  R  P  I  L  K  R  L  E  R  P  Q  D  R  D  T  P
Query                 1199  GCAGCGTGATCCGGCCCATCCTCAAGAGGCTGGAGCGGCCCCAGGACAGGGACACGCCCG  1258
Sbjct                 1675  ............................................................  1734
CDS:Cell division cy  326   C  S  V  I  R  P  I  L  K  R  L  E  R  P  Q  D  R  D  T  P

CDS:M-phase inducer   346   V  Q  N  K  R  R  R  S  V  T  P  P  E  E  Q  Q  E  A  E  E
Query                 1259  TGCAGAATAAGCGGAGGCGGAGCGTGACCCCTCCTGAGGAGCAGCAGGAGGCTGAGGAAC  1318
Sbjct                 1735  ............................................................  1794
CDS:Cell division cy  346   V  Q  N  K  R  R  R  S  V  T  P  P  E  E  Q  Q  E  A  E  E

CDS:M-phase inducer   366   P  K  A  R  V  L  R  S  K  S  L  C  H  D  E  I  E  N  L  L
Query                 1319  CTAAAGCCCGCGTCCTCCGCTCAAAATCACTGTGTCACGATGAGATCGAGAACCTCCTGG  1378
Sbjct                 1795  ............................................................  1854
CDS:Cell division cy  366   P  K  A  R  V  L  R  S  K  S  L  C  H  D  E  I  E  N  L  L

CDS:M-phase inducer   386   D  S  D  H  R  E  L  I  G  D  Y  S  K  A  F  L  L  Q  T  V
Query                 1379  ACAGTGACCACCGAGAGCTGATTGGAGATTACTCTAAGGCCTTCCTCCTACAGACAGTAG  1438
Sbjct                 1855  ............................................................  1914
CDS:Cell division cy  386   D  S  D  H  R  E  L  I  G  D  Y  S  K  A  F  L  L  Q  T  V

CDS:M-phase inducer   406   D  G  K  H  Q  D  L  K  Y  I  S  P  E  T  M  V  A  L  L  T
Query                 1439  ACGGAAAGCACCAAGACCTCAAGTACATCTCACCAGAAACGATGGTGGCCCTATTGACGG  1498
Sbjct                 1915  ............................................................  1974
CDS:Cell division cy  406   D  G  K  H  Q  D  L  K  Y  I  S  P  E  T  M  V  A  L  L  T

CDS:M-phase inducer   426   G  K  F  S  N  I  V  D  K  F  V  I  V  D  C  R  Y  P  Y  E
Query                 1499  GCAAGTTCAGCAACATCGTGGATAAGTTTGTGATTGTAGACTGCAGATACCCCTATGAAT  1558
Sbjct                 1975  ............................................................  2034
CDS:Cell division cy  426   G  K  F  S  N  I  V  D  K  F  V  I  V  D  C  R  Y  P  Y  E

CDS:M-phase inducer   446   Y  E  G  G  H  I  K  T  A  V  N  L  P  L  E  R  D  A  E  S
Query                 1559  ATGAAGGCGGGCACATCAAGACTGCGGTGAACTTGCCCCTGGAACGCGACGCCGAGAGCT  1618
Sbjct                 2035  ............................................................  2094
CDS:Cell division cy  446   Y  E  G  G  H  I  K  T  A  V  N  L  P  L  E  R  D  A  E  S

CDS:M-phase inducer   466   F  L  L  K  S  P  I  A  P  C  S  L  D  K  R  V  I  L  I  F
Query                 1619  TCCTACTGAAGAGCCCCATCGCGCCCTGTAGCCTGGACAAGAGAGTCATCCTCATTTTCC  1678
Sbjct                 2095  ............................................................  2154
CDS:Cell division cy  466   F  L  L  K  S  P  I  A  P  C  S  L  D  K  R  V  I  L  I  F

CDS:M-phase inducer   486   H  C  E  F  S  S  E  R  G  P  R  M  C  R  F  I  R  E  R  D
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Query                1679  ACTGTGAATTCTCATCTGAGCGTGGGCCCCGCATGTGCCGTTTCATCAGGGAACGAGACC  1738
Sbjct                2155  ............................................................  2214
CDS:Cell division cy 486   H  C  E  F  S  S  E  R  G  P  R  M  C  R  F  I  R  E  R  D

CDS:M-phase inducer  506   R  A  V  N  D  Y  P  S  L  Y  Y  P  E  M  Y  I  L  K  G  G
Query                1739  GTGCTGTCAACGACTACCCCAGCCTCTACTACCCTGAGATGTATATCCTGAAAGGCGGCT  1798
Sbjct                2215  ............................................................  2274
CDS:Cell division cy 506   R  A  V  N  D  Y  P  S  L  Y  Y  P  E  M  Y  I  L  K  G  G

CDS:M-phase inducer  526   Y  K  E  F  F  P  Q  H  P  N  F  C  E  P  Q  D  Y  R  P  M
Query                1799  ACAAGGAGTTCTTCCCTCAGCACCCGAACTTCTGTGAACCCCAGGACTACCGGCCCATGA  1858
Sbjct                2275  ............................................................  2334
CDS:Cell division cy 526   Y  K  E  F  F  P  Q  H  P  N  F  C  E  P  Q  D  Y  R  P  M

