Introduction to applied bioinformatics

PETRA MATOUŠKOVÁ

2023/2024

9/10

Exam

Thursday 2.5.2024 16:30

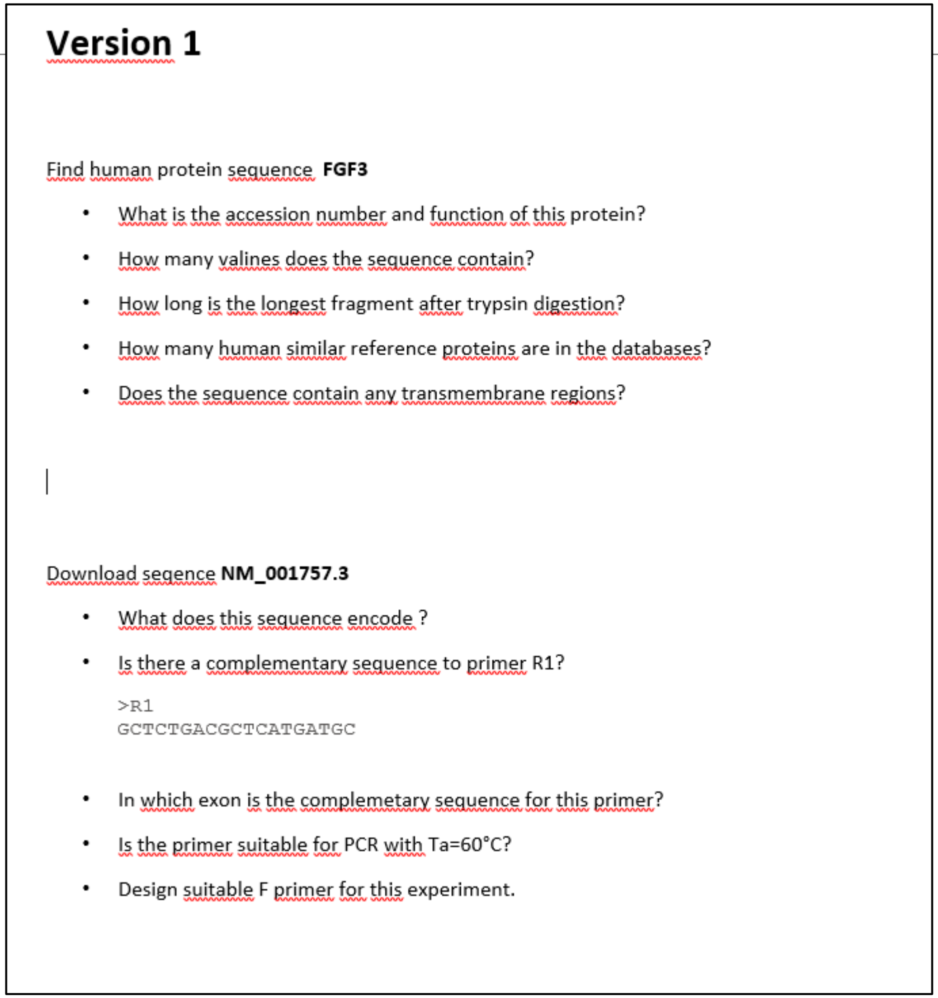
Moodle: files with the version
open „task“ for submission (like for homeworks).

Usual Exam test:

2 parts, each five points

Maximum 10 points

8.5-10p:	1
7-8p:	2
5-6.5p:	3



Version 1

Find human protein sequence **FGF3**

- What is the accession number and function of this protein?
- How many valines does the sequence contain?
- How long is the longest fragment after trypsin digestion?
- How many human similar reference proteins are in the databases?
- Does the sequence contain any transmembrane regions?

Download seqence **NM_001757.3**

- What does this sequence encode ?
- Is there a complementary sequence to primer R1?

```
>R1
GCTCTGACGCTCATGATGC
```

- In which exon is the complemetary sequence for this primer?
- Is the primer suitable for PCR with Ta=60°C?
- Design suitable F primer for this experiment.

Previous Exams

Find human protein sequence **FGF3**

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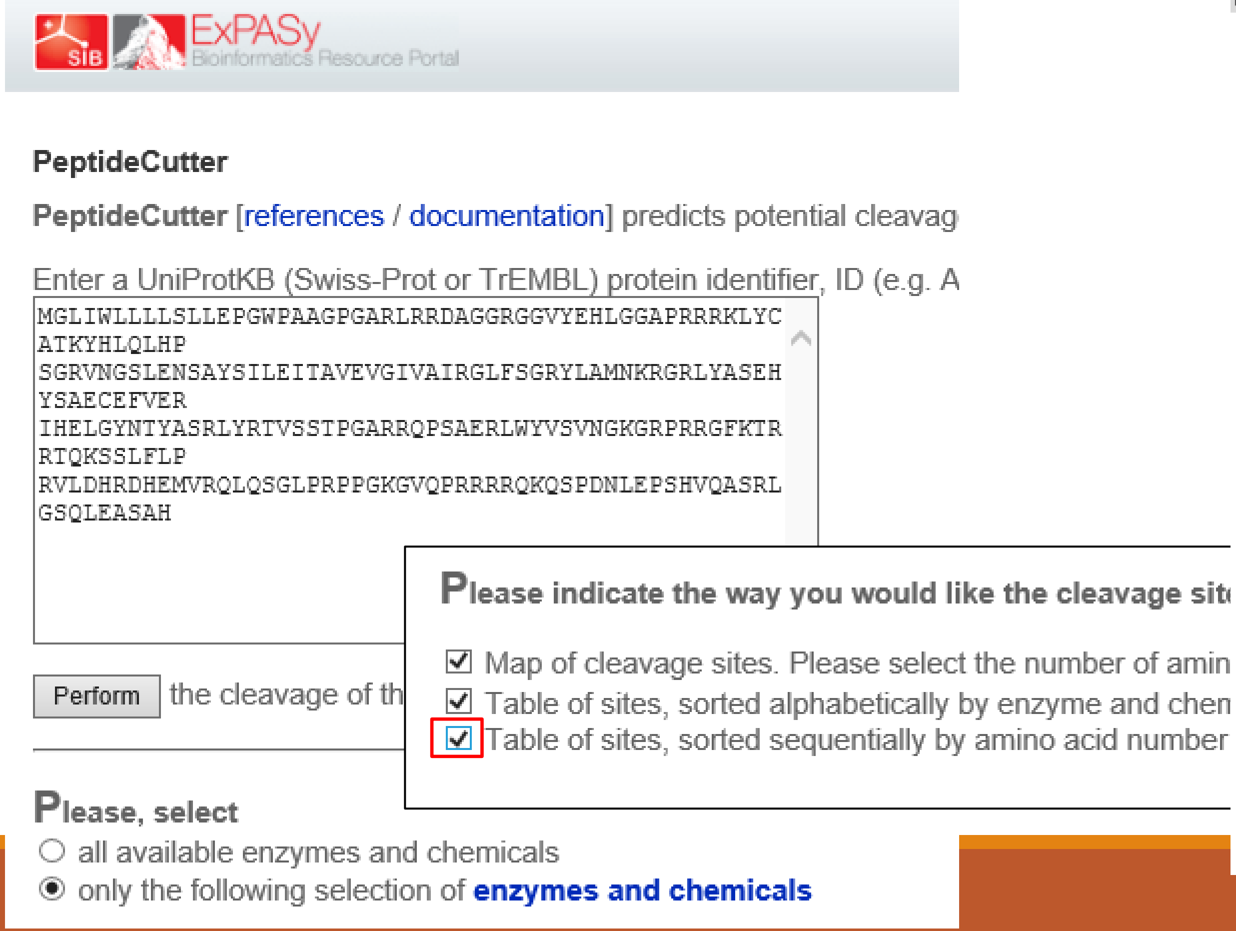


PeptideCutter

PeptideCutter [references / documentation] predicts potential cleavag

Enter a UniProtKB (Swiss-Prot or TrEMBL) protein identifier, ID (e.g. A

```
MGLIWLLLLSLLEPGWPAAGPGARLRRDAGGRGGVYEHLGGAPRRRKLYC
ATKYHLQLHP
SGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGRLYASEH
YSAECEFVER
IHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRPRRGFKTR
RTQKSSLFLP
RVLDHRDHEMVRQLQSGLPRPPGKGVQPRRRRQKQSPDNLEPSHVQASRL
GSQLEASAH
```

the cleavage of th

Please indicate the way you would like the cleavage sit

☑ Map of cleavage sites. Please select the number of amin

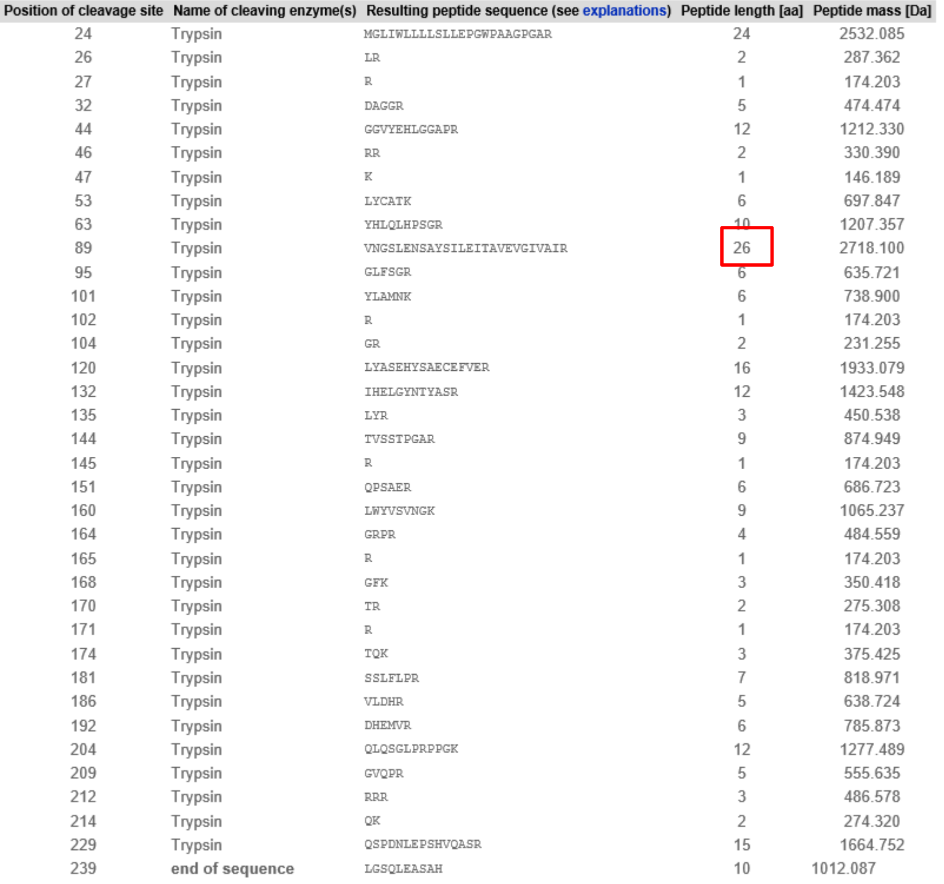
☑ Table of sites, sorted alphabetically by enzyme and chen

☑ Table of sites, sorted sequentially by amino acid number

Please, select

○ all available enzymes and chemicals

● only the following selection of **enzymes and chemicals**



Position of cleavage site	Name of cleaving enzyme(s)	Resulting peptide sequence (see explanations)	Peptide length [aa]	Peptide mass [Da]
24	Trypsin	MGLIWLLLLSLLEPGWPAAGPGAR	24	2532.085
26	Trypsin	LR	2	287.362
27	Trypsin	R	1	174.203
32	Trypsin	DAGGR	5	474.474
44	Trypsin	GGVYEHLGGAPR	12	1212.330
46	Trypsin	RR	2	330.390
47	Trypsin	K	1	146.189
53	Trypsin	LYCATK	6	697.847
63	Trypsin	YHLQLHPSGR	10	1207.357
89	Trypsin	VNGSLENSAYSILEITAVEVGIVAIR	26	2718.100
95	Trypsin	GLFSGR	6	635.721
101	Trypsin	YLAMNK	6	738.900
102	Trypsin	R	1	174.203
104	Trypsin	GR	2	231.255
120	Trypsin	LYASEHYSAECEFVER	16	1933.079
132	Trypsin	IHELGYNTYASR	12	1423.548
135	Trypsin	LYR	3	450.538
144	Trypsin	TVSSTPGAR	9	874.949
145	Trypsin	R	1	174.203
151	Trypsin	QPSAER	6	686.723
160	Trypsin	LWYVSVNGK	9	1065.237
164	Trypsin	GRPR	4	484.559
165	Trypsin	R	1	174.203
168	Trypsin	GFK	3	350.418
170	Trypsin	TR	2	275.308
171	Trypsin	R	1	174.203
174	Trypsin	TQK	3	375.425
181	Trypsin	SSLFLPR	7	818.971
186	Trypsin	VLDHR	5	638.724
192	Trypsin	DHEMVR	6	785.873
204	Trypsin	QLQSGLPRPPGK	12	1277.489
209	Trypsin	GVQPR	5	555.635
212	Trypsin	RRR	3	486.578
214	Trypsin	QK	2	274.320
229	Trypsin	QSPDNLEPSHVQASR	15	1664.752
239	**end of sequence**	LGSQLEASAH	10	1012.087

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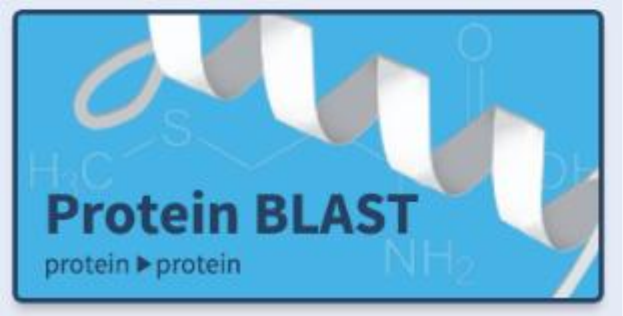
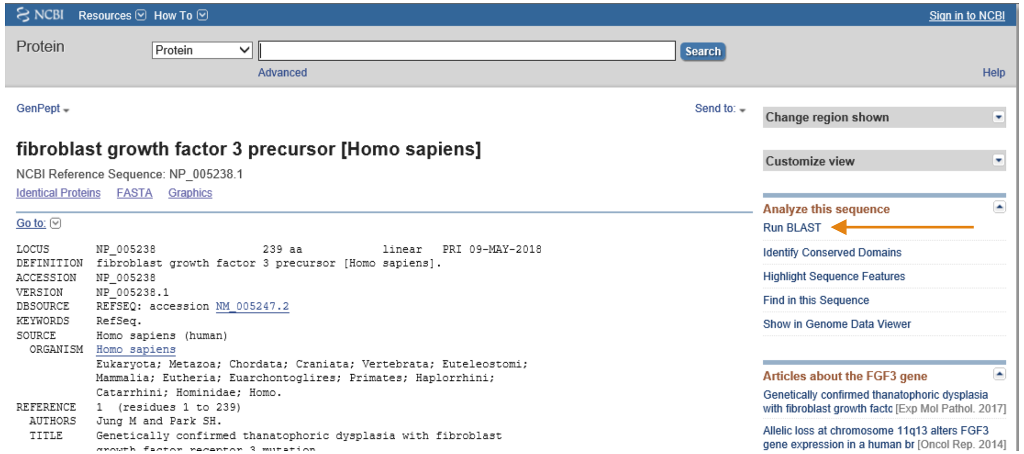




fibroblast growth factor 3 precursor [Homo sapiens]

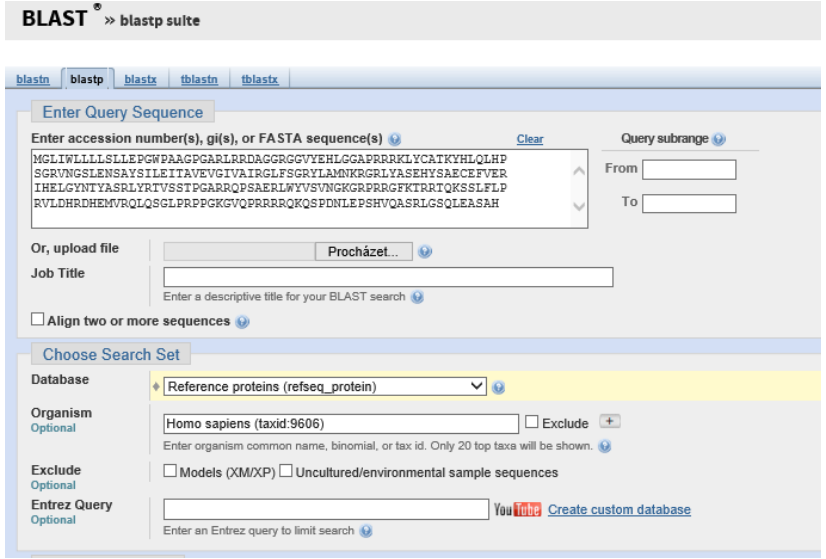
NCBI Reference Sequence: NP_005238.1

```
LOCUS       NP_005238                239 aa            linear   PRI 09-MAY-2018
DEFINITION  fibroblast growth factor 3 precursor [Homo sapiens].
ACCESSION   NP_005238
VERSION     NP_005238.1
DBSOURCE    REFSEQ: accession NM_005247.2
KEYWORDS    RefSeq.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 239)
  AUTHORS   Jung M and Park SH.
  TITLE     Genetically confirmed thanatophoric dysplasia with fibroblast
```

Articles about the FGF3 gene

Genetically confirmed thanatophoric dysplasia with fibroblast growth factc [Exp Mol Pathol. 2017]

Allelic loss at chromosome 11q13 alters FGF3 gene expression in a human br [Oncol Rep. 2014]



Enter accession number(s), gi(s), or FASTA sequence(s)

```
MGLIWLLLLSLLEPGWPAAGPGARLRRDAGGRGGVYEHLGGAPRRRKLYCATKYHLQLHP
SGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGRLYASEHYSAECEFVER
IHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRPRRGFKTRRTQKSSLFLP
RVLDHRDHEMVRQLQSGLPRPPGKGVQPRRRRQKQSPDNLEPSHVQASRLGSQLEASAH
```

Or, upload file

Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Database: Reference proteins (refseq_protein)

Organism (Optional): Homo sapiens (taxid:9606) ☐ Exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

