

Homo sapiens cyclin D1 (CCND1), mRNA

Sequence ID: [NM_053056.3](#) Length: 4238 Number of Matches: 1Range 1: 1 to 2030 [GenBank](#) [Graphics](#)

Next Match Previous Match

Related

Information

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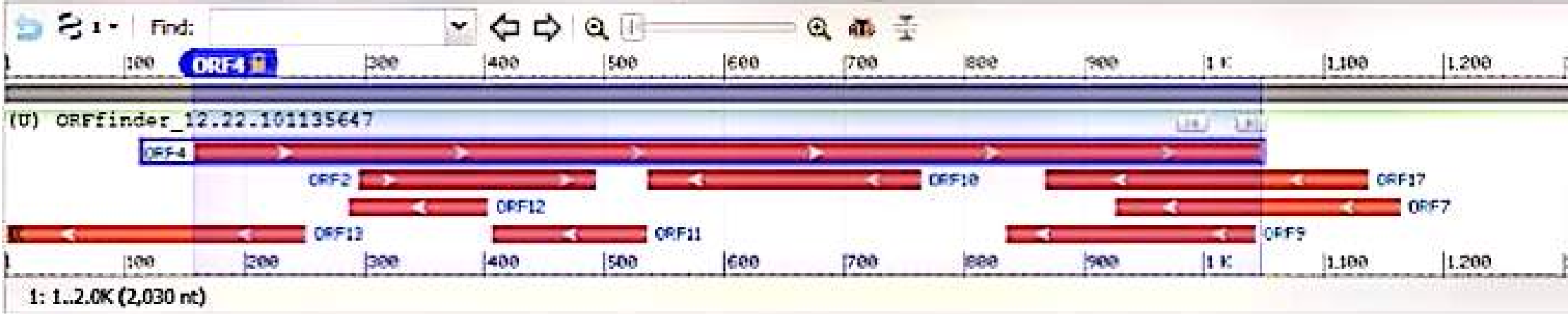
| Score | Expect | Identities | Gaps |
|-----------------|---|----------------|-------------|
| 3480 bits(1884) | 0.0 | 1988/2030(98%) | 41/2030(2%) |
| Query 1 | AGAGGGCTGTCGGCGCAGTAGCAGCGAGCAGCAGAGTCCG | | |
| Sbjct 1 | AGAGGGCTGTCGGCGCAGTAGCAGCGAGCAGCAGAGTCCG | | |
| Query 61 | AAGAGCGCGAGGGAGCGCGGGGAGCAGAGAAGCGAGAGCCG | | |
| Sbjct 61 | AAGAGCGCGAGGGAGCGCGGGGAGCAGAGAAGCGAGAGCCG | | |
| Query 121 | CCACAGCCCTCCCGAGCTGCCAGGAAGAGCCCCAGCCATC | | |
| Sbjct 121 | CCACAGCCCTCCCGAGCTGCCAGGAAGAGCCCCAGCCATC | | |
| Query 181 | GCGAAGTGGAAACCATCCGCCGCGCGTA-CCCAGTGCCAA | | |
| Sbjct 181 | GCGAAGTGGAAACCATCCGCCGCGCGTACCCAGTGCCAA | | |
| Query 240 | TGCGGGCCATGCTGAAGG-GGAGGAGACCTGCGCGCCCTC | | |
| Sbjct 241 | TGCGGGCCATGCTGAAGGCGGAGGAGACCTGCGCGCCCTC | | |
| Query 298 | TGCAGAAGGAGGTCTCGCTCCATGCGGAAGATCGTCGCC | | |
| Sbjct 301 | TGCAGAAGGAGGTCTCGCTCCATGCGGAAGATCGTCGCC | | |
| Query 358 | GCGAGGAACAGAAGTGCAGGAGGAGGTCTTCCCGCTGGCC | | |
| Sbjct 361 | GCGAGGAACAGAAGTGCAGGAGGAGGTCTTCCCGCTGGCC | | |
| Query 417 | TCCTGTCGCTGGAGCCCGTGAAAAAGAGCCGCTGCAGCTC | | |
| Sbjct 421 | TCCTGTCGCTGGAGCCCGTGAAAAAGAGCCGCTGCAGCTC | | |
| Query 477 | TCGTBGCCTCTAAGATGAAGGAGACCATCCCCCTGACGGCC | | |
