

## WEEK 2 ASSIGNMENT

Introduction to Computational Biology – BIOL 509000 | Fall 1 2020

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**Question #1: What is the length of your query sequence?**

The length of the query sequence is 113962 bp.

Job Title	Practice Sequence
RID	<a href="#">NMBST5KR016</a> Search expires on 09-11 21:50 pm <a href="#">Download All</a> ▼
Program	BLASTN <a href="#">?</a> <a href="#">Citation</a> ▼
Database	Human G+T (2 databases) <a href="#">See details</a> ▼
Query ID	lcl Query_53659
Description	Practice Sequence
Molecule type	dna
Query Length	113962
Other reports	<a href="#">Distance tree of results</a> <a href="#">MSA viewer</a> <a href="#">?</a>

Figure 1. Summary header from BLAST query.

**Question #2: The query sequence should match a subject sequence that is catalogued in the database as part of the “GRCh38.p12 Primary Assembly.” What chromosome is this alignment located on?**

The alignment is located on *Homo sapiens* chromosome 6 as part of GRCh38.p12 Primary Assembly.

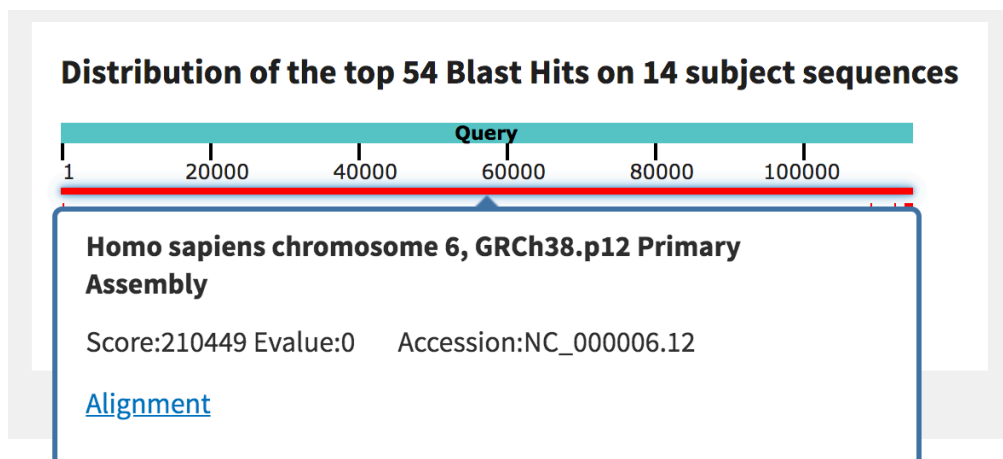


Figure 2. Graphical section representing strong (identical) alignment of query sequence as highlighted by the red bar.

[GenBank](#)   [FASTA](#)

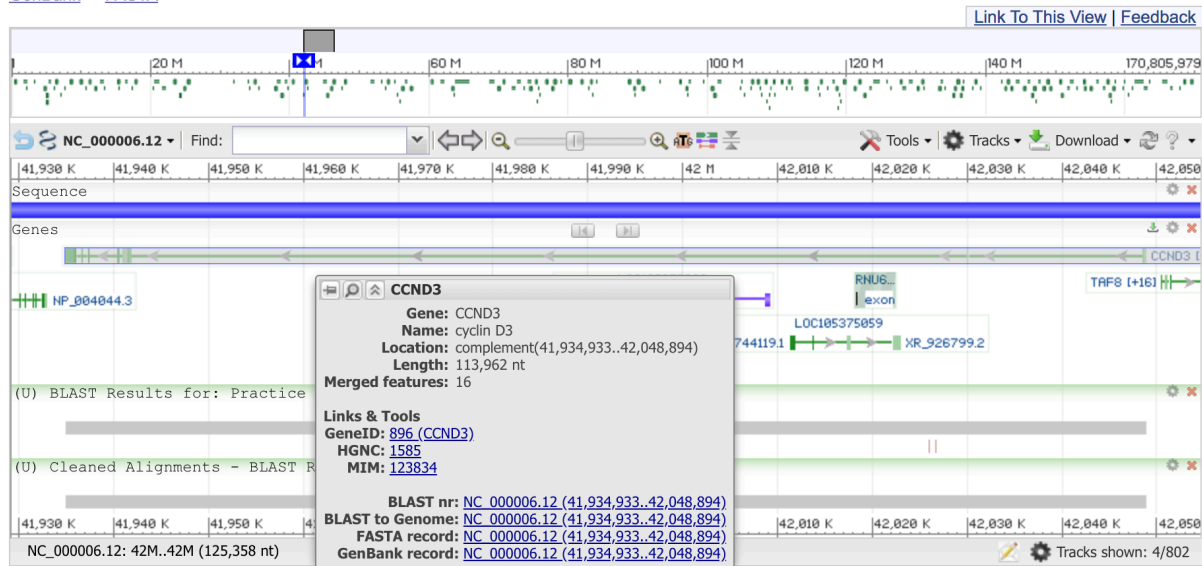


Figure 3. Alignment of query sequence corresponds to cyclin D3 protein.