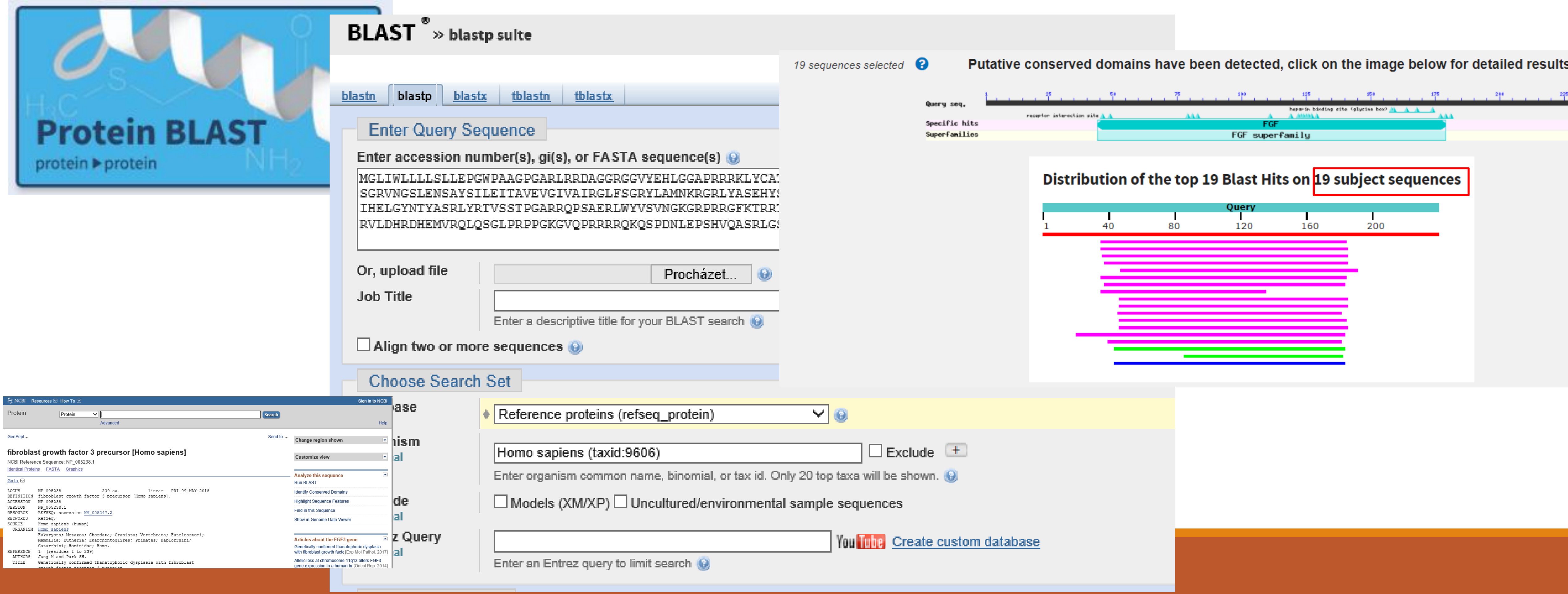
Exclude (Optional): ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Entrez Query (Optional):

Enter an Entrez query to limit search

Find human protein sequence **FGF3**

How many human similar reference proteins are in the databases?



Protein BLAST

protein ▸ protein

BLAST ® » **blastp suite**

blastn | **blastp** | blastx | tblastn | tblastx

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

```
MGLIWLLLLSLLEPGWPAAGPGARLRRDAGGRGGVYEHLGGAPRRRKLYCA
SGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGRLYASEHY
IHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRPRRGFKTRR
RVLDHRDHEMVRQLQSGLPRPPGKGVQPRRRRQKQSPDNLEPSHVQASRLG
```

Or, upload file: Procházet...

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☐ Align two or more sequences

Choose Search Set

ase: Reference proteins (refseq_protein)

nism / al: Homo sapiens (taxid:9606) ☐ Exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

de / al: ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

z Query / al:

Enter an Entrez query to limit search

Create custom database

19 sequences selected

Putative conserved domains have been detected, click on the image below for detailed results

Distribution of the top 19 Blast Hits on 19 subject sequences

NCBI Resources How To Sign in to NCBI

Protein | Protein | Search

Advanced | Help

GenPept | Send to:

fibroblast growth factor 3 precursor [Homo sapiens]

NCBI Reference Sequence: NP_005238.1

Identical Proteins FASTA Graphics

Go to:

```
LOCUS       NP_005238                239 aa            linear   PRI 09-MAY-2018
DEFINITION  fibroblast growth factor 3 precursor [Homo sapiens].
ACCESSION   NP_005238
VERSION     NP_005238.1
DBSOURCE    REFSEQ: accession NM_005247.2
KEYWORDS    RefSeq.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 239)
  AUTHORS   Jung M and Park SH.
  TITLE     Genetically confirmed thanatophoric dysplasia with fibroblast
```

Change region shown

Customize view

Analyze this sequence

- Run BLAST
- Identify Conserved Domains
- Highlight Sequence Features
- Find in this Sequence
- Show in Genome Data Viewer

Articles about the FGF3 gene

- Genetically confirmed thanatophoric dysplasia with fibroblast growth factc [Exp Mol Pathol. 2017]
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Solution:
FGF3: P11487 (NP_005238.1), Fibroblast growth factor 3-role in the regulation of embryonic development…
Contains 13 valins.
Longest fragment after trypsin digestion has 26 aminoacids.
In the databes of reference sequences, there is 19 similar proteins.
There is no transmembrane helices.

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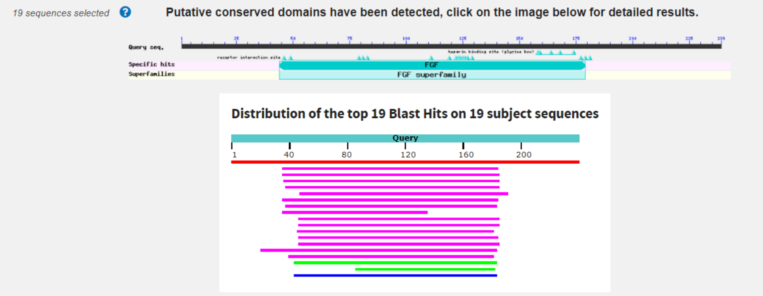
P11487 (FGF3_HUMAN) / NP_005238.1

Fibroblast growth factor 3

-role in the regulation of embryonic development…

V	13

Trypsin	VNGSLENSAYSILEITAVEVGIVAIR	26



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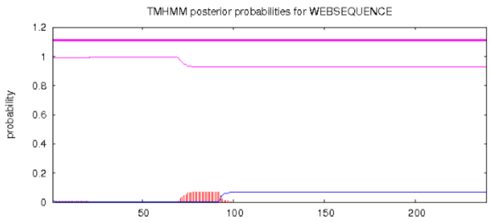

Exam test:

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7-8p:	2
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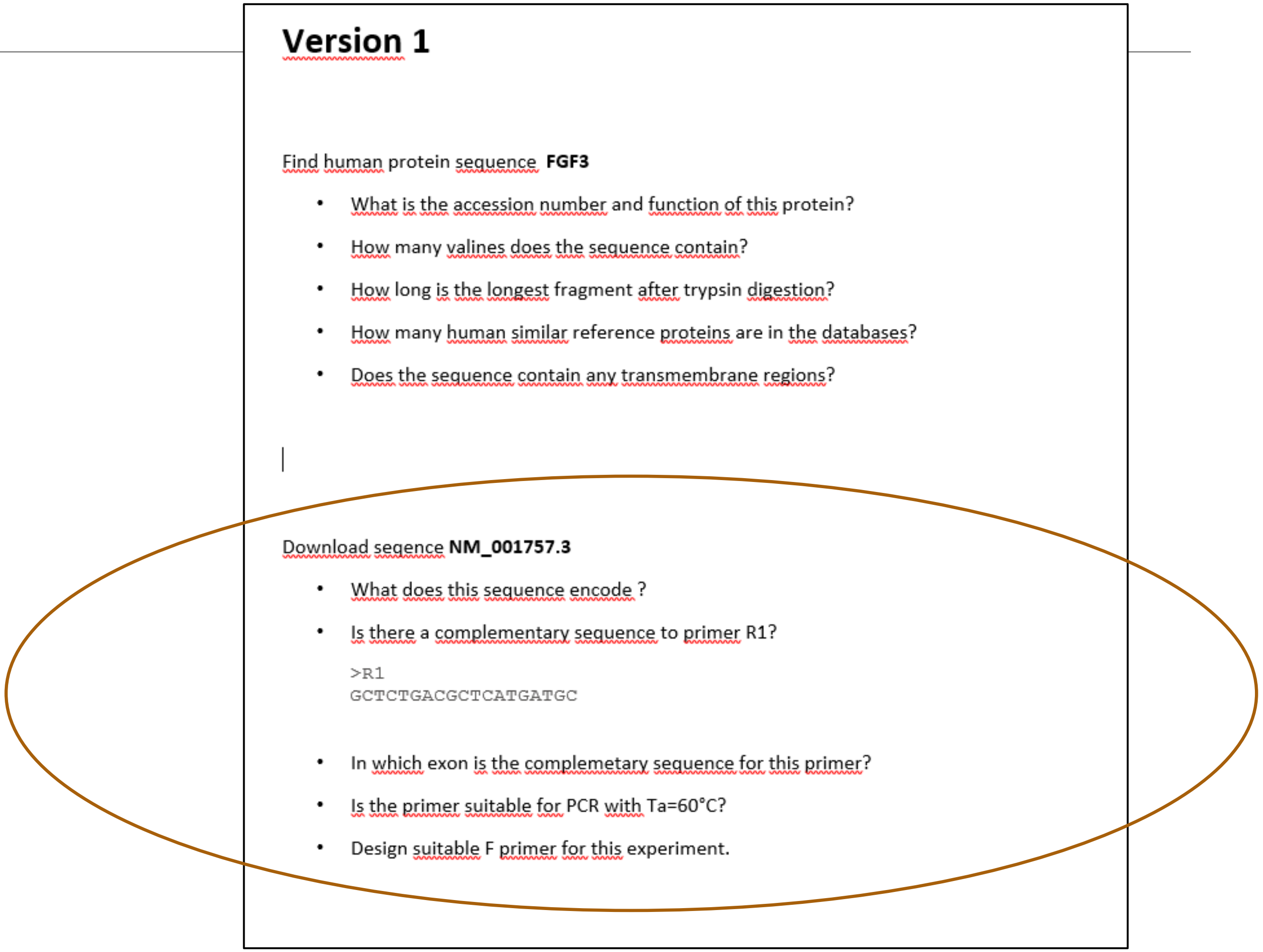

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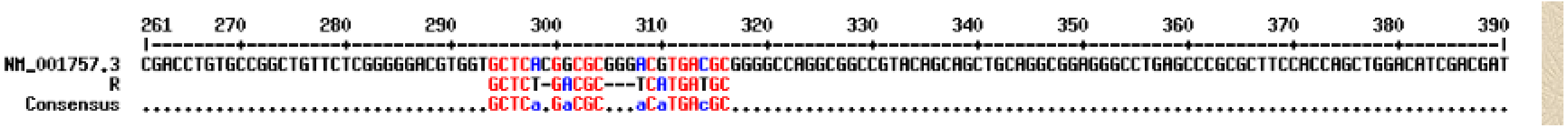
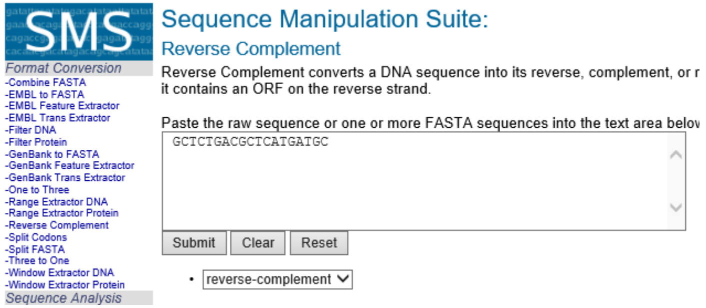
Multalin:



```
               261    270       280       290       300       310       320       330       340       350       360       370       380       390
               |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
NM_001757.3    CGACCTGTGCCGGCTGTTCTCGGGGGACGTGGTGCTCACGGCGCGGGACGTGACGCGGGGCCAGGCGGCCGTACAGCAGCTGCAGGCGGAGGGCCTGAGCCCGCGCTTCCACCAGCTGGACATCGACGAT
          R                                     GCTCT-GACGC---TCATGATGC
  Consensus    .................................GCTCa.GaCGC...aCaTGAcGC..........................................................................
```



Sequence Manipulation Suite:

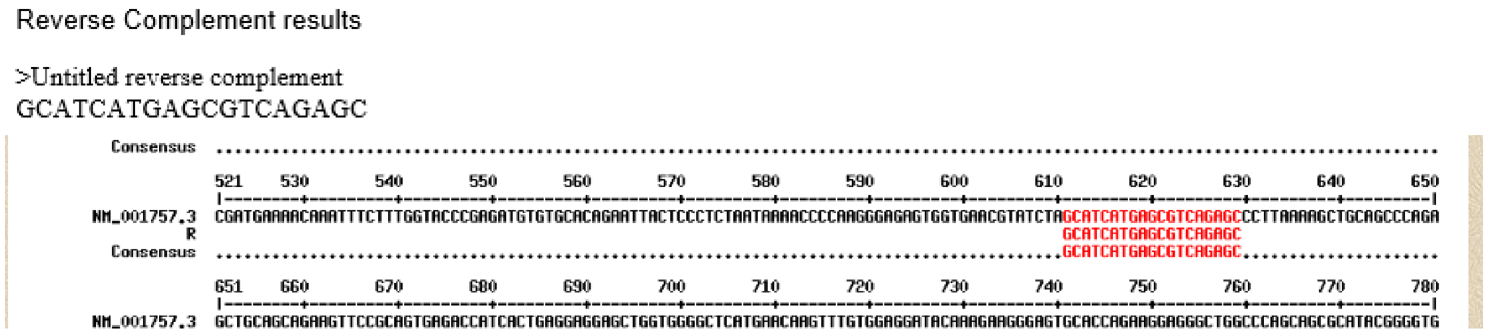
Reverse Complement

Reverse Complement converts a DNA sequence into its reverse, complement, or r
it contains an ORF on the reverse strand.

Paste the raw sequence or one or more FASTA sequences into the text area belov

GCTCTGACGCTCATGATGC

- reverse-complement



Reverse Complement results

>Untitled reverse complement
GCATCATGAGCGTCAGAGC

```
  Consensus    ..................................................................................................................................

               521    530       540       550       560       570       580       590       600       610       620       630       640       650
               |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
NM_001757.3    CGATGAAAACAAATTTCTTTGGTACCCGAGATGTGTGCACAGAATTACTCCCTCTAATAAAACCCCAAGGGAGAGTGGTGAACGTATCTAGCATCATGAGCGTCAGAGCCCTTAAAAGCTGCAGCCCAGA
          R                                                                                                GCATCATGAGCGTCAGAGC
  Consensus    ..........................................................................................GCATCATGAGCGTCAGAGC.....................

               651    660       670       680       690       700       710       720       730       740       750       760       770       780
               |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
NM_001757.3    GCTGCAGCAGAAGTTCCGCAGTGAGACCATCACTGAGGAGGAGCTGGTGGGGCTCATGAACAAGTTTGTGGAGGATACAAAGAAGGGAGTGCACCAGAAGGAGGGCTGGCCCAGCAGCGCATACGGGGTG
```

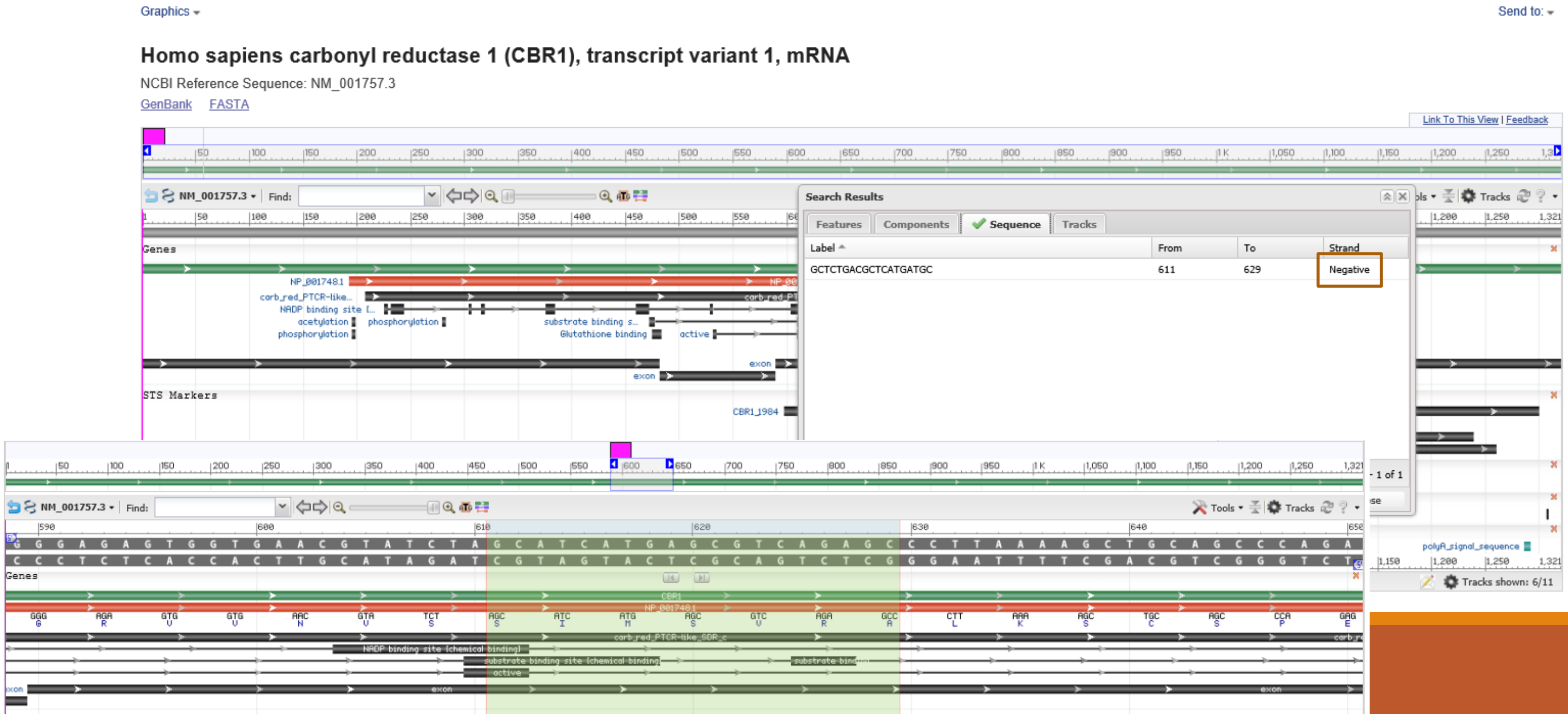
→yes.