CDS:M-phase inducer  546   N  H  E  A  F  K  D  E  L  K  T  F  R  L  K  T  R  S  W  A
Query                1859  ACCACGAGGCCTTCAAGGATGAGCTAAAGACCTTCCGCCTCAAGACTCGCAGCTGGGCTG  1918
Sbjct                2335  ............................................................  2394
CDS:Cell division cy 546   N  H  E  A  F  K  D  E  L  K  T  F  R  L  K  T  R  S  W  A

CDS:M-phase inducer  566   G  E  R  S  R  R  E  L  C  S  R  L  Q  D  Q
Query                1919  GGGAGCGGAGCCGGCGGGAGCTCTGTAGCCGGCTGCAGGACCAGTGAGGGGCCTGCGCCA  1978
Sbjct                2395  ............................................................  2454
CDS:Cell division cy 566   G  E  R  S  R  R  E  L  C  S  R  L  Q  D  Q

Query                1979  GTCCTGCTACCTCCCTTGCCTTTCGAGGCCTGAAGCCAGCTGCCCTATGGGCCTGCCGGG  2038
Sbjct                2455  ............................................................  2514

Query                2039  CTGAGGGCCTGCTGGAGGCCTCAGGTGCTGTCCATGGGAAAGATGGTGTGGGTGTCCTGC  2098
Sbjct                2515  ............................................................  2574

Query                2099  CTGTCTGCCCCAGCCCAGATTCCCCTGTGTCATCCCATCATTTTCCATATCCTGGTGCCC  2158
Sbjct                2575  ............................................................  2634

Query                2159  CCCACCCCTGGAAGAGCCCAGTCTGTTGAGTTAGTTAAGTTGGGTTAATACCAGCTTAAA  2218
Sbjct                2635  ............................................................  2694

Query                2219  GGCAGTATTTTGTGTCCTCCAGGAGCTTCTTGTTTCCTTGTTAGGGTTAACCCTTCATCT  2278
Sbjct                2695  ............................................................  2754

Query                2279  TCCTGTGTCCTGAAACGCTCCTTTGTGTGTGTGTCAGCTGAGGCTGGGGGAGAGCCGTGG  2338
Sbjct                2755  ............................................................  2814

Query                2339  TCCCTGAGGATGGGTCAGAGCTAAACTCCTTCCTGGCCTGAGAGTCAGCTCTCTGCCCTG  2398
Sbjct                2815  ............................................................  2874

Query                2399  TGTACTTCCCGGGCCAGGGCTGCCCCTAATCTCTGTAGGAACCGTGGTATGTCTGCCATG  2458
Sbjct                2875  ............................................................  2934

Query                2459  TTGCCCCTTTCTCTTTTCCCCTTTCCTGTCCCACCATACGAGCACCTCCAGCCTGAACAG  2518
Sbjct                2935  ...............................A............................  2994

Query                2519  AAGCTCTTACTCTTTCCTATTTCAGTGTTACCTGTGTGCTTGGTCTGTTTGACTTTACGC  2578
Sbjct                2995  ............................................................  3054

Query                2579  CCATCTCAGGACACTTCCGTAGACTGTTTAGGTTCCCCTGTCAAATATCAGTTACCCACT  2638
Sbjct                3055  ............................................................  3114

Query                2639  CGGTCCCAGTTTTGTTGCCCCAGAAAGGGATGTTATTATCCTTGGGGGCTCCCAGGGCAA  2698
Sbjct                3115  ............................................................  3174
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Query                2699  GGGTTAAGGCCTGAATCATGAGCCTGCTGGAAGCCCAGCCCCTACTGCTGTGAACCCTGG  2758
Sbjct                3175  ............................................................  3234

Query                2759  GGCCTGACTGCTCAGAACTTGCTGCTGTCTTGTTGCggatggatggaaggttggatggat  2818
Sbjct                3235  ............................................................  3294

Query                2819  gggtggatggccgtggatggccgtggatgCGCAGTGCCTTGCATACCCAAACCAGGTGGG  2878
Sbjct                3295  ............................................................  3354

Query                2879  AGCGTTTTGTTGAGCATGACAGCCTGCAGCAGGAATATATGTGTGCCTATTTGTGTGGAC  2938
Sbjct                3355  ............................................................  3414

Query                2939  AAAAATATTTACACTTAGGGTTTGGAGCTATTCAAGAGGAAATGTCACAGAAGCAGCTAA  2998
Sbjct                3415  ............................................................  3474

Query                2999  ACCAAGGACTGAGCACCCTCTGGATTCTGAATCTCAAGATGGGGGCAGGGCTGTGCTTGA  3058
Sbjct                3475  ............................................................  3534

Query                3059  AGGCCCTGCTGAGTCATCTGTTAGGGCCTTGGTTCAATAAAGCACTGAGCAAGTTGAGAA  3118
Sbjct                3535  ............................................................  3594

Query                3119  A  3119
Sbjct                3595  .  3595
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