**Question #3: The protein encoded by this gene is part of a family known as the cyclins. It is important as a regulator of CDK kinases and plays a role in cell cycle regulation. In particular, cyclin D3 is a regulator of what two CDKs?**

Cyclin D3 acts as a regulator of CDK4 and CDK6.

**Question #4: Complete the following sentence. “This protein has been shown to interact with and be involved in the phosphorylation of tumor suppressor protein retinoblastoma (Rb).”**

**Question #5: Homology describes the similarity in sequence between organisms of the same or different species. When the CCND3 gene is compared to the gene in other organisms, which organisms are reported to be homologous?**

The CCND3 gene has homologs in chimpanzee, Rhesus monkey, dog, cow, mouse, rat, chicken, and mosquito.

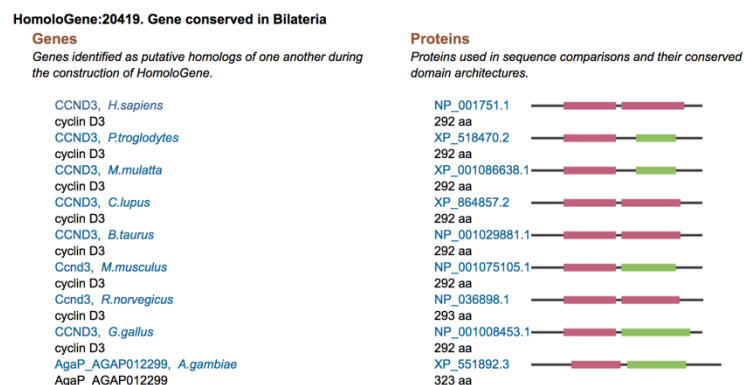


Figure 4. Homologs of CCND3.

**Question #6: Report the following information for primer pairs that can be used to specifically amplify variant 1. Provide separate A-C answers for each pair. Do not report information for primer pairs that can amplify other unintended templates (either cyclin D-related targets or other places within the human genome).**

All 6 returned primer sequences amplify the CCND3 transcript variant 1 selectively. However, there are differences in melting temperature and GC-content for the different primer pairs.

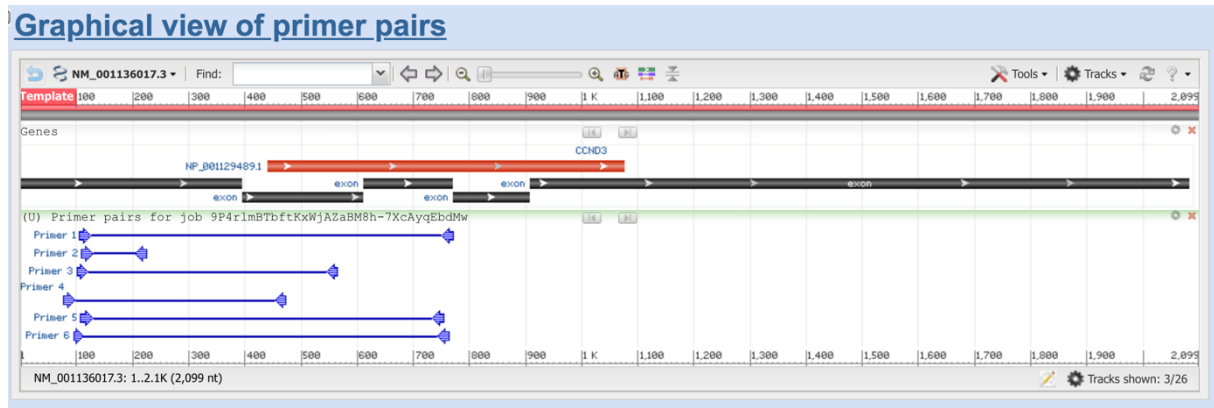


Figure 5. With Primer-BLAST generated primer pairs for amplification of CCND3 transcript variant 1.

I suggest primer pair 1 to be most suitable because of the small difference in melting temperature and the same GC-content (55%)

#### Primer pair 1

	Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	CCGAAACTTGGCTGAGCAGA	Plus	20	106	125	60.60	55.00	5.00	3.00
Reverse primer	CTGTAGCACAGAGGGCCAAA	Minus	20	770	751	59.96	55.00	6.00	1.00
Product length	665								

#### Products on intended targets

>NM\_001136017.3 Homo sapiens cyclin D3 (CCND3), transcript variant 1, mRNA

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product length = 665
Forward primer 1 CCGAAACTTGGCTGAGCAGA 20
Template       106 ..... 125

Reverse primer 1 CTGTAGCACAGAGGGCCAAA 20
Template       770 ..... 751
  
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Figure 6. Primer pair for amplification of CCND3, transcript variant 1.

**A. Forward primer sequence CCGAAACTTGGCTGAGCAGA**

**B. Reverse primer sequence CTGTAGCACAGAGGGCCAAA**

**C. Product length 665**