Download seqence **NM_001757.3**

Is there a complementary sequence to primer R1?

>R1
GCTCTGACGCTCATGATGC

NCBI: Graphic



Homo sapiens carbonyl reductase 1 (CBR1), transcript variant 1, mRNA

NCBI Reference Sequence: NM_001757.3

Search Results

Label	From	To	Strand
GCTCTGACGCTCATGATGC	611	629	Negative

→yes.

Download seqence **NM_001757.3**

What does this sequence encode ?

Is there a complementary sequence to primer R1?

In which exon is the complemetary sequence for this primer?

Is the primer suitable for PCR with Ta=60°C?

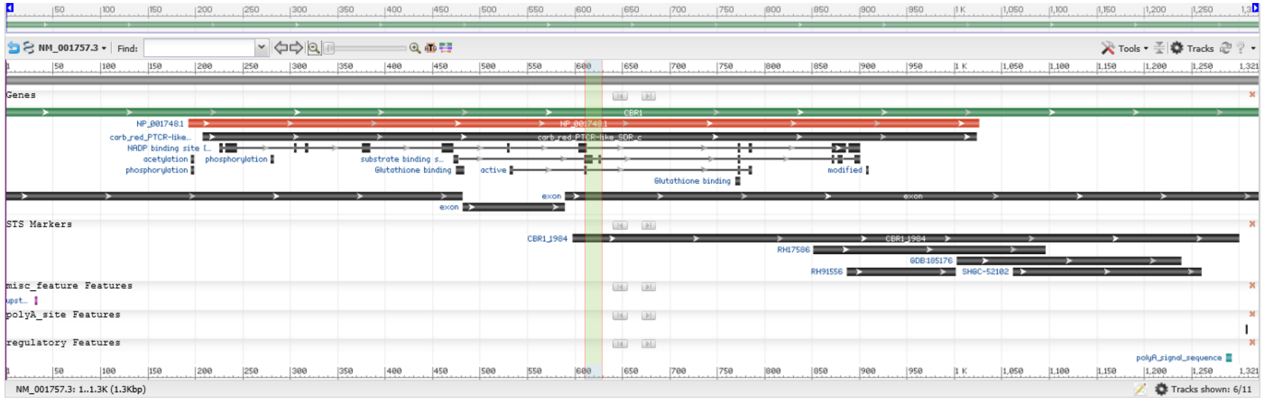
Design suitable F primer for this experiment.

```
>R1
GCTCTGACGCTCATGATGC
```

Download seqence **NM_001757.3**

In which exon is the complemetary sequence for this primer?

NCBI: Graphic



>R1
GCTCTGACGCTCATGATGC

→ third exon

Download seqence **NM_001757.3**

What does this sequence encode ?

Is there a complementary sequence to primer R1?

In which exon is the complemetary sequence for this primer?

Is the primer suitable for PCR with Ta=60°C?

(Design suitable F primer for this experiment.)

2025: We did not cover this one

>R1
`GCTCTGACGCTCATGATGC`

Download seqence **NM_001757.3**

<u>Solution:</u>

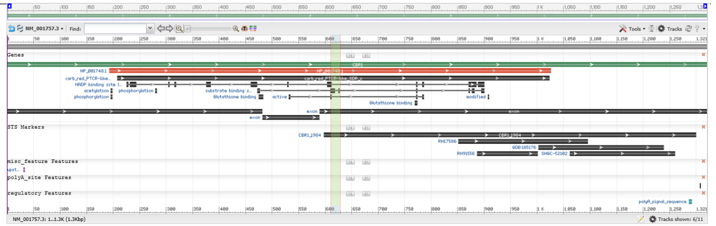
This sequence encodes carbonyl reductase 1 (CBR1).

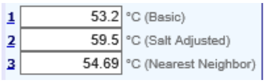
Yes, there is complementary sequence to primer R1.

It is within 3rd exon.

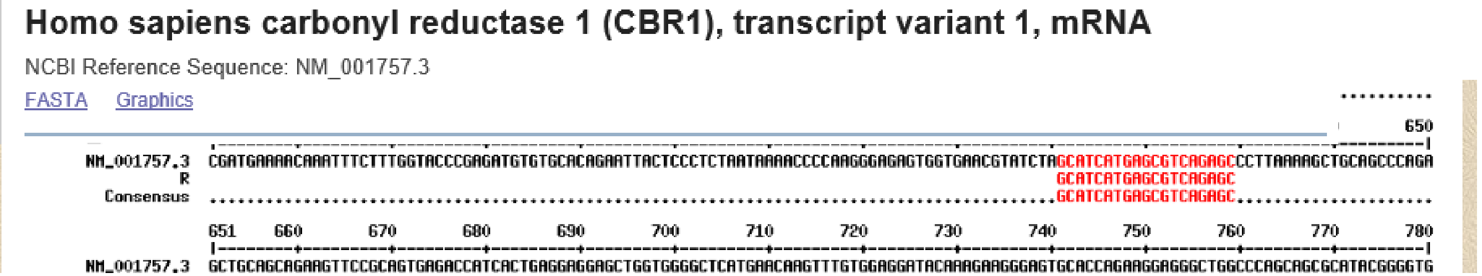
At Ta=60°C the primer should work.

An example of suitable F primer: F:`CAAGGTTGCTGATCCCACAC`





1 53.2 °C (Basic)
2 59.5 °C (Salt Adjusted)
3 54.69 °C (Nearest Neighbor)



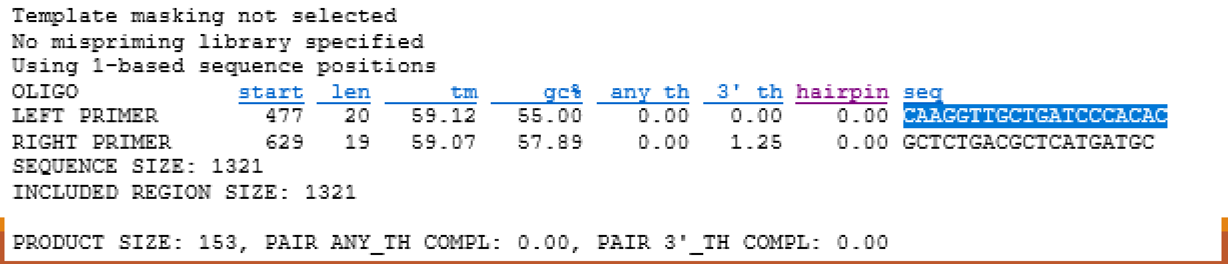
Homo sapiens carbonyl reductase 1 (CBR1), transcript variant 1, mRNA

NCBI Reference Sequence: NM_001757.3

FASTA Graphics

```
                                                                                                                       ..........
                                                                                                                              650
             |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  NM_001757.3 CGATGAAAACAAATTTCTTTGGTACCCGAGATGTGTGCACAGAATTACTCCCTCTAATAAAACCCCAAGGGAGAGTGGTGAACGTATCTAGCATCATGAGCGTCAGAGCCCTTAAAAGCTGCAGCCCAGA
            R                                                                                         GCATCATGAGCGTCAGAGC
    Consensus ..........................................................................................GCATCATGAGCGTCAGAGC.....................

              651     660       670       680       690       700       710       720       730       740       750       760       770       780
             |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  NM_001757.3 GCTGCAGCAGAAGTTCCGCAGTGAGACCATCACTGAGGAGGAGCTGGTGGGGCTCATGAACAAGTTTGTGGAGGATACAAAGAAGGGAGTGCACCAGAAGGAGGGCTGGCCCAGCAGCGCATACGGGGTG
```



```
Template masking not selected
No mispriming library specified
Using 1-based sequence positions
OLIGO              start  len      tm     gc%  any th  3' th hairpin seq
LEFT PRIMER          477   20   59.12   55.00    0.00   0.00    0.00 CAAGGTTGCTGATCCCACAC
RIGHT PRIMER         629   19   59.07   57.89    0.00   1.25    0.00 GCTCTGACGCTCATGATGC
SEQUENCE SIZE: 1321
INCLUDED REGION SIZE: 1321

PRODUCT SIZE: 153, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00
```

Exam test II:

2 parts, each five points

Maximum 10 points

8.5-10p:	1
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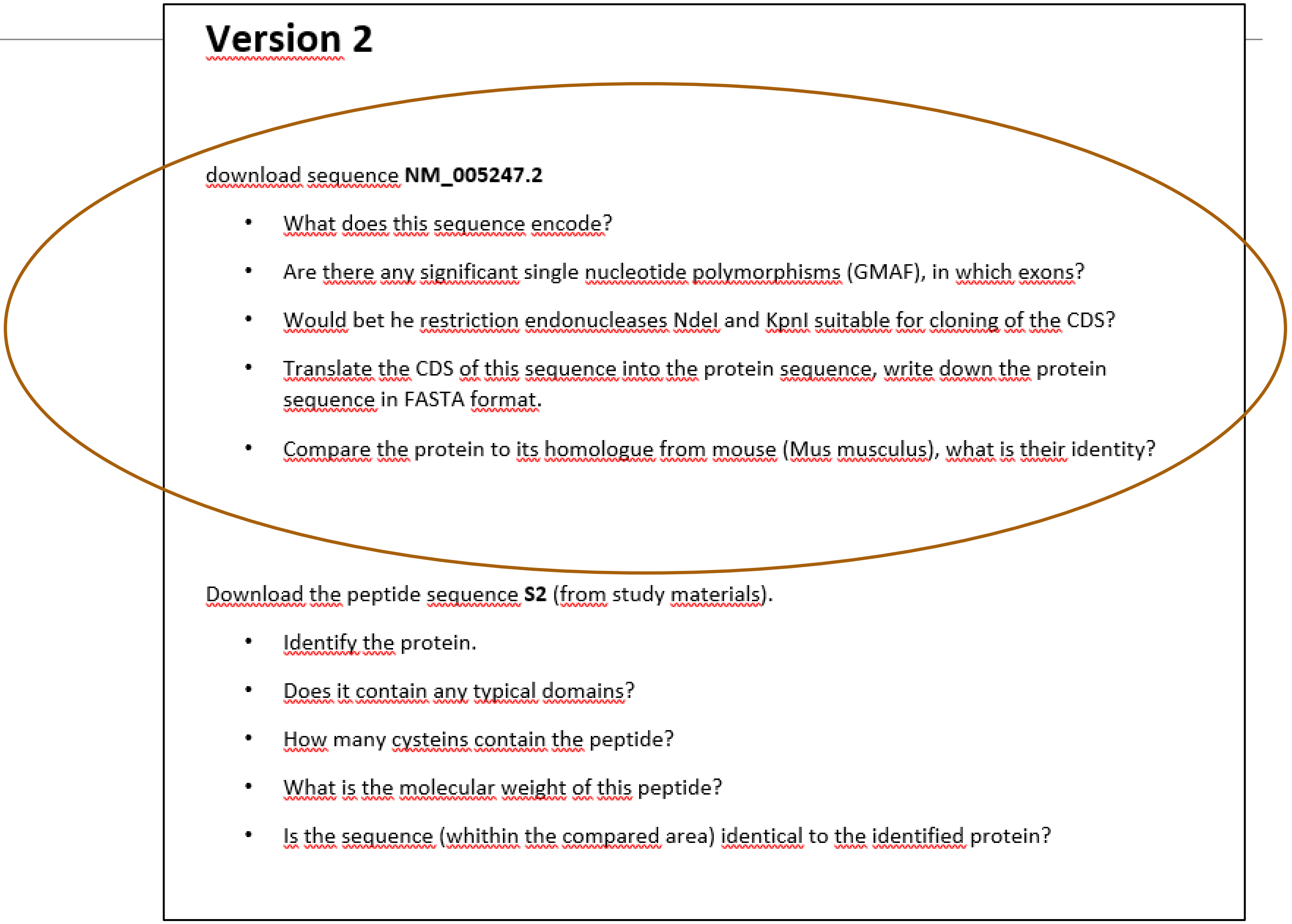

Version 2

download sequence **NM_005247.2**

- What does this sequence encode?
- Are there any significant single nucleotide polymorphisms (GMAF), in which exons?
- Would bet he restriction endonucleases NdeI and KpnI suitable for cloning of the CDS?
- Translate the CDS of this sequence into the protein sequence, write down the protein sequence in FASTA format.
- Compare the protein to its homologue from mouse (Mus musculus), what is their identity?

Download the peptide sequence **S2** (from study materials).

- Identify the protein.
- Does it contain any typical domains?
- How many cysteins contain the peptide?
- What is the molecular weight of this peptide?
- Is the sequence (whithin the compared area) identical to the identified protein?

Download sequence **NM_005247.2**

What does this sequence encode?

(Are there any significant single nucleotide polymorphisms (GMAF), in which exons?)

2025: We did not cover this one

Would be the restriction endonucleases NdeI and KpnI suitable for cloning of the CDS?

Translate the CDS of this sequence into the protein sequence, write down the protein sequence in FASTA format.

Compare the protein to its homologue from mouse (Mus musculus), what is their identity?

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What does this sequence encode?

Are there any significant single nucleotide polymorphisms (GMAF), in which exons?

Would be the restriction endonucleases NdeI and KpnI suitable for cloning of the CDS?

Translate the CDS of this sequence into the protein sequence, write down the protein sequence in FASTA format.

Compare the protein to its homologue from mouse (Mus musculus), what is their identity?

Restriction summary:

KpnI ggtac|c	289
NdeI ca|tatg	none

→ KpnI is not suitable

Download sequence **NM_005247.2**

What does this sequence encode?

Are there any significant single nucleotide polymorphisms (GMAF), in which exons?

Would be the restriction endonucleases NdeI and KpnI suitable for cloning of the CDS?

Translate the CDS of this sequence into the protein sequence, write down the protein sequence in FASTA format.

Compare the protein to its homologue from mouse (Mus musculus), what is their identity?

<u>Solution:</u>
This gene encodes Fibroblast Growth Factor 3
GMAF are in the 1st and 3rd exon.
Restriction endonuclease KpnI is not suitable for cloning.
The FASTA of the protein is:
The indentity of human and mouse FGF3 proteins is 79.1 %.

```
>protein-FGF3
MGLIWLLLLSLLEPGWPAAGPGARLRRDAGGRGGVYEHLGGAPRRRKLYCATKYHLQLHP
SGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGRLYASEHYSAECEFVER
IHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRPRRGFKTRRTQKSSLFLP
RVLDHRDHEMVRQLQSGLPRPPGKGVQPRRRRQKQSPDNLEPSHVQASRLGSQLEASAH*
```

Download sequence **NM_005247.2**

<u>Solution:</u>

This gene encodes Fibroblast Growth Factor 3

GMAF are in the 1st and 3rd exon.

Restriction endonuclease KpnI is not suitable for cloning.

The FASTA of the protein is:

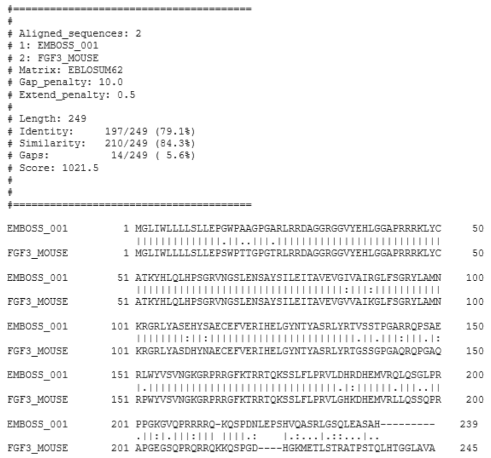
The indentity of human and mouse FGF3 proteins is 79.1 %.

```
>protein-FGF3
MGLIWLLLLSLLEPGWPAAGPGARLRRDAGGRGGVYEHLGGAPRRRKLYCATKYHLQLHP
SGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGRLYASEHYSAECEFVER
IHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRPRRGFKTRRTQKSSLFLP
RVLDHRDHEMVRQLQSGLPRPPGKGVQPRRRRQKQSPDNLEPSHVQASRLGSQLEASAH*
```

Homo sapiens fibroblast growth factor 3 (FGF3), mRNA

NCBI Reference Sequence: NM_005247.2

NdeI ca|tatg	none
KpnI ggtac|c	289



```
#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: FGF3_MOUSE
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 249
# Identity:     197/249 (79.1%)
# Similarity:   210/249 (84.3%)
# Gaps:          14/249 ( 5.6%)
# Score: 1021.5
#
#
#=======================================

EMBOSS_001         1 MGLIWLLLLSLLEPGWPAAGPGARLRRDAGGRGGVYEHLGGAPRRRKLYC     50
                     ||||||||||||||.||..|||.|||||||||||||||||||||||||||
FGF3_MOUSE         1 MGLIWLLLLSLLEPSWPTTGPGTRLRRDAGGRGGVYEHLGGAPRRRKLYC     50

EMBOSS_001        51 ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMN    100
                     ||||||||||||||||||||||||||||||||||:|||:|||||||||||
FGF3_MOUSE        51 ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMN    100

EMBOSS_001       101 KRGRLYASEHYSAECEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAE    150
                     ||||||||:||:|||||||||||||||||||||||||.||.|||:|||.|:
FGF3_MOUSE       101 KRGRLYASDHYNAECEFVERIHELGYNTYASRLYRTGSSGPGAQRQPGAQ    150

EMBOSS_001       151 RLWYVSVNGKGRPRRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPR    200
                     |.|||||||||||||||||||||||||||||||.|:||||||.|||..||
FGF3_MOUSE       151 RPWYVSVNGKGRPRRGFKTRRTQKSSLFLPRVLGHKDHEMVRLLQSSQPR    200

EMBOSS_001       201 PPGKGVQPRRRRQ-KQSPDNLEPSHVQASRLGSQLEASAH---------    239
                     .||:|.|||:||| ||||.:    |.:...|.::...|..
FGF3_MOUSE       201 APGEGSQPRQRRQKKQSPGD----HGKMETLSTRATPSTQLHTGGLAVA    245
```

Exam test:

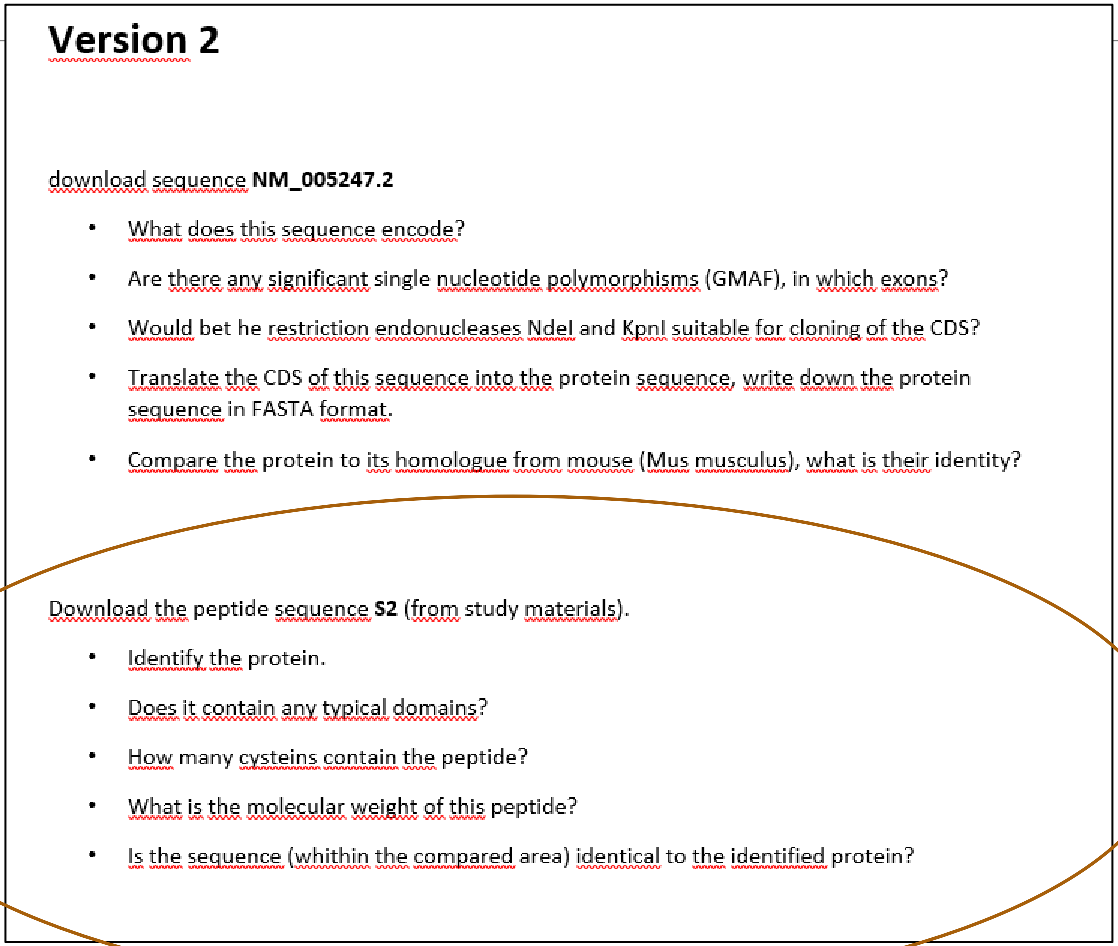
2 parts, each five points

<u>Maximum 10 points</u>

9-10p: 1

7-8p: 2

5-6p: 3



Version 2

download sequence **NM_005247.2**

- What does this sequence encode?
- Are there any significant single nucleotide polymorphisms (GMAF), in which exons?
- Would bet he restriction endonucleases NdeI and KpnI suitable for cloning of the CDS?
- Translate the CDS of this sequence into the protein sequence, write down the protein sequence in FASTA format.
- Compare the protein to its homologue from mouse (Mus musculus), what is their identity?

Download the peptide sequence **S2** (from study materials).

- Identify the protein.
- Does it contain any typical domains?
- How many cysteins contain the peptide?
- What is the molecular weight of this peptide?
- Is the sequence (whithin the compared area) identical to the identified protein?

Download the peptide sequence **S2** (from study materials).

Identify the protein.

Does it contain any typical domains?

How many cysteins contain the peptide?

What is the molecular weight of this peptide?

Is the sequence (whithin the compared area) identical to the identified protein?

```
>S2
CGPSTSGTTSGPGPARPARARPRRPREETLTPEEEEKRRVRRERNKLAAAKCRNRRRELT
DRLQAETDQLEEEKAELESEIAELQKEKERLEFVLVAHKPGCKIPYEEGPGPLAEVRD
LPGSAPAKEDGFSWLLPPPPPPPLPFQTSQDAPPNLTASLFTHSEVQVLGDPFPVVNPSC
```

Download the peptide sequence **S2** (from study materials).

Identify the protein.

Does it contain any typical domains?

How many cysteins contain the peptide?

What is the molecular weight of this peptide?

Is the sequence (whithin the compared area) identical to the identified protein?

Solution:
Peptide is probably human FosB homologue.
Yes, it contains leucine zipper bZIP.
Contains four cysteins
Mw=19.1 kDa.
It differs from the human homologue in the first and the last aminoacid.

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Solution:

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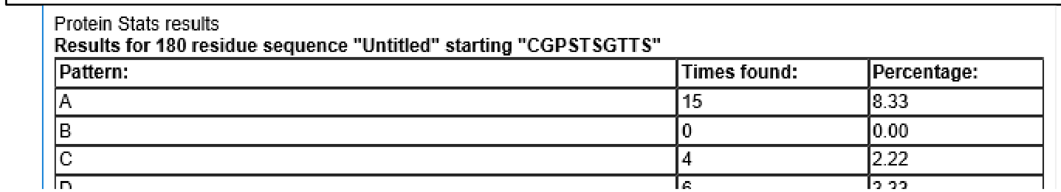
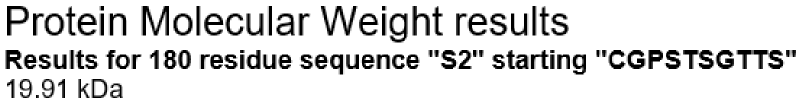


Protein Stats results

Results for 180 residue sequence "Untitled" starting "CGPSTSGTTS"

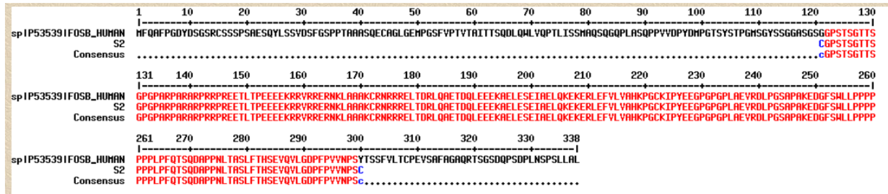
Pattern:	Times found:	Percentage:
A	15	8.33
B	0	0.00
C	4	2.22



Protein Molecular Weight results

Results for 180 residue sequence "S2" starting "CGPSTSGTTS"

19.91 kDa

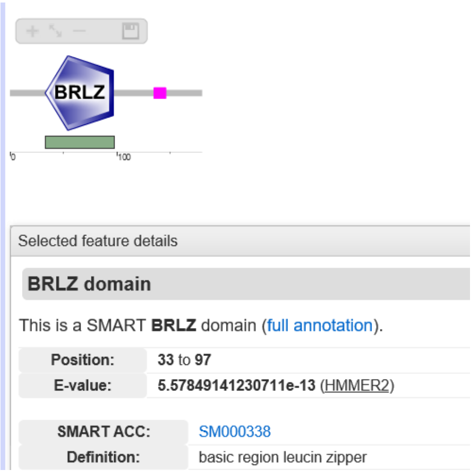


```
                    1        10        20        30        40        50        60        70        80        90        100       110       120       130
                    |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
sp|P53539|FOSB_HUMAN MFQAFPGDYDSGSRCSSSPSAESQYLSSVDSFGSPPTAAASQECAGLGEMPGSFVPTVTAITTSQDLQWLVQPTLISSMAQSQGQPLASQPPVVDPYDMPGTSYSTPGMSGYSSGGASGSGGPSTSGTTS
                  S2                                                                                                                          CGPSTSGTTS
           Consensus ........................................................................................................................cGPSTSGTTS

                    131      140       150       160       170       180       190       200       210       220       230       240       250       260
                    |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
sp|P53539|FOSB_HUMAN GPGPARPARARPRRPREETLTPEEEEKRRVRRERNKLAAAKCRNRRRELTDRLQAETDQLEEEKAELESEIAELQKEKERLEFVLVAHKPGCKIPYEEGPGPGPLAEVRDLPGSAPAKEDGFSWLLPPPP
                  S2 GPGPARPARARPRRPREETLTPEEEEKRRVRRERNKLAAAKCRNRRRELTDRLQAETDQLEEEKAELESEIAELQKEKERLEFVLVAHKPGCKIPYEEGPGPGPLAEVRDLPGSAPAKEDGFSWLLPPPP
           Consensus GPGPARPARARPRRPREETLTPEEEEKRRVRRERNKLAAAKCRNRRRELTDRLQAETDQLEEEKAELESEIAELQKEKERLEFVLVAHKPGCKIPYEEGPGPGPLAEVRDLPGSAPAKEDGFSWLLPPPP

                    261      270       280       290       300       310       320       330      338
                    |---------+---------+---------+---------+---------+---------+---------+--------|
sp|P53539|FOSB_HUMAN PPPLPFQTSQDAPPNLTASLFTHSEVQVLGDPFPVVNPSYTSSFVLTCPEVSAFAGAQRTSGSDQPSDPLNSPSLLAL
                  S2 PPPLPFQTSQDAPPNLTASLFTHSEVQVLGDPFPVVNPSC
           Consensus PPPLPFQTSQDAPPNLTASLFTHSEVQVLGDPFPVVNPSc.......................................
```

protein fosB isoform 1 [Homo sapiens]

NCBI Reference Sequence: NP_006723.2

Identical Proteins FASTA Graphics



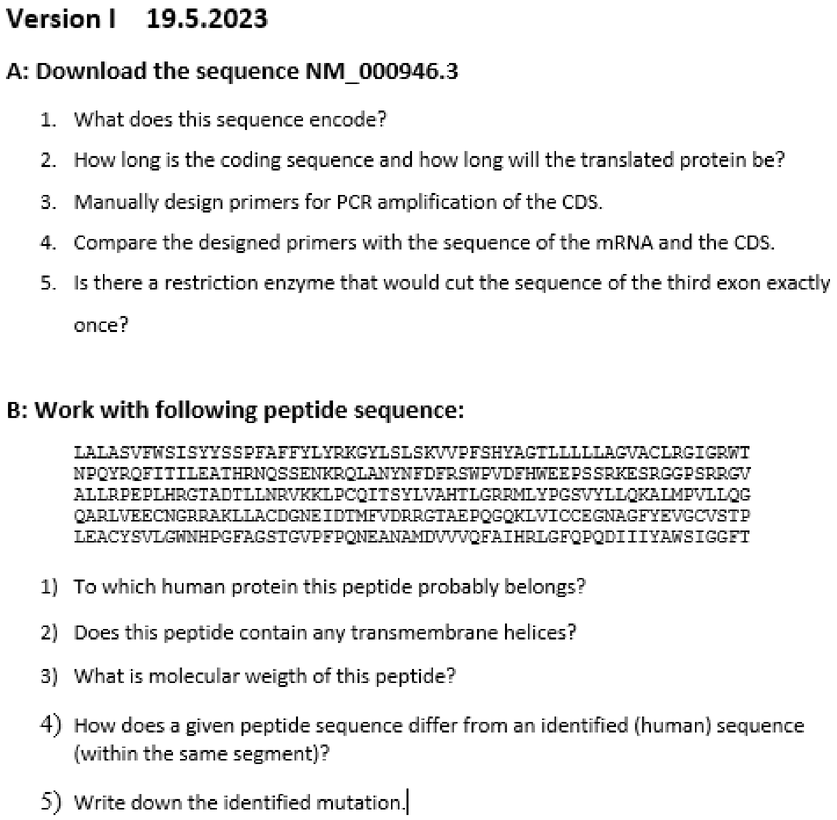
Selected feature details

BRLZ domain

This is a SMART **BRLZ** domain (full annotation).

Position:	33 to 97
E-value:	5.57849141230711e-13 (HMMER2)
SMART ACC:	SM000338
Definition:	basic region leucin zipper

Version from 2023_new to Moodle



Version I 19.5.2023

A: Download the sequence NM_000946.3

1. What does this sequence encode?
2. How long is the coding sequence and how long will the translated protein be?
3. Manually design primers for PCR amplification of the CDS.
4. Compare the designed primers with the sequence of the mRNA and the CDS.
5. Is there a restriction enzyme that would cut the sequence of the third exon exactly once?

B: Work with following peptide sequence:

```
LALASVFWSISYYSSPFAFFYLYRKGYLSLSKVVPFSHYAGTLLLLLAGVACLRGIGRWT
NPQYRQFITILEATHRNQSSENKRQLANYNFDFRSWPVDFHWEEPSSRKESRGGPSRRGV
ALLRPEPLHRGTADTLLNRVKKLPCQITSYLVAHTLGRRMLYPGSVYLLQKALMPVLLQG
QARLVEECNGRRAKLLACDGNEIDTMFVDRRGTAEPQGQKLVICCEGNAGFYEVGCVSTP
LEACYSVLGWNHPGFAGSTGVPFPQNEANAMDVVVQFAIHRLGFQPQDIIIYAWSIGGFT
```

1) To which human protein this peptide probably belongs?
2) Does this peptide contain any transmembrane helices?
3) What is molecular weigth of this peptide?
4) How does a given peptide sequence differ from an identified (human) sequence (within the same segment)?
5) Write down the identified mutation.

A: Download the sequence NM_000946.3

1. What does this sequence encode?
2. How long is the coding sequence and how long will the translated protein be?
3. Manually design primers for PCR amplification of the CDS.
4. Compare the designed primers with the sequence of the mRNA and the CDS.
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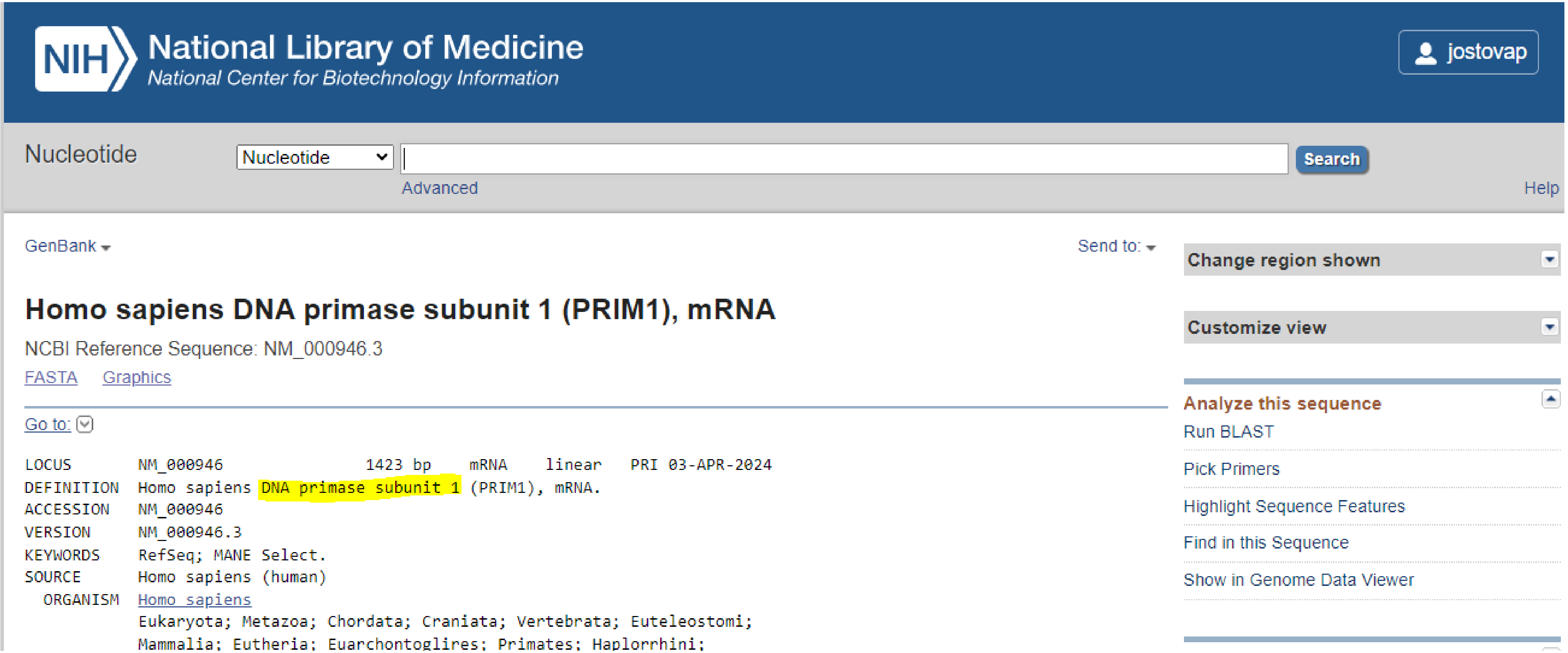
5. Is there a restriction enzyme that would cut the sequence of the third exon exactly once?

What does this sequence encode?



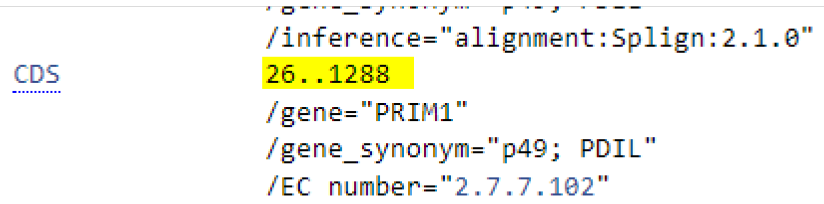
Homo sapiens DNA primase subunit 1 (PRIM1), mRNA

NCBI Reference Sequence: NM_000946.3

```
LOCUS       NM_000946               1423 bp    mRNA    linear   PRI 03-APR-2024
DEFINITION  Homo sapiens DNA primase subunit 1 (PRIM1), mRNA.
ACCESSION   NM_000946
VERSION     NM_000946.3
KEYWORDS    RefSeq; MANE Select.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
```

How long is the coding sequence and how long will the translated protein be?