| Sbjct 481 | TCGTGGCCTCTAAGATGAAGGAGACCATCCCCCTGACGGCC | | |
| Query 537 | CCGACAACCTCCATCCGGCCCGAGGAGCTGCTGCAATGGAC | | |
| Sbjct 541 | CCGACAACCTCCATCCGGCCCGAGGAGCTGCTGCAATGGAC | | |
| Query 597 | TCAAGTGGAACTTGGCCGCAATGACCCCGCACGA-TTCAT | | |
| Sbjct 601 | TCAAGTGGAACTTGGCCGCAATGACCCCGCACGATTTTCAT | | |
| Query 656 | TGCCAGAGGCGGAGGAGAACAACAGATCATCCGCAAACAC | | |
| Sbjct 661 | TGCCAGAGGCGGAGGAGAACAACAGATCATCCGCAAACAC | | |
| Query 716 | TCTGTGCCACAGATGTGAAGTTCAATTTCCAATCCGCCCTC | | |
| Sbjct 721 | TCTGTGCCACAGATGTGAAGTTCAATTTCCAATCCGCCCTC | | |
| Query 776 | TGGTGGCCGAGTGCAAGGCCTGAACCTGAGGAGCCCCAAC | | |
| Sbjct 781 | TGGTGGCCGAGTGCAAGGCCTGAACCTGAGGAGCCCCAAC | | |
| Query 836 | GCCTCACACGCTTCTCTCCAGAGTGATCAAGTGTGACCCC | | |
| Sbjct 841 | GCCTCACACGCTTCTCTCCAGAGTGATCAAGTGTGACCCC | | |
| Query 896 | AGGAGCAGATCGAAGCCCTGCTGGAGTCAAGCCTGCGCCAC | | |
| Sbjct 901 | AGGAGCAGATCGAAGCCCTGCTGGAGTCAAGCCTGCGCCAC | | |
| Query 956 | CCAAGGCCGCCgaggaggagggaaggaggaggaggaggT | | |
| Sbjct 961 | CCAAGGCCGCCGAGGAGGAGGAAGAGGAGGAGGAGGAGGT | | |
| Query 1016 | CCGACGTGCGGGACGTGGACATCTGAGGGCGCCAGGCAGGC | | |
| Sbjct 1021 | CCGACGTGCGGGACGTGGACATCTGAGGGCGCCAGGCAGGC | | |
| Query 1076 | AGCGAGGGCGGAGCCGGCCCCAGGTGCTCCCCCTGACAGT- | | |
| Sbjct 1081 | AGCGAGGGCGGAGCCGGCCCCAGGTGCTCCCCCTGACAGT | | |
| Query 1135 | GATACCAGAAGGGAAAGCTTCATTCTCCTTGTGTTGGTT | | |
| Sbjct 1141 | GATACCAGAAGGGAAAGCTTCATTCTCCTTGTGTTGGTT | | |

