

## 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](#)[Strand](#)[Gene/Protein](#)[Gene details](#)[Genome Data](#)[Viewer](#) - aligned[genomic context](#)

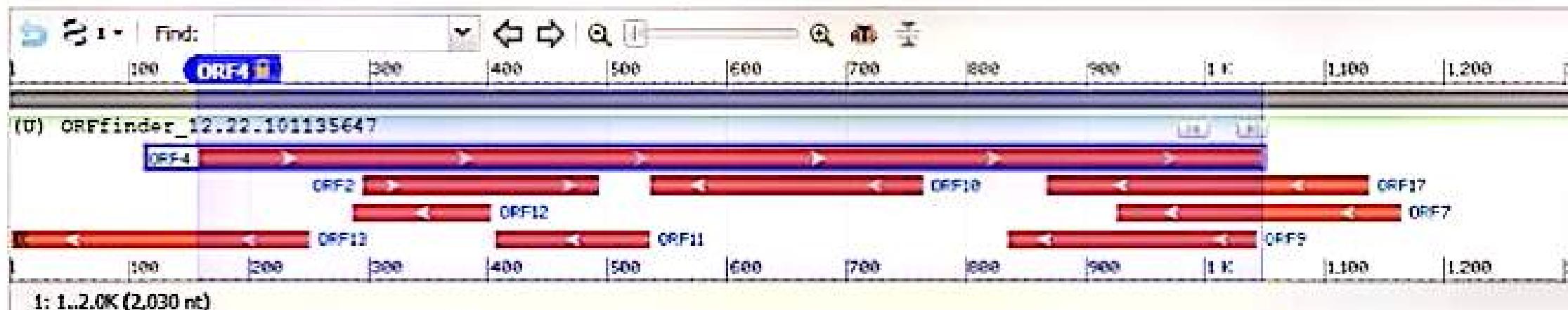
Score 3480 bits(1884)	Expect 0.0	Identities 1988/2030(98%)	Gaps 41/2030(2%)
Query 1	AGAGGGCTGTCGGCGCAGTAGCAGCAGCAGCAGAGTCGG		
Sbjct 1	AGAGGGCTGTCGGCGCAGTAGCAGCAGCAGCAGAGTCGG		
Query 61	AAGAGCGCGAGGGAGCGCGGGCAGCAGAAGCGAGAGCCG		
Sbjct 61	AAGAGCGCGAGGGAGCGCGGGCAGCAGAAGCGAGAGCCG		
Query 121	CCACAGCCCTCCCCAGCTGCCAGGAAGAGCCCCAGCCATC		
Sbjct 121	CCACAGCCCTCCCCAGCTGCCAGGAAGAGCCCCAGCCATC		
Query 181	GCGAAGTGGAAACCATCCGCCGCCTA-CCCGATGCCAAC		
Sbjct 181	GCGAAGTGGAAACCATCCGCCGCCTA-CCCGATGCCAAC		
Query 240	TGCGGGCCATGCTGAAGG-GGAGGAGACCTGCGGCCCTC		
Sbjct 241	TGCGGGCCATGCTGAAGGCGGAGGAGACCTGCGGCCCTC		
Query 298	TGCAGAAGGAGGTCTGCCGTCCATGCGGAAGATGTCGCC		
Sbjct 301	TGCAGAAGGAGGTCTGCCGTCCATGCGGAAGATGTCGCC		
Query 358	GCGAGGAACAGAACAGTGCAGGGAGGTCTTCCCCTGGCC		
Sbjct 361	GCGAGGAACAGAACAGTGCAGGGAGGTCTTCCCCTGGCC		
Query 417	TCCTTGTGCTGGAGCCCGTGAAGGAGACCTGCGCCCTGCAGCT		
Sbjct 421	TCCTTGTGCTGGAGCCCGTGAAGGAGACCTGCGCCCTGCAGCT		
Query 477	TCTGTGCCCTTAAGATGAAGGAGACCATCCCCCTGACGGCC		
Sbjct 481	TCTGTGCCCTTAAGATGAAGGAGACCATCCCCCTGACGGCC		
Query 537	CCGACAACCTCCATCCGGCCCGAGGGAGCTGCTGCAAATGGAC		
Sbjct 541	CCGACAACCTCCATCCGGCCCGAGGGAGCTGCTGCAAATGGAC		
Query 597	TCAAGTGGAACCTGGCCGCAATGACCCCGCACGA-TTCAT		
Sbjct 601	TCAAGTGGAACCTGGCCGCAATGACCCCGCACGATTTCAT		
Query 656	TGCCAGAGGCGGAGGAGAACAAAACAGATCATCCGCAAACAC		
Sbjct 661	TGCCAGAGGCGGAGGAGAACAAAACAGATCATCCGCAAACAC		
Query 716	TCTGTGCCACAGATGTGAAGTTCAATTCCAATCCGCCCTC		
Sbjct 721	TCTGTGCCACAGATGTGAAGTTCAATTCCAATCCGCCCTC		
Query 776	TGGTGGCCGCAGTGCAAGGCCTGAACCTGAGGAGCCCCAAC		
Sbjct 781	TGGTGGCCGCAGTGCAAGGCCTGAACCTGAGGAGCCCCAAC		
Query 836	GCCTCACACGCTTCCCTCCAGAGTGTCAAGTGTGACCC		
Sbjct 841	GCCTCACACGCTTCCCTCCAGAGTGTCAAGTGTGACCC		
Query 896	AGGAGCAGATCGAAGCCCTGCTGGAGTCAAGCCTGCCAC		
Sbjct 901	AGGAGCAGATCGAAGCCCTGCTGGAGTCAAGCCTGCCAC		
Query 956	CCAAGGCCGCCgaggaggaggaaagaggaggaggaggagg		
Sbjct 961	CCAAGGCCGCCgaggaggaggaaagaggaggaggaggagg		
Query 1016	CCGACGTGCGGGACGTGGACATCTGAGGGCGCCAGGCAGG		
Sbjct 1021	CCGACGTGCGGGACGTGGACATCTGAGGGCGCCAGGCAGG		
Query 1076	AGCGAGGGCGGAGCCGGCCCGAGGTGCTCCCTGACAGT-C		
Sbjct 1081	AGCGAGGGCGGAGCCGGCCCGAGGTGCTCCCTGACAGT-C		
Query 1135	GATACCAGAAGGGAAAGCTTCAATTCTCCTTGTGTTGGTT		
Sbjct 1141	GATACCAGAAGGGAAAGCTTCAATTCTCCTTGTGTTGGTT		