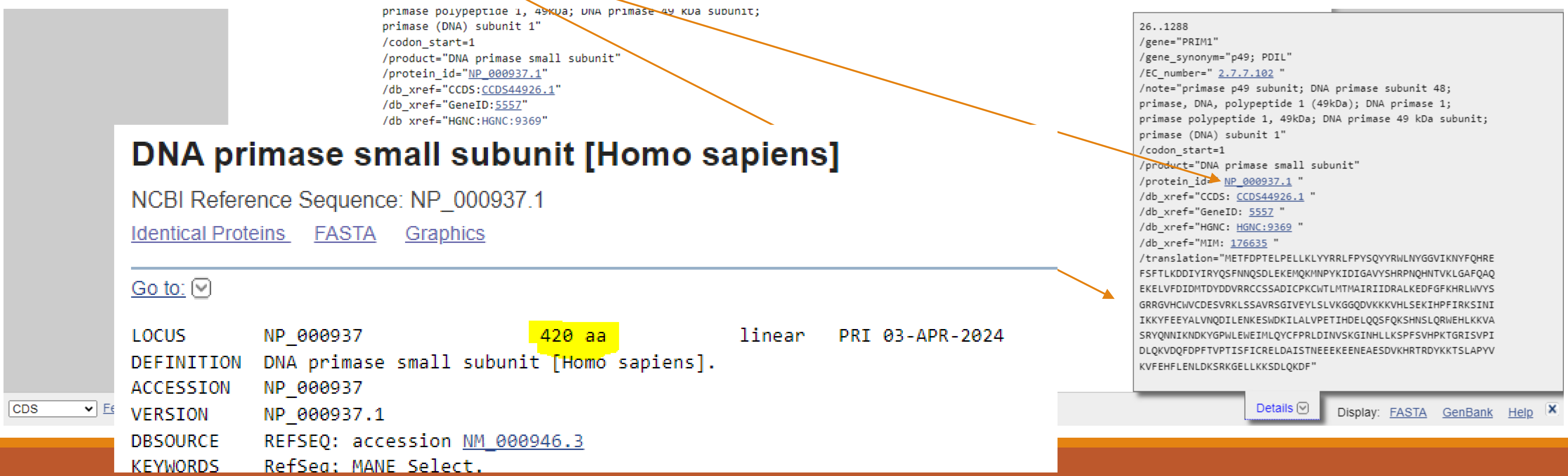
CDS:



```
CDS             /inference="alignment:Splign:2.1.0"
                26..1288
                /gene="PRIM1"
                /gene_synonym="p49; PDIL"
                /EC_number="2.7.7.102"
```

1) 1288-26+1= 1263nt (bp)

Translated protein



```
primase (DNA) subunit 1"
/codon_start=1
/product="DNA primase small subunit"
/protein_id="NP_000937.1"
/db_xref="CCDS:CCDS44926.1"
/db_xref="GeneID:5557"
/db_xref="HGNC:HGNC:9369"
```

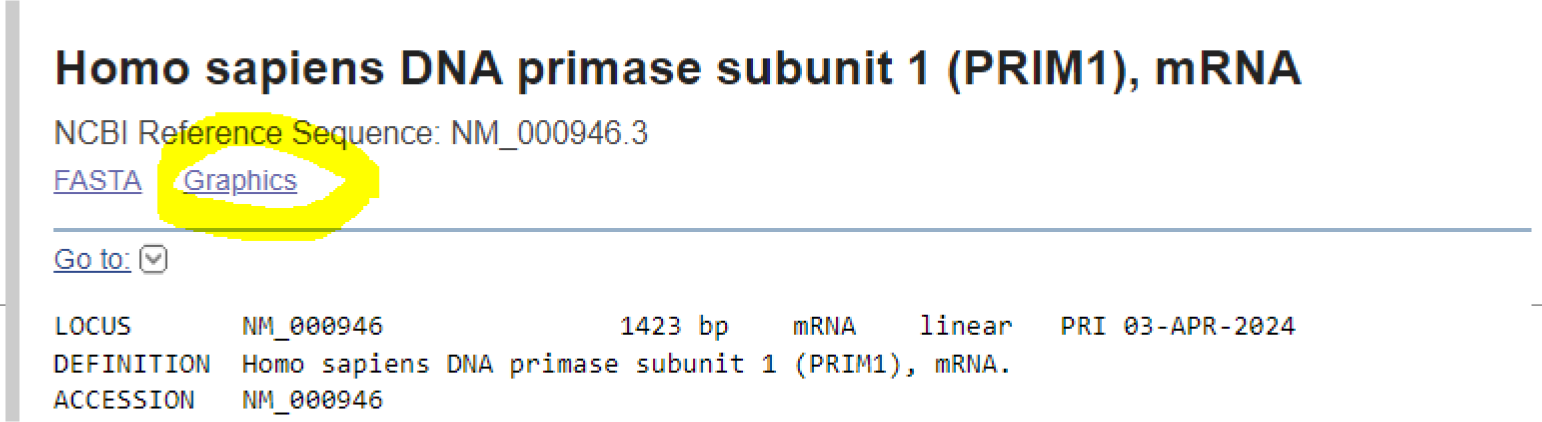
DNA primase small subunit [Homo sapiens]

NCBI Reference Sequence: NP_000937.1

```
LOCUS       NP_000937                420 aa            linear   PRI 03-APR-2024
DEFINITION  DNA primase small subunit [Homo sapiens].
ACCESSION   NP_000937
VERSION     NP_000937.1
DBSOURCE    REFSEQ: accession NM_000946.3
KEYWORDS    RefSeq; MANE Select.
```

```
26..1288
/gene="PRIM1"
/gene_synonym="p49; PDIL"
/EC_number=" 2.7.7.102 "
/note="primase p49 subunit; DNA primase subunit 48;
primase, DNA, polypeptide 1 (49kDa); DNA primase 1;
primase polypeptide 1, 49kDa; DNA primase 49 kDa subunit;
primase (DNA) subunit 1"
/codon_start=1
/product="DNA primase small subunit"
/protein_id=" NP_000937.1 "
/db_xref="CCDS: CCDS44926.1 "
/db_xref="GeneID: 5557 "
/db_xref="HGNC: HGNC:9369 "
/db_xref="MIM: 176635 "
/translation="METFDPTELPELLKLYYRRLFPYSQYYRWLNYGGVIKNYFQHRE
FSFTLKDDIYIRYQSFNNQSDLEKEMQKMNPYKIDIGAVYSHRPNQHNTVKLGAFQAQ
EKELVFDIDMTDYDDVRRCCSSADICPKCWTLMTMAIRIIDRALKEDFGFKHRLWVYS
GRRGVHCWVCDESVRKLSSAVRSGIVEYLSLVKGGQDVKKKVHLSEKIHPFIRKSINI
IKKYFEEYALVNQDILENKESWDKILALVPETIHDELQQSFQKSHNSLQRWEHLKKVA
SRYQNNIKNDKYGPWLEWEIMLQYCFPRLDINVSKGINHLLKSPFSVHPKTGRISVPI
DLQKVDQFDPFTVPTISFICRELDAISTNEEEKEENEAESDVKHRTRDYKKTSLAPYV
KVFEHFLENLDKSRKGELLKKSDLQKDF"
```

Other possibility:



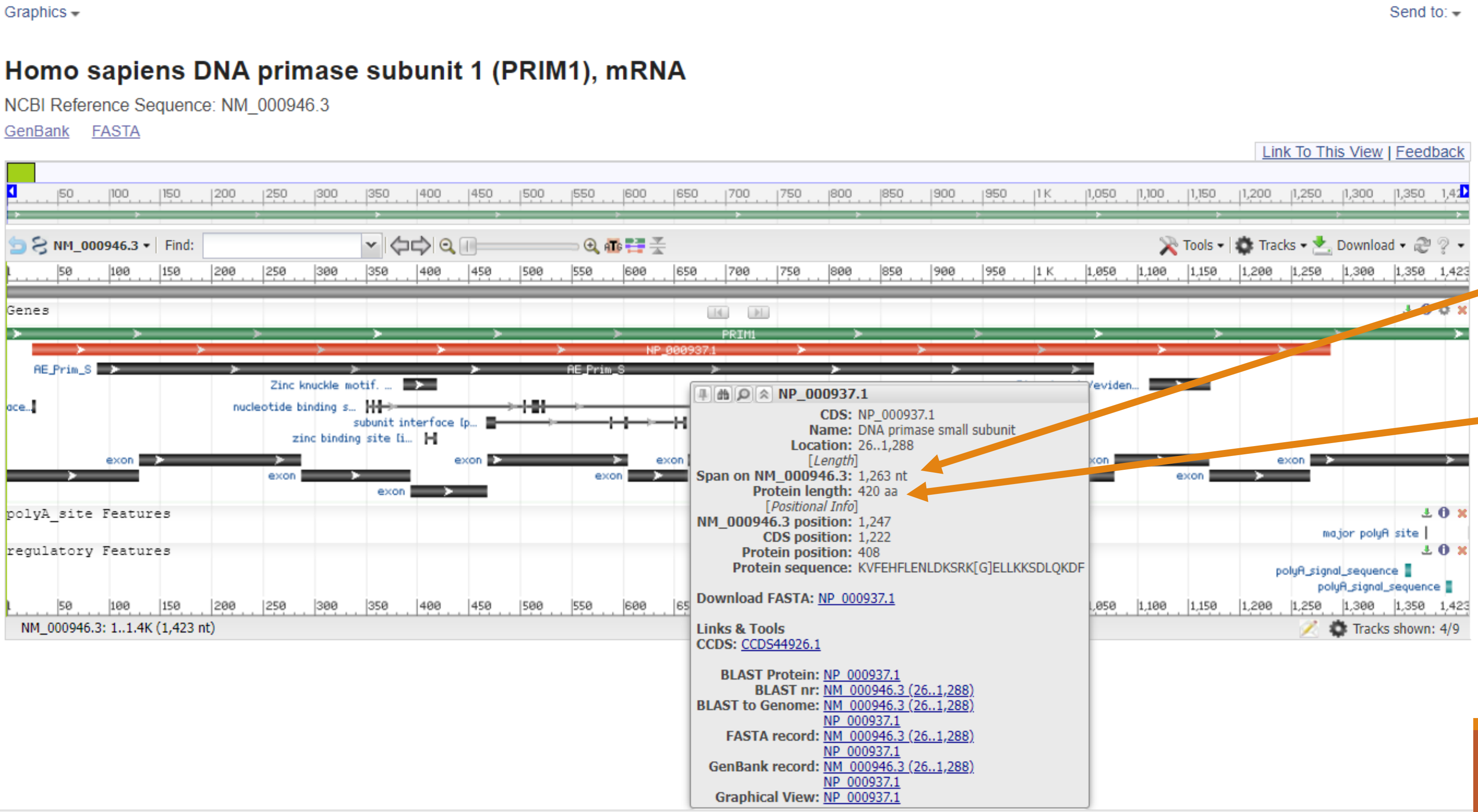
Homo sapiens DNA primase subunit 1 (PRIM1), mRNA

NCBI Reference Sequence: NM_000946.3

FASTA Graphics

Go to:

```
LOCUS       NM_000946                1423 bp    mRNA    linear   PRI 03-APR-2024
DEFINITION  Homo sapiens DNA primase subunit 1 (PRIM1), mRNA.
ACCESSION   NM_000946
```



Homo sapiens DNA primase subunit 1 (PRIM1), mRNA

NCBI Reference Sequence: NM_000946.3

GenBank FASTA

NP_000937.1

CDS: NP_000937.1
Name: DNA primase small subunit
Location: 26..1,288
[Length]
Span on NM_000946.3: 1,263 nt
Protein length: 420 aa
[Positional Info]
NM_000946.3 position: 1,247
CDS position: 1,222
Protein position: 408
Protein sequence: KVFEHFLENLDKSRK[G]ELLKKSDLQKDF

Download FASTA: NP_000937.1

Links & Tools
CCDS: CCDS44926.1

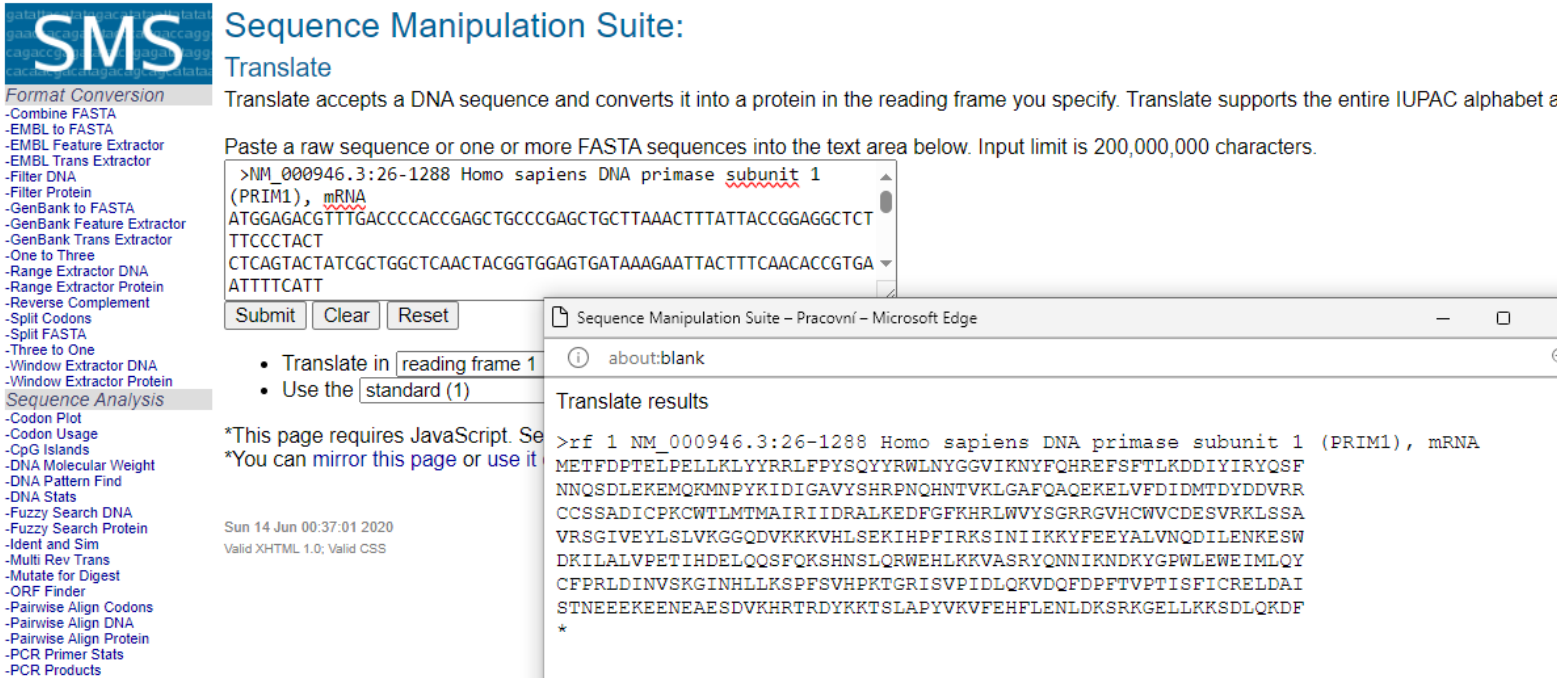
BLAST Protein: NP_000937.1
BLAST nr: NM_000946.3 (26..1,288)
BLAST to Genome: NM_000946.3 (26..1,288)
NP_000937.1
FASTA record: NM_000946.3 (26..1,288)
NP_000937.1
GenBank record: NM_000946.3 (26..1,288)
NP_000937.1
Graphical View: NP_000937.1

CDS

protein

Other option for translated protein:

Translate CDS:



Sequence Manipulation Suite:

Translate

Translate accepts a DNA sequence and converts it into a protein in the reading frame you specify. Translate supports the entire IUPAC alphabet a

Paste a raw sequence or one or more FASTA sequences into the text area below. Input limit is 200,000,000 characters.

```
 >NM_000946.3:26-1288 Homo sapiens DNA primase subunit 1
(PRIM1), mRNA
ATGGAGACGTTTGACCCCACCGAGCTGCCCGAGCTGCTTAAACTTTATTACCGGAGGCTCT
TTCCCTACT
CTCAGTACTATCGCTGGCTCAACTACGGTGGAGTGATAAAGAATTACTTTCAACACCGTGA
ATTTTCATT
```

- Translate in reading frame 1
- Use the standard (1)

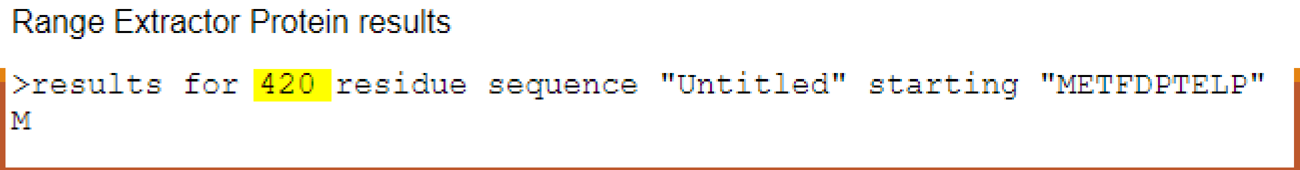
*This page requires JavaScript. Se
*You can mirror this page or use it

Sun 14 Jun 00:37:01 2020
Valid XHTML 1.0; Valid CSS

Translate results

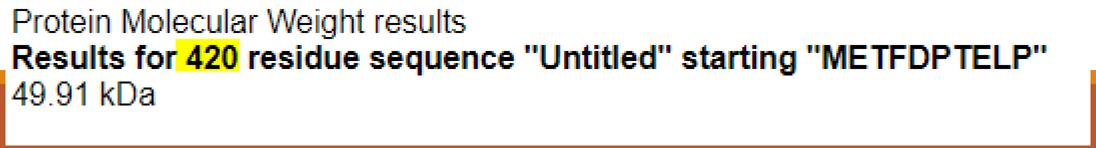
```
>rf 1 NM_000946.3:26-1288 Homo sapiens DNA primase subunit 1 (PRIM1), mRNA
METFDPTELPELLKLYYRRLFPYSQYYRWLNYGGVIKNYFQHREFSFTLKDDIYIRYQSF
NNQSDLEKEMQKMNPYKIDIGAVYSHRPNQHNTVKLGAFQAQEKELVFDIDMTDYDDVRR
CCSSADICPKCWTLMTMAIRIIDRALKEDFGFKHRLWVYSGRRGVHCWVCDESVRKLSSA
VRSGIVEYLSLVKGGQDVKKKVHLSEKIHPFIRKSINIIKKYFEEYALVNQDILENKESW
DKILALVPETIHDELQQSFQKSHNSLQRWEHLKKVASRYQNNIKNDKYGPWLEWEIMLQY
CFPRLDINVSKGINHLLKSPFSVHPKTGRISVPIDLQKVDQFDPFTVPTISFICRELDAI
STNEEEKEENEAESDVKHRTRDYKKTSLAPYVKVFEHFLENLDKSRKGELLKKSDLQKDF
*
```