| | Description | Scientific Name | Max Score | Total Score | Query Cover | E value | Per Ident | Acc Len | Accession |
|-------------------------------------|--|------------------------------|-----------|-------------|-------------|---------|-----------|---------|-----------------------------|
| <input checked="" type="checkbox"/> | Homo sapiens cyclin D1 (CCND1) mRNA | Homo sapiens | 3749 | 3749 | 100% | 0.0 | 100.00% | 4238 | NM_053056.3 |
| <input checked="" type="checkbox"/> | H.sapiens of BCL1 mRNA encoding cyclin | Homo sapiens | 3722 | 3722 | 99% | 0.0 | 99.95% | 3813 | Z23022.1 |
| <input checked="" type="checkbox"/> | Human PRAD1 mRNA for cyclin | Homo sapiens | 3712 | 3712 | 99% | 0.0 | 99.85% | 4244 | X59793.1 |

Open Reading Frame Viewer

Sequence

ORFs found: 17 Genetic code: 1 Start codon: 'ATG' only



| | |
|-------------------------|------|
| Total count, all bases: | 2030 |
| Adenine (A) count | 497 |
| Thymine (T) count | 437 |
| Guanine (G) count | 542 |
| Cytosine (C) count | 554 |
| %G-C content | 54 |

Results of translation

- Open reading frames are highlighted in red
- Select your initiator on one of the following frames to retrieve your amino acid sequence

Download all the translated frames

5'3' Frame 1

RGLSAQ-QRAAESARSGEGOKSARERGAEEARAERGPSQDPQSPAAQEEPOFWNTSSCAAKNKPSAARTFMPTSSTTGCCGFC-RR
RRPARPRCPTSNVCRARRSCRPCGRSSPPGCWRSARNRSARRRSSRWP-TTWTASCRWSP-KRAACSCWGPLACSWPLR-RRPSP-RP
RSCASTPTTPSGPRSCCKWSCSN-TSSSGTWPO-PRTISLNTSSPKCQRRRRRTNRSSANTRRPSLPSVPCM-SSFPIRPFWWQRGAM
WPOCKA-T-GAPTTSCPTTASHASSPE-SSVTRTASGPARSRSKPCWSQACARPSRTWTFRPFRRRRKRRRRRWTLAHPFTCGTWT
EGARQAGATATRSEGGAGPRCSPDSSPSSPEHFDTRRESFILLVVGCFPLCSFPLPSLT-AKENDYPKTVFKREREREKKIVFA-P-AV
GEEGCATDDRGFYTPPIINSFLY-CTCFSVVRIGINTKEASRERIRFHPLRV-KKA-KHFNIEKFSKPELK-KRVLGRKTYSCAFPD
KAQL-WGSRHLCTLLAHMHVVTL-VIVCYIIP-VDV-PLHLING-SHLLVIVA-RARVHVLCACDHHPNKPSSDKPSSGGLSGTSQR
SRVGKGHLSHSYDTLL-REDEIVT-YILEFLYSSYFCSDLEMRWFESTQRPCSQLTSRENPQLLGLCS

5'3' Frame 2

EGCRRSSSEQOSPHAPARGRRARGSAGQOKREPSADPARTHSPPQLPRKSPSHGTPAPVLRSGNHPPRVPRCOPPPORPGAAGHAEGG
GDLRALGVLLCMCAEGGPAVHAEDRRHLDAGGLRGTEVRGGGLPAGHELPGPLPVAGAREKEPPAAAGGHLHVRGL-DEGDHPPDGR
EAVHLHRQLHPARGAAANGAAPGEQAQVEPGRNDPARFH-TLPLQNARGGGEQTDHPQTRADLRCP LCHRCEVHFQSALHGGSGERG
GRSARPEPEEPQQLPVLLPPTHLPLOSDQV-PGLPPGLPGADRSPAGVKPAPGPAEHGPQGRRGGGGGGGGGGGLHTHRRAGRHL
RAPGRRAPPPPAARAE PAPGAPLTVPPLRSILIPEGKASEFLLLVEFSEFALSPEHL-LKQKKKITQALS LKERERKKK-YLHNPFRW

1;B:>|c|ORF4

MEHQLLCCEVETIRRAYPDANLLNDR

VLRAMLKAEETCAPSVSYFKCVQK

EVLPSMRKIVATWMLEVCEEQKCEEE

VFPLAMNYLDRFLSLEPVKKSRLO

LLGATCMFVASKMKETIPLTAEKLCIYT

DNSIRPEELLQMELLVNKLKW

NLAAMTPHDFIEHFLSKMPEAEENKQ

IIRKHAQTFVALCATDVKFISNPP

SMVAAGSVVAQGLNLRSPNNFLSY

YRLTRFLSRVIKCDPDCLRACQEQ

IEALLESSLRQAQQNMDPKAAEEEEEE