	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	<a href="#">Homo sapiens</a>	3749	3749	100%	0.0	100.00%	4238	NM_053056.3
<input checked="" type="checkbox"/>	Hsap005 of BCL1 mRNA encoding cyclin	<a href="#">Homo sapiens</a>	3722	3722	99%	0.0	99.95%	3013	Z23022.1
<input checked="" type="checkbox"/>	Human PRAD1 mRNA for cyclin	<a href="#">Homo sapiens</a>	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-QRAAESARSGEQKSARERGAAEARAERGPSQDPQPSPAAQEEPOPWNTSSCAAKWKEAARTPMPTSSTGCCGPC-RR  
RRPARPRCPTSNVCRRLSCRPCGRSSPPGCWRSARNRSARRSSRWP-TTWTASCRWSP-KRAACSCWGPLACSWPLR-RRFSP-RP  
RSCASTPTTPSGPRSCCKWCSW-TSSSGTWPO-PRTISINTSSPKCQRRTNRSSANTRRPSLPSVPOM-SSFPIRFWWQRGAM  
WPOCKA-T-CAPTTSCPTTASHASSPE-SSVTRTASGPARSRSKPCWSOACARPSRTWTPRPPRRRKRRRRRWTLAHPPTCGTWTS  
EGARQAGATATRSEGGAGPRCSPDSPSSPEHFDTRRESFILLVVGCFPLCSFPLPSLT-AKEKDYPKTVFKREREKKIVFA-P-AV  
GEEGCATDDRGFYTPIINSFLY-CTCFSVVRIGINTKEASRERIRFHPLRV-KFA-KHFFNIEKFSKPFLK-KRVLGRKTYSCAFPD  
MAQL-WGSRHILCTLLAHHVVTL-VIVCYYIP-VDV-PLHLHG-SHLLVTVA-RARVHVILCACDHHPPNEPSSDKPSSGGLSGTSQR  
SRVGKGHLHSYDTLL-REDEIVT-YILFLYSSYFCSDLERCWFSQLTSRFNPQLLGLCS

### 5'3' Frame 2

EGCRRSSSEOCSPHAPARGRRARGSAGQCKREPSADPARTHSPPOLPRKSPSHGTPAPVLRSGNHPPRVPRCOPPCORPGAAAGHAEEGG  
GDLRALGVLLCMCAEGGPAVHAEDRRHLDAGGLRGTEVRGGGLPAGHELPGPLPVAGAREKEPPAAAGGHLHVRGL-DEGDHPPDGR  
EAVHLHRQLHPARGAAANGAAPGEQAQVEPGRNDPARFH-TIPLQNARGGGEQTDHPQTRADLRCPLCHRCEVHFQSALHGGSGERGtat  
GRSARPEPEEPQQLPVLLPPHTLPLOSDQV-PGLPPGLPGADRSPAGVKPAPGPAEHGPQGRGGGRGGGGPGLHTRRAGRGHLto Ge  
RAPGRRAPPAAARAEPAPGAPLTVPPRLSILIPEGKASESLLLVVESEALSPFHL-LKQKKKITQKLSLKERERKKK-YLNPERM

1;B:>Icl|ORF4

MEHQLLCCEVETIRRAYPDANLLNDR  
VLRAMLKAEETCAPSVSYFKCVQK  
EVLPMSMRKIVATWMLEVCEEQKCEEE  
VFPLAMNYLDRFLSLEPVKKSRQLQ  
LLGATCMFVASKMKETIPLTAEKLCIYT  
DNSIRPEELLQMELLLVNKWK  
NLAAMTPHDFIEHFLSKMPEAEENKQ  
IIRKHAQTFVALCATDVKFISNPP  
SMVAAGSVVAAVQGLNLRSPNNFLSY  
YRLTRFLSRVIKCDPDCLRACQEQQ  
IEALLESSLRQAQQNMDPKAAEEEEEEE