And copy the protein to protein stats or range extractor protein Mw…all will tell you the length:



Range Extractor Protein results

```
>results for 420 residue sequence "Untitled" starting "METFDPTELP"
M
```



Protein Molecular Weight results

Results for 420 residue sequence "Untitled" starting "METFDPTELP"

49.91 kDa

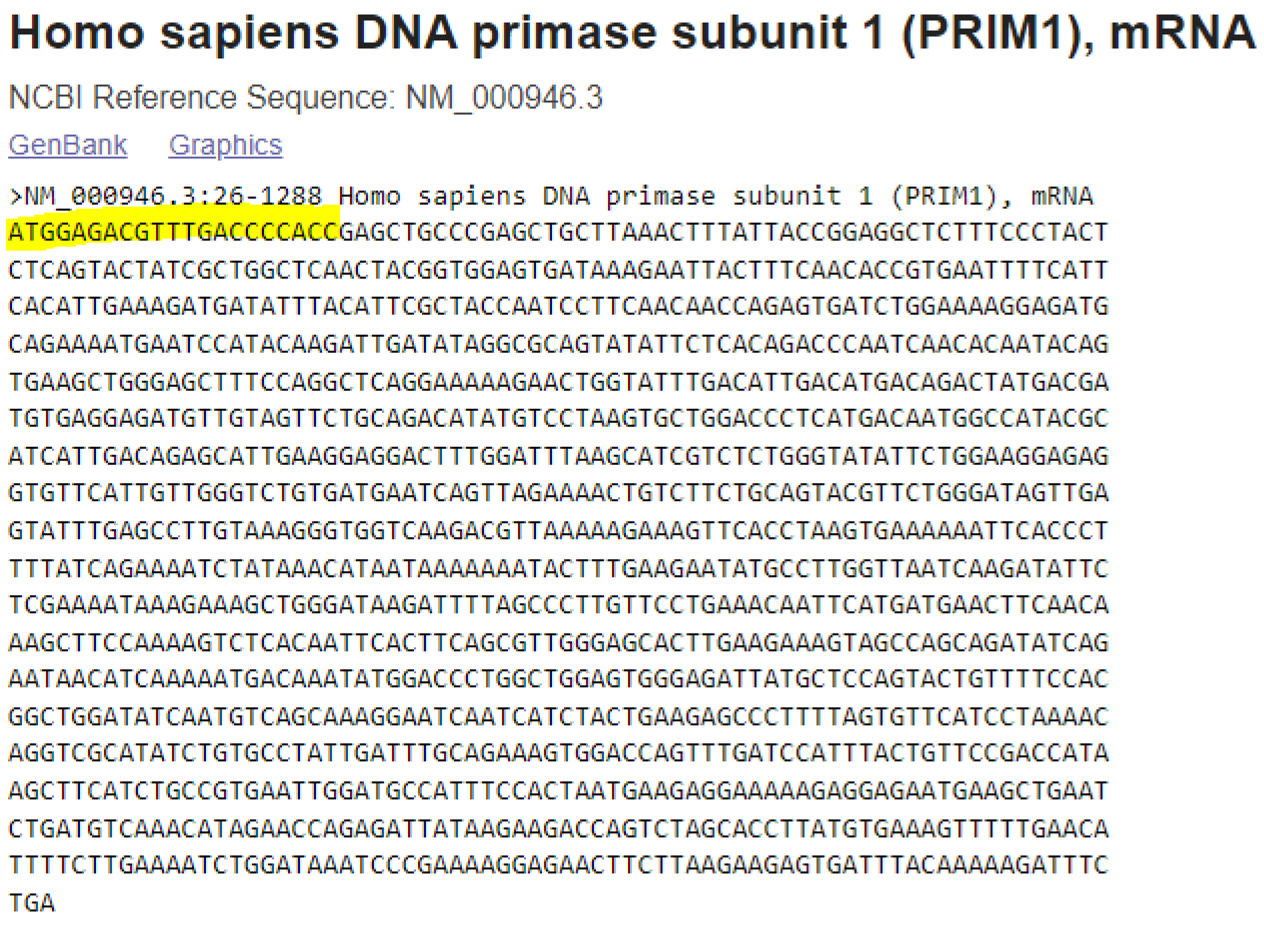
Other option for translated protein: **math**

CDS=1263nt

Triplets for each AA: 1263/3=421 - 1 stop codon (no AA) = 420 AA

Manually design primers for PCR amplification of the CDS.

F: ATG GAG ACG TTT GAC CCC AC

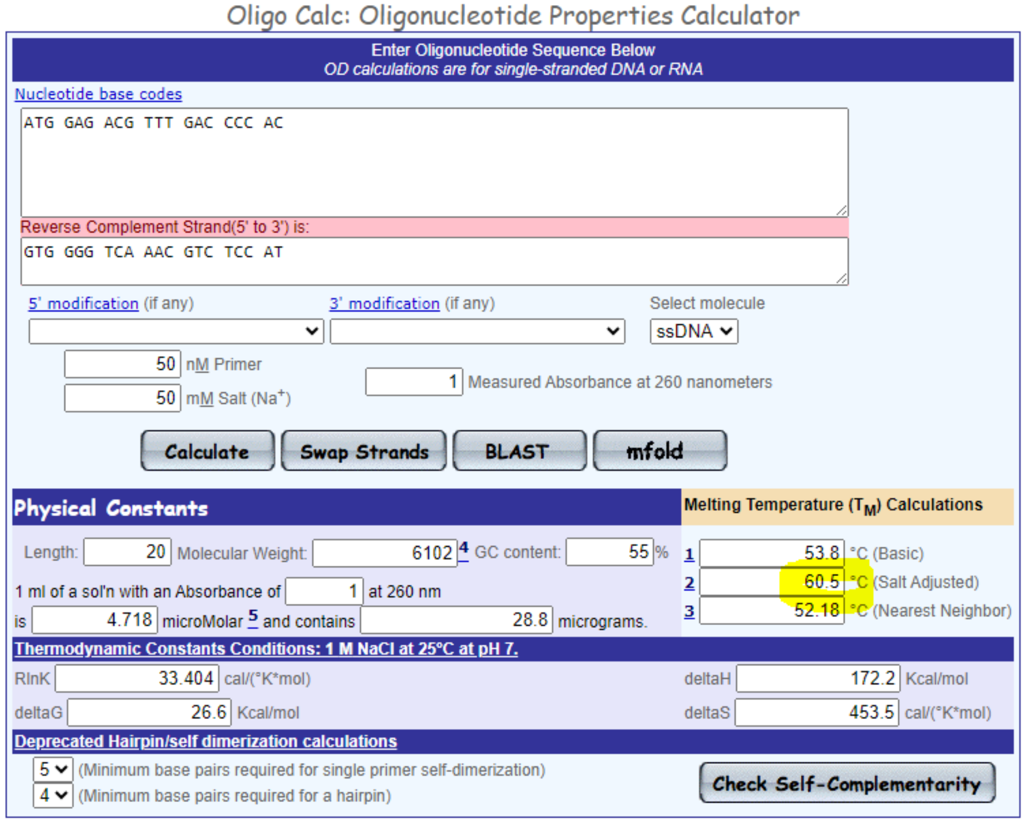


Homo sapiens DNA primase subunit 1 (PRIM1), mRNA

NCBI Reference Sequence: NM_000946.3

GenBank Graphics

```
>NM_000946.3:26-1288 Homo sapiens DNA primase subunit 1 (PRIM1), mRNA
ATGGAGACGTTTGACCCCACCGAGCTGCCCGAGCTGCTTAAACTTTATTACCGGAGGCTCTTTCCCTACT
CTCAGTACTATCGCTGGCTCAACTACGGTGGAGTGATAAAGAATTACTTTCAACACCGTGAATTTTCATT
CACATTGAAAGATGATATTTACATTCGCTACCAATCCTTCAACAACCAGAGTGATCTGGAAAAGGAGATG
CAGAAAATGAATCCATACAAGATTGATATAGGCGCAGTATATTCTCACAGACCCAATCAACACAATACAG
TGAAGCTGGGAGCTTTCCAGGCTCAGGAAAAAGAACTGGTATTTGACATTGACATGACAGACTATGACGA
TGTGAGGAGATGTTGTAGTTCTGCAGACATATGTCCTAAGTGCTGGACCCTCATGACAATGGCCATACGC
ATCATTGACAGAGCATTGAAGGAGGACTTTGGATTTAAGCATCGTCTCTGGGTATATTCTGGAAGGAGAG
GTGTTCATTGTTGGGTCTGTGATGAATCAGTTAGAAAACTGTCTTCTGCAGTACGTTCTGGGATAGTTGA
GTATTTGAGCCTTGTAAAGGGTGGTCAAGACGTTAAAAAGAAAGTTCACCTAAGTGAAAAAATTCACCCT
TTTATCAGAAAATCTATAAACATAATAAAAAAATACTTTGAAGAATATGCCTTGGTTAATCAAGATATTC
TCGAAAATAAAGAAAGCTGGGATAAGATTTTAGCCCTTGTTCCTGAAACAATTCATGATGAACTTCAACA
AAGCTTCCAAAAGTCTCACAATTCACTTCAGCGTTGGGAGCACTTGAAGAAAGTAGCCAGCAGATATCAG
AATAACATCAAAAATGACAAATATGGACCCTGGCTGGAGTGGGAGATTATGCTCCAGTACTGTTTTCCAC
GGCTGGATATCAATGTCAGCAAAGGAATCAATCATCTACTGAAGAGCCCTTTTAGTGTTCATCCTAAAAC
AGGTCGCATATCTGTGCCTATTGATTTGCAGAAAGTGGACCAGTTTGATCCATTTACTGTTCCGACCATA
AGCTTCATCTGCCGTGAATTGGATGCCATTTCCACTAATGAAGAGGAAAAAGAGGAGAATGAAGCTGAAT
CTGATGTCAAACATAGAACCAGAGATTATAAGAAGACCAGTCTAGCACCTTATGTGAAAGTTTTTGAACA
TTTTCTTGAAAATCTGGATAAATCCCGAAAAGGAGAACTTCTTAAGAAGAGTGATTTACAAAAAGATTTC
TGA
```



Oligo Calc: Oligonucleotide Properties Calculator

Enter Oligonucleotide Sequence Below
OD calculations are for single-stranded DNA or RNA

Nucleotide base codes

ATG GAG ACG TTT GAC CCC AC

Reverse Complement Strand(5' to 3') is:

GTG GGG TCA AAC GTC TCC AT

5' modification (if any)

3' modification (if any)

Select molecule: ssDNA

50 nM Primer

50 mM Salt (Na^+)

1 Measured Absorbance at 260 nanometers

Physical Constants

Length: 20 Molecular Weight: 6102 4 GC content: 55 %

1 ml of a sol'n with an Absorbance of 1 at 260 nm

is 4.718 microMolar 5 and contains 28.8 micrograms.

Melting Temperature (T_M) Calculations

1 53.8 °C (Basic)

2 60.5 °C (Salt Adjusted)

3 52.18 °C (Nearest Neighbor)

Thermodynamic Constants Conditions: 1 M NaCl at 25°C at pH 7.

RlnK 33.404 cal/(°K*mol)

deltaH 172.2 Kcal/mol

deltaG 26.6 Kcal/mol

deltaS 453.5 cal/(°K*mol)

Deprecated Hairpin/self dimerization calculations

5 (Minimum base pairs required for single primer self-dimerization)

4 (Minimum base pairs required for a hairpin)

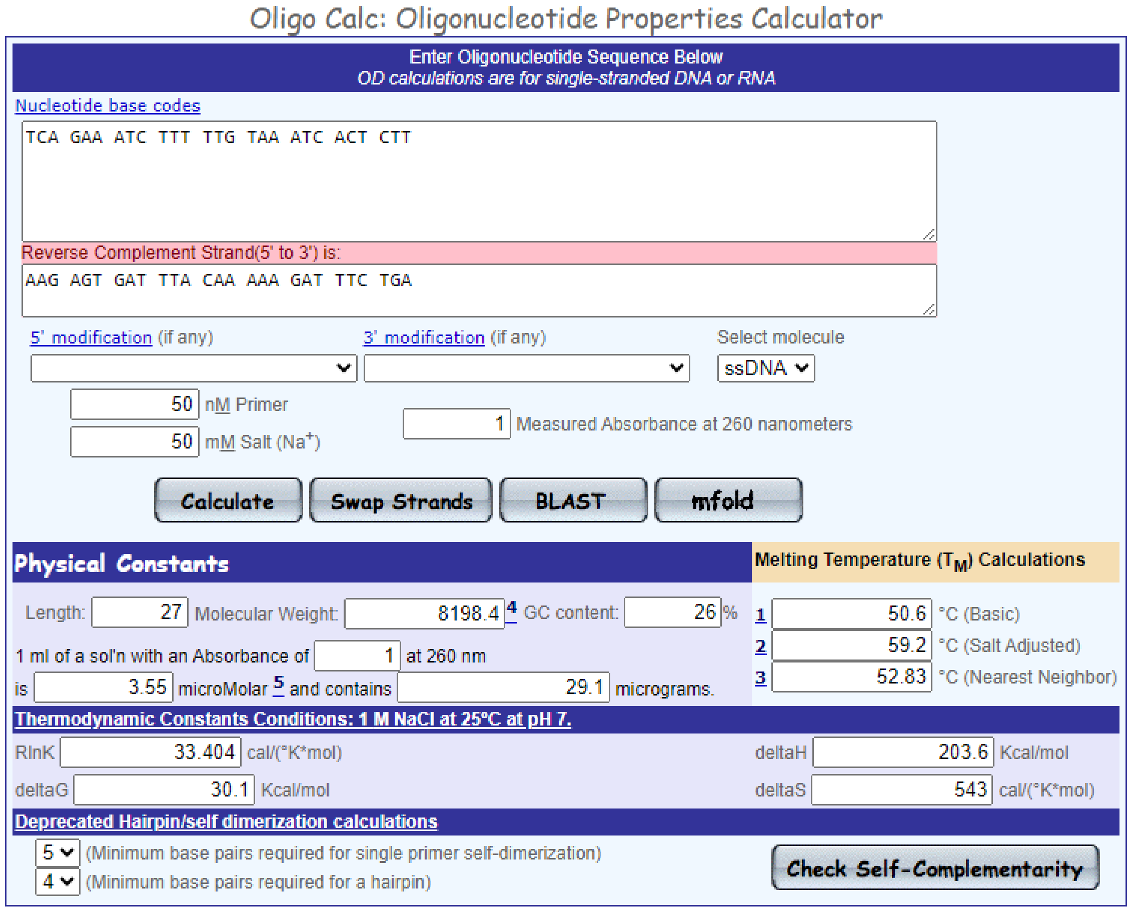
Citation: Kibbe WA. 'OligoCalc: an online oligonucleotide properties calculator'. (2007)

R:TCA GAA ATC TTT TTG TAA ATC ACT CTT

Reverse complement the whole CDS:

Reverse Complement results

```
>NM_000946.3:26-1288 Homo sapiens DNA primase subunit 1 (PRIM1),
TCAGAAATCTTTTTGTAAATCACTCTTCTTAAGAAGTTCTCCTTTTCGGGATTTATCCAG
ATTTTCAAGAAAATGTTCAAAAACTTTCACATAAGGTGCTAGACTGGTCTTCTTATAATC
TCTGGTTCTATGTTTGACATCAGATTCAGCTTCATTCTCCTCTTTTTCCTCTTCATTAGT
GGAAATGGCATCCAATTCACGGCAGATGAAGCTTATGGTCGGAACAGTAAATGGATCAAA
CTGGTCCACTTTCTGCAAATCAATAGGCACAGATATGCGACCTGTTTTAGGATGAACACT
AAAAGGGCTCTTCAGTAGATGATTGATTCCTTTGCTGACATTGATATCCAGCCGTGGAAA
ACAGTACTGGAGCATAATCTCCCACTCCAGCCAGGGTCCATATTTGTCATTTTTGATGTT
ATTCTGATATCTGCTGGCTACTTTCTTCAAGTGCTCCCAACGCTGAAGTGAATTGTGAGA
CTTTTGGAAGCTTTGTTGAAGTTCATCATGAATTGTTTCAGGAACAAGGGCTAAAATCTT
ATCCCAGCTTTCTTTATTTTCGAGAATATCTTGATTAACCAAGGCATATTCTTCAAAGTA
TTTTTTTATTATGTTTATAGATTTTCTGATAAAAGGGTGAATTTTTTCACTTAGGTGAAC
TTTCTTTTTAACGTCTTGACCACCCTTTACAAGGCTCAAATACTCAACTATCCCAGAACG
TACTGCAGAAGACAGTTTTCTAACTGATTCATCACAGACCCAACAATGAACACCTCTCCT
TCCAGAATATACCCAGAGACGATGCTTAAATCCAAAGTCCTCCTTCAATGCTCTGTCAAT
GATGCGTATGGCCATTGTCATGAGGGTCCAGCACTTAGGACATATGTCTGCAGAACTACA
ACATCTCCTCACATCGTCATAGTCTGTCATGTCAATGTCAAATACCAGTTCTTTTTCCTG
AGCCTGGAAAGCTCCCAGCTTCACTGTATTGTGTTGATTGGGTCTGTGAGAATATACTGC
GCCTATATCAATCTTGTATGGATTCATTTTCTGCATCTCCTTTTCCAGATCACTCTGGTT
```



Oligo Calc: Oligonucleotide Properties Calculator

Enter Oligonucleotide Sequence Below
OD calculations are for single-stranded DNA or RNA

Nucleotide base codes

```
TCA GAA ATC TTT TTG TAA ATC ACT CTT
```

Reverse Complement Strand(5' to 3') is:

```
AAG AGT GAT TTA CAA AAA GAT TTC TGA
```

5' modification (if any):
3' modification (if any):
Select molecule: ssDNA

50 nM Primer
50 mM Salt (Na$^+$)
1 Measured Absorbance at 260 nanometers

Physical Constants

Length: 27 Molecular Weight: 8198.4 [4] GC content: 26 %

1 ml of a sol'n with an Absorbance of 1 at 260 nm

is 3.55 microMolar [5] and contains 29.1 micrograms.

Melting Temperature (T_M) Calculations

[1] 50.6 °C (Basic)
[2] 59.2 °C (Salt Adjusted)
[3] 52.83 °C (Nearest Neighbor)

Thermodynamic Constants Conditions: 1 M NaCl at 25°C at pH 7.

RlnK 33.404 cal/(°K*mol)
deltaH 203.6 Kcal/mol
deltaG 30.1 Kcal/mol
deltaS 543 cal/(°K*mol)

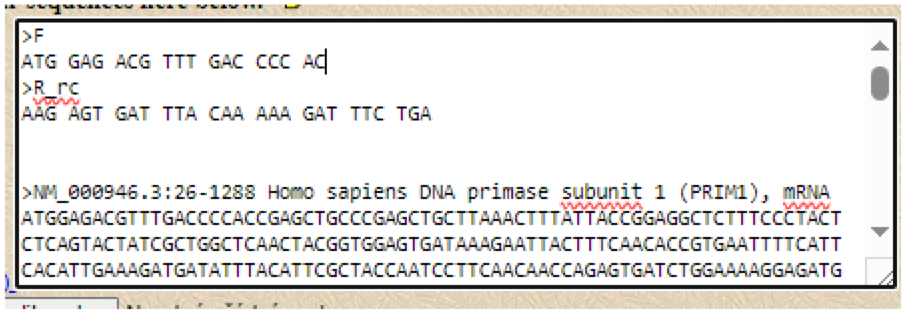
Deprecated Hairpin/self dimerization calculations

5 (Minimum base pairs required for single primer self-dimerization)
4 (Minimum base pairs required for a hairpin)

Citation: Kibbe WA. 'OligoCalc: an online oligonucleotide properties calculator'. (2007).

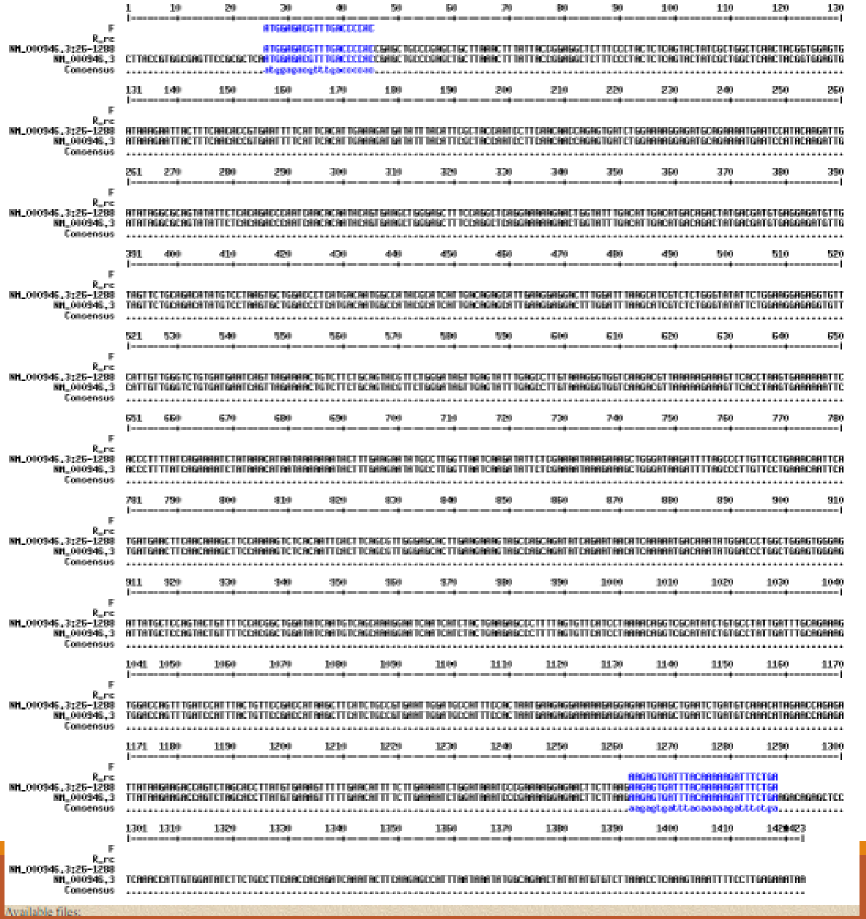
Compare the designed primers with the sequence of the mRNA and the CDS.

Multalin (don´t forget to reverse complement the primer for comparison



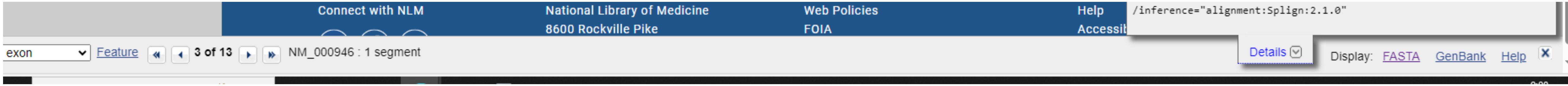
```
>F
ATG GAG ACG TTT GAC CCC AC
>R_rc
AAG AGT GAT TTA CAA AAA GAT TTC TGA


>NM_000946.3:26-1288 Homo sapiens DNA primase subunit 1 (PRIM1), mRNA
ATGGAGACGTTTGACCCCACCGAGCTGCCCGAGCTGCTTAAACTTTATTACCGGAGGCTCTTTCCCTACT
CTCAGTACTATCGCTGGCTCAACTACGGTGGAGTGATAAAGAATTACTTTCAACACCGTGAATTTTCATT
CACATTGAAAGATGATATTTACATTCGCTACCAATCCTTCAACAACCAGAGTGATCTGGAAAAGGAGATG
```



Is there a restriction enzyme that would cut the sequence of **the third exon** exactly once?

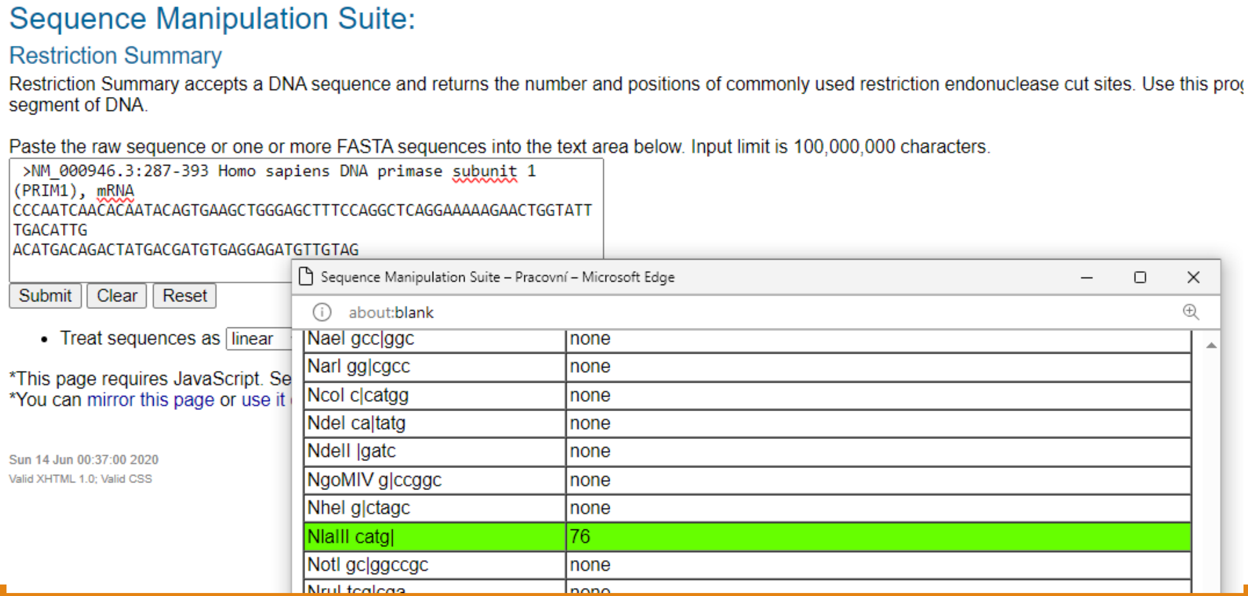
Get the 3rd exon:



```
/inference="alignment:Splign:2.1.0"
```

Restriction summary:

Answer:yes NlaIII



Sequence Manipulation Suite:

Restriction Summary

Restriction Summary accepts a DNA sequence and returns the number and positions of commonly used restriction endonuclease cut sites. Use this prog segment of DNA.

Paste the raw sequence or one or more FASTA sequences into the text area below. Input limit is 100,000,000 characters.

```
 >NM_000946.3:287-393 Homo sapiens DNA primase subunit 1
(PRIM1), mRNA
CCCAATCAACACAATACAGTGAAGCTGGGAGCTTTCCAGGCTCAGGAAAAAGAACTGGTATT
TGACATTG
ACATGACAGACTATGACGATGTGAGGAGATGTTGTAG
```

- Treat sequences as linear

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NaeI gcc|ggc	none
NarI gg|cgcc	none
NcoI c|catgg	none
NdeI ca|tatg	none
NdeII |gatc	none
NgoMIV g|ccggc	none
NheI g|ctagc	none
NlaIII catg|	76
NotI gc|ggccgc	none
NruI tcg|cga	none

B: Work with following peptide sequence:

LALASVFWSISYYSSPFAFFYLYRKGYLSLSKVVPFSHYAGTLLLLLAGVACLRGIGRWT

NPQYRQFITILEATHRNQSSENKRQLANYNFDFRSWPVDFHWEEPSSRKESRGGPSRRGV

ALLRPEPLHRGTADTLLNRVKKLPCQITSYLVAHTLGRRMLYPGSVYLLQKALMPVLLQG

QARLVEECNGRRAKLLACDGNEIDTMFVDRRGTAEPQGQKLVICCEGNAGFYEVGCVSTP

LEACYSVLGWNHPGFAGSTGVPFPQNEANAMDVVVQFAIHRLGFQPQDIIIYAWSIGGFT

1) To which human protein this peptide probably belongs?
2) Does this peptide contain any transmembrane helices?
3) What is molecular weigth of this peptide?
4) How does a given peptide sequence differ from an identified (human) sequence (within the same segment)? **2025:** We did not cover this one
5) Write down the identified mutation. **2025:** We did not cover this one

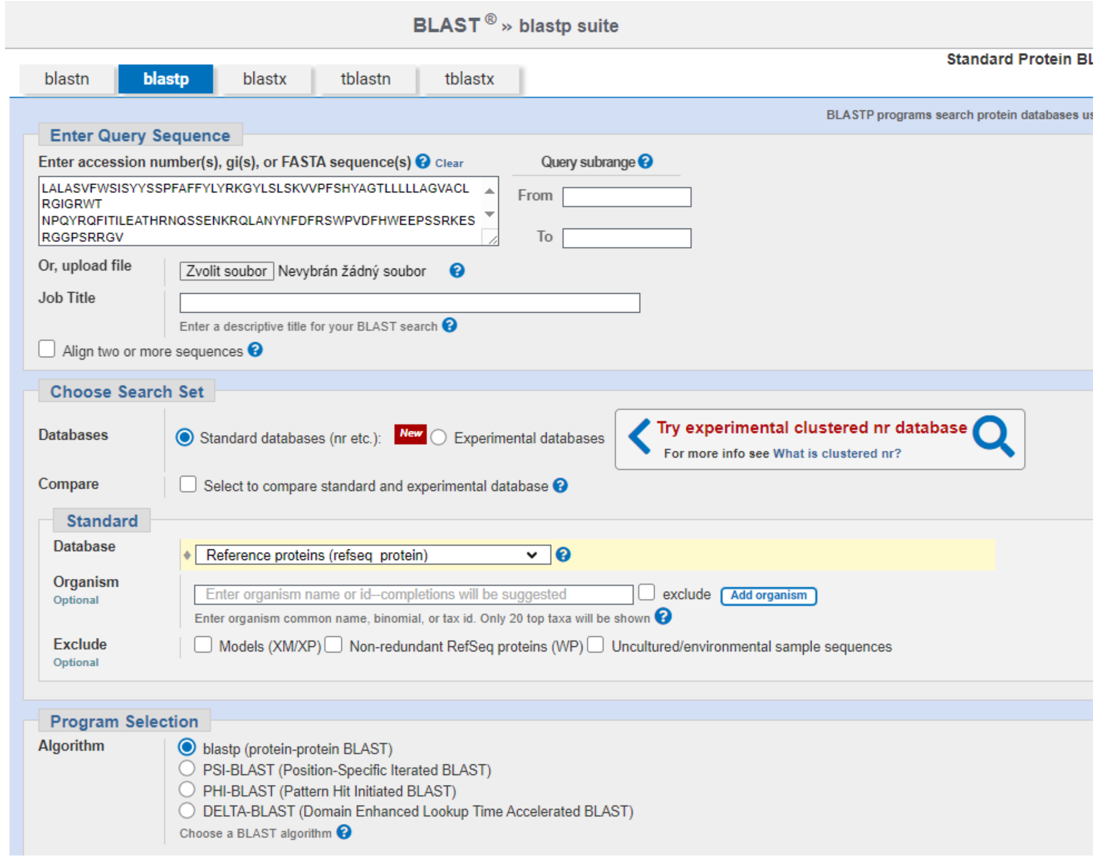
B: Work with following peptide sequence:

```
LALASVFWSISYYSSPFAFFYLYRKGYLSLSKVVPFSHYAGTLLLLLAGVACLRGIGRWT

NPQYRQFITILEATHRNQSSENKRQLANYNFDFRSWPVDFHWEEPSSRKESRGGPSRRGV

ALLRPEPLHRGTADTLLNRVKKLPCQITSYLVAHTLGRRMLYPGSVYLLQKALMPVLLQG

QARLVEECNGRRAKLLACDGNEIDTMFVDRRGTAEPQGQKLVICCEGNAGFYEVGCVSTP

LEACYSVLGWNHPGFAGSTGVPFPQNEANAMDVVVQFAIHRLGFQPQDIIIYAWSIGGFT
```

1) To which human protein this peptide probably belongs? →BLASTp
2) Does this peptide contain any transmembrane helices? →TMHMM, TopCons…
3) What is molecular weigth of this peptide? →SMS/Protein Molecular weight
4) How does a given peptide sequence differ from an identified (human) sequence (within the same segment)? **2025:** We did not cover this one
5) Write down the identified mutation. **2025:** We did not cover this one

To which human protein this peptide probably belongs?

BLASTp



Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) Clear

```
LALASVFWSISYYSSPFAFFYLYRKGYLSLSKVVPFSHYAGTLLLLLAGVACL
RGIGRWT
NPQYRQFITILEATHRNQSSENKRQLANYNFDFRSWPVDFHWEEPSSRKES
RGGPSRRGV
```

Query subrange

From

To

Or, upload file: Zvolit soubor Nevybrán žádný soubor

Job Title: Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Databases: ● Standard databases (nr etc.): New ○ Experimental databases

Try experimental clustered nr database
For more info see What is clustered nr?

Compare: ☐ Select to compare standard and experimental database

Standard

Database: Reference proteins (refseq_protein)

Organism (Optional): Enter organism name or id--completions will be suggested ☐ exclude Add organism

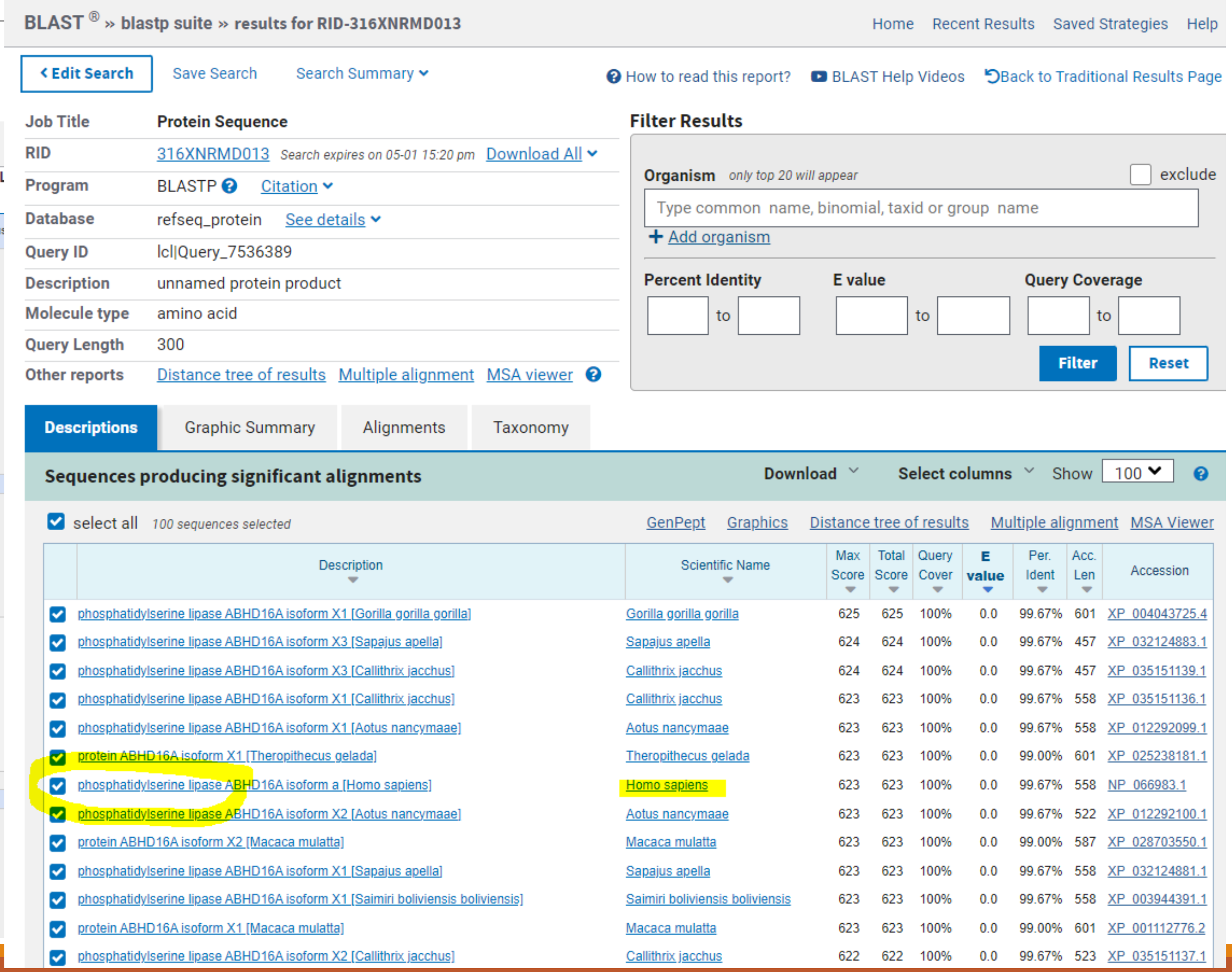
Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

Exclude (Optional): ☐ Models (XM/XP) ☐ Non-redundant RefSeq proteins (WP) ☐ Uncultured/environmental sample sequences

Program Selection

Algorithm:
● blastp (protein-protein BLAST)
○ PSI-BLAST (Position-Specific Iterated BLAST)
○ PHI-BLAST (Pattern Hit Initiated BLAST)
○ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm



Job Title	Protein Sequence
RID	316XNRMD013 Search expires on 05-01 15:20 pm Download All
Program	BLASTP Citation
Database	refseq_protein See details
Query ID	lcl|Query_7536389
Description	unnamed protein product
Molecule type	amino acid
Query Length	300
Other reports	Distance tree of results Multiple alignment MSA viewer

Filter Results

Organism only top 20 will appear ☐ exclude

Type common name, binomial, taxid or group name

+ Add organism

Percent Identity ___ to ___ E value ___ to ___ Query Coverage ___ to ___

Filter Reset

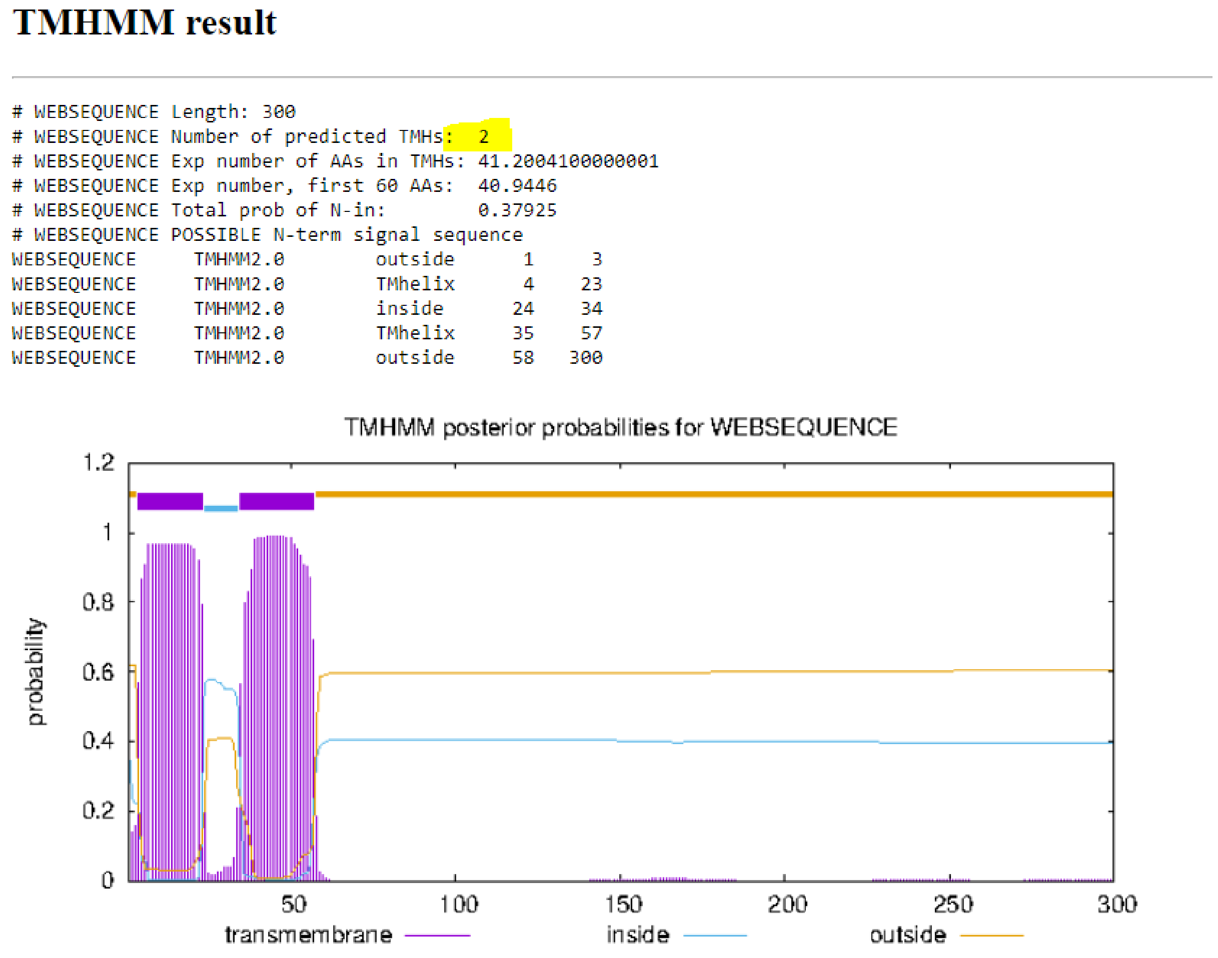
Sequences producing significant alignments

☑ select all 100 sequences selected

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	phosphatidylserine lipase ABHD16A isoform X1 [Gorilla gorilla gorilla]	Gorilla gorilla gorilla	625	625	100%	0.0	99.67%	601	XP_004043725.4
☑	phosphatidylserine lipase ABHD16A isoform X3 [Sapajus apella]	Sapajus apella	624	624	100%	0.0	99.67%	457	XP_032124883.1
☑	phosphatidylserine lipase ABHD16A isoform X3 [Callithrix jacchus]	Callithrix jacchus	624	624	100%	0.0	99.67%	457	XP_035151139.1
☑	phosphatidylserine lipase ABHD16A isoform X1 [Callithrix jacchus]	Callithrix jacchus	623	623	100%	0.0	99.67%	558	XP_035151136.1
☑	phosphatidylserine lipase ABHD16A isoform X1 [Aotus nancymaae]	Aotus nancymaae	623	623	100%	0.0	99.67%	558	XP_012292099.1
☑	protein ABHD16A isoform X1 [Theropithecus gelada]	Theropithecus gelada	623	623	100%	0.0	99.00%	601	XP_025238181.1
☑	phosphatidylserine lipase ABHD16A isoform a [Homo sapiens]	Homo sapiens	623	623	100%	0.0	99.67%	558	NP_066983.1
☑	phosphatidylserine lipase ABHD16A isoform X2 [Aotus nancymaae]	Aotus nancymaae	623	623	100%	0.0	99.67%	522	XP_012292100.1
☑	protein ABHD16A isoform X2 [Macaca mulatta]	Macaca mulatta	623	623	100%	0.0	99.00%	587	XP_028703550.1
☑	phosphatidylserine lipase ABHD16A isoform X1 [Sapajus apella]	Sapajus apella	623	623	100%	0.0	99.67%	558	XP_032124881.1
☑	phosphatidylserine lipase ABHD16A isoform X1 [Saimiri boliviensis boliviensis]	Saimiri boliviensis boliviensis	623	623	100%	0.0	99.67%	558	XP_003944391.1
☑	protein ABHD16A isoform X1 [Macaca mulatta]	Macaca mulatta	623	623	100%	0.0	99.00%	601	XP_001112776.2
☑	phosphatidylserine lipase ABHD16A isoform X2 [Callithrix jacchus]	Callithrix jacchus	622	622	100%	0.0	99.67%	523	XP_035151137.1

Does this peptide contain any transmembrane helices?

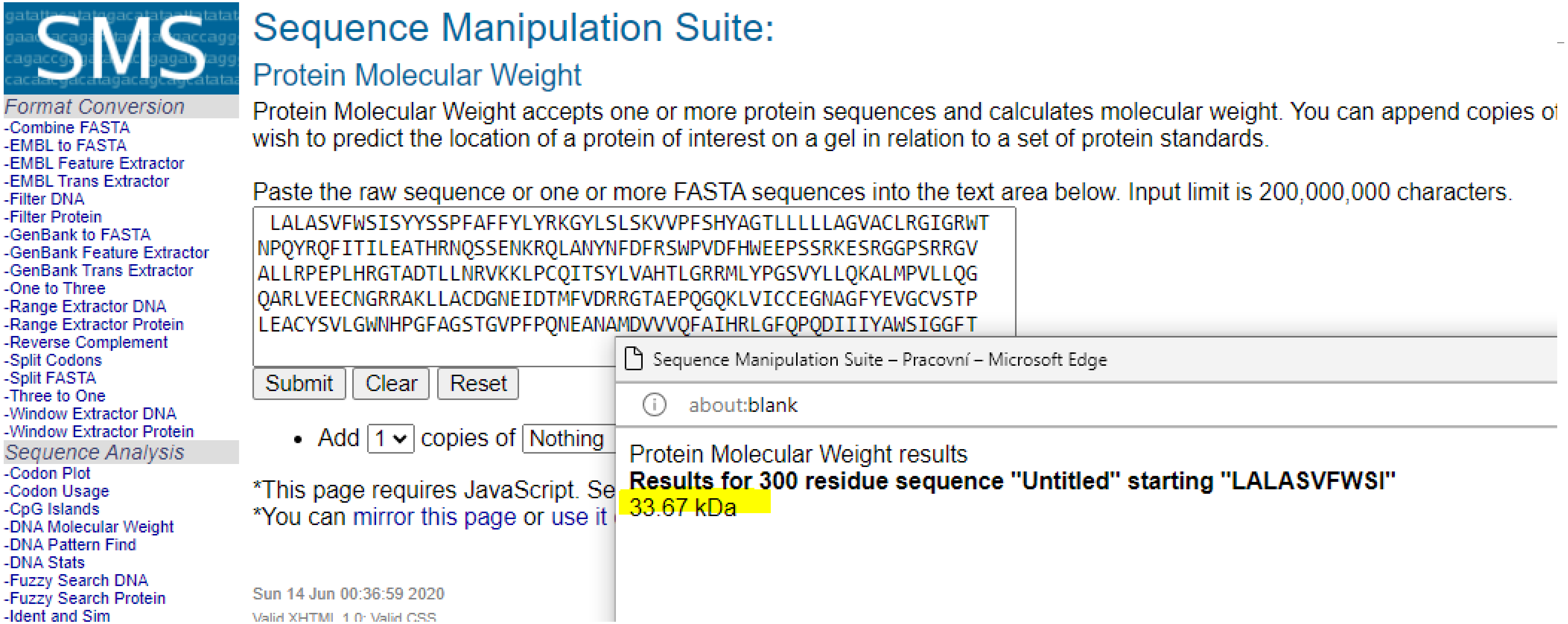
Yes 2.



TMHMM result

```
# WEBSEQUENCE Length: 300
# WEBSEQUENCE Number of predicted TMHs:  2
# WEBSEQUENCE Exp number of AAs in TMHs: 41.2004100000001
# WEBSEQUENCE Exp number, first 60 AAs:  40.9446
# WEBSEQUENCE Total prob of N-in:        0.37925
# WEBSEQUENCE POSSIBLE N-term signal sequence
WEBSEQUENCE     TMHMM2.0        outside      1     3
WEBSEQUENCE     TMHMM2.0        TMhelix      4    23
WEBSEQUENCE     TMHMM2.0        inside      24    34
WEBSEQUENCE     TMHMM2.0        TMhelix     35    57
WEBSEQUENCE     TMHMM2.0        outside     58   300
```

What is molecular weigth of this peptide?



Sequence Manipulation Suite:

Protein Molecular Weight

Protein Molecular Weight accepts one or more protein sequences and calculates molecular weight. You can append copies o
wish to predict the location of a protein of interest on a gel in relation to a set of protein standards.

Paste the raw sequence or one or more FASTA sequences into the text area below. Input limit is 200,000,000 characters.

```
 LALASVFWSISYYSSPFAFFYLYRKGYLSLSKVVPFSHYAGTLLLLLAGVACLRGIGRWT
NPQYRQFITILEATHRNQSSENKRQLANYNFDFRSWPVDFHWEEPSSRKESRGGPSRRGV
ALLRPEPLHRGTADTLLNRVKKLPCQITSYLVAHTLGRRMLYPGSVYLLQKALMPVLLQG
QARLVEECNGRRAKLLACDGNEIDTMFVDRRGTAEPQGQKLVICCEGNAGFYEVGCVSTP
LEACYSVLGWNHPGFAGSTGVPFPQNEANAMDVVVQFAIHRLGFQPQDIIIYAWSIGGFT
```

- Add 1 copies of Nothing

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Valid XHTML 1.0; Valid CSS

Sequence Manipulation Suite – Pracovní – Microsoft Edge

about:blank

Protein Molecular Weight results

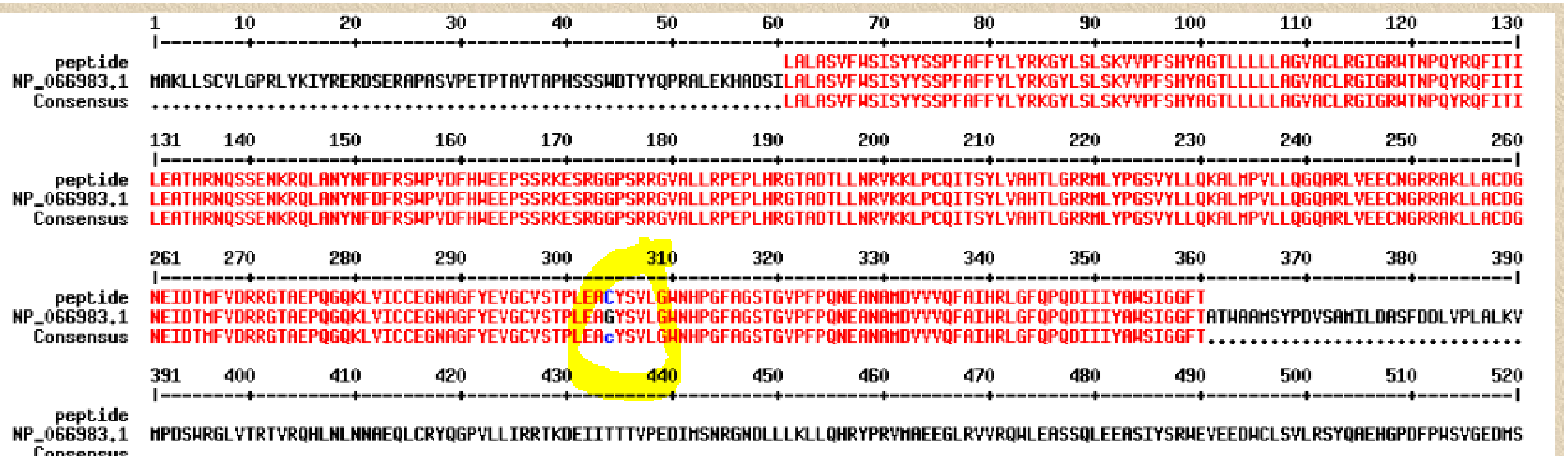
Results for 300 residue sequence "Untitled" starting "LALASVFWSI"

33.67 kDa

How does a given peptide sequence differ from an identified (human) sequence (within the same segment)?

Differs in 1 aminoacid

2025: We did not cover this one



```
            1       10        20        30        40        50        60        70        80        90       100       110       120       130
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
    peptide                                                             LALASVFWSISYYSSPFAFFYLYRKGYLSLSKVVPFSHYAGTLLLLLAGVACLRGIGRWTNPQYRQFITI
NP_066983.1 MAKLLSCVLGPRLYKIYRERDSERAPASVPETPTAVTAPHSSSWDTYYQPRALEKHADSILALASVFWSISYYSSPFAFFYLYRKGYLSLSKVVPFSHYAGTLLLLLAGVACLRGIGRWTNPQYRQFITI
  Consensus ............................................................LALASVFWSISYYSSPFAFFYLYRKGYLSLSKVVPFSHYAGTLLLLLAGVACLRGIGRWTNPQYRQFITI

            131    140       150       160       170       180       190       200       210       220       230       240       250       260
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
    peptide LEATHRNQSSENKRQLANYNFDFRSWPVDFHWEEPSSRKESRGGPSRRGVALLRPEPLHRGTADTLLNRVKKLPCQITSYLVAHTLGRRMLYPGSVYLLQKALMPVLLQGQARLVEECNGRRAKLLACDG
NP_066983.1 LEATHRNQSSENKRQLANYNFDFRSWPVDFHWEEPSSRKESRGGPSRRGVALLRPEPLHRGTADTLLNRVKKLPCQITSYLVAHTLGRRMLYPGSVYLLQKALMPVLLQGQARLVEECNGRRAKLLACDG
  Consensus LEATHRNQSSENKRQLANYNFDFRSWPVDFHWEEPSSRKESRGGPSRRGVALLRPEPLHRGTADTLLNRVKKLPCQITSYLVAHTLGRRMLYPGSVYLLQKALMPVLLQGQARLVEECNGRRAKLLACDG

            261    270       280       290       300       310       320       330       340       350       360       370       380       390
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
    peptide NEIDTMFVDRRGTAEPQGQKLVICCEGNAGFYEVGCVSTPLEACYSVLGWNHPGFAGSTGVPFPQNEANAMDVVVQFAIHRLGFQPQDIIIYAWSIGGFT
NP_066983.1 NEIDTMFVDRRGTAEPQGQKLVICCEGNAGFYEVGCVSTPLEAGYSVLGWNHPGFAGSTGVPFPQNEANAMDVVVQFAIHRLGFQPQDIIIYAWSIGGFTATWAAMSYPDVSAMILDASFDDLVPLALKV
  Consensus NEIDTMFVDRRGTAEPQGQKLVICCEGNAGFYEVGCVSTPLEAcYSVLGWNHPGFAGSTGVPFPQNEANAMDVVVQFAIHRLGFQPQDIIIYAWSIGGFT..............................

            391    400       410       420       430       440       450       460       470       480       490       500       510       520
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
    peptide
NP_066983.1 MPDSWRGLVTRTVRQHLNLNNAEQLCRYQGPVLLIRRTKDEIITTTVPEDIMSNRGNDLLLKLLQHRYPRVMAEEGLRVVRQWLEASSQLEEASIYSRWEVEEDWCLSVLRSYQAEHGPDFPWSVGEDMS
  Consensus
```