Освоение компьютерных программ анализа нуклеотидных и аминокислотных последовательностей: SnapGene (GeneRunner; Vector NTI 11; CLC Sequence Viewer 8)

Преподаватель: старший преподаватель
кафедры молекулярной биологии и генетики,
PhD, Смекенов И.Т.
Дисциплина: Рекомбинация ДНК

(*Лекция 9*)

Цель

Изучить компьютерные программы для анализа нуклеотидных и аминокислотных последовательностей с целью повышения эффективности молекулярно-биологических исследований.

Задачи

1.Ознакомиться с функциональными возможностями программы SnapGene для визуализации и аннотирования ДНК-клонирования.

2.Рассмотреть программу GeneRunner и её применение для анализа нуклеотидных последовательностей.

3.Изучить возможности Vector NTI 11 для работы с последовательностями и проектирования векторов.

4.Оценить функционал CLC Sequence Viewer 8 для многократного выравнивания последовательностей и анализа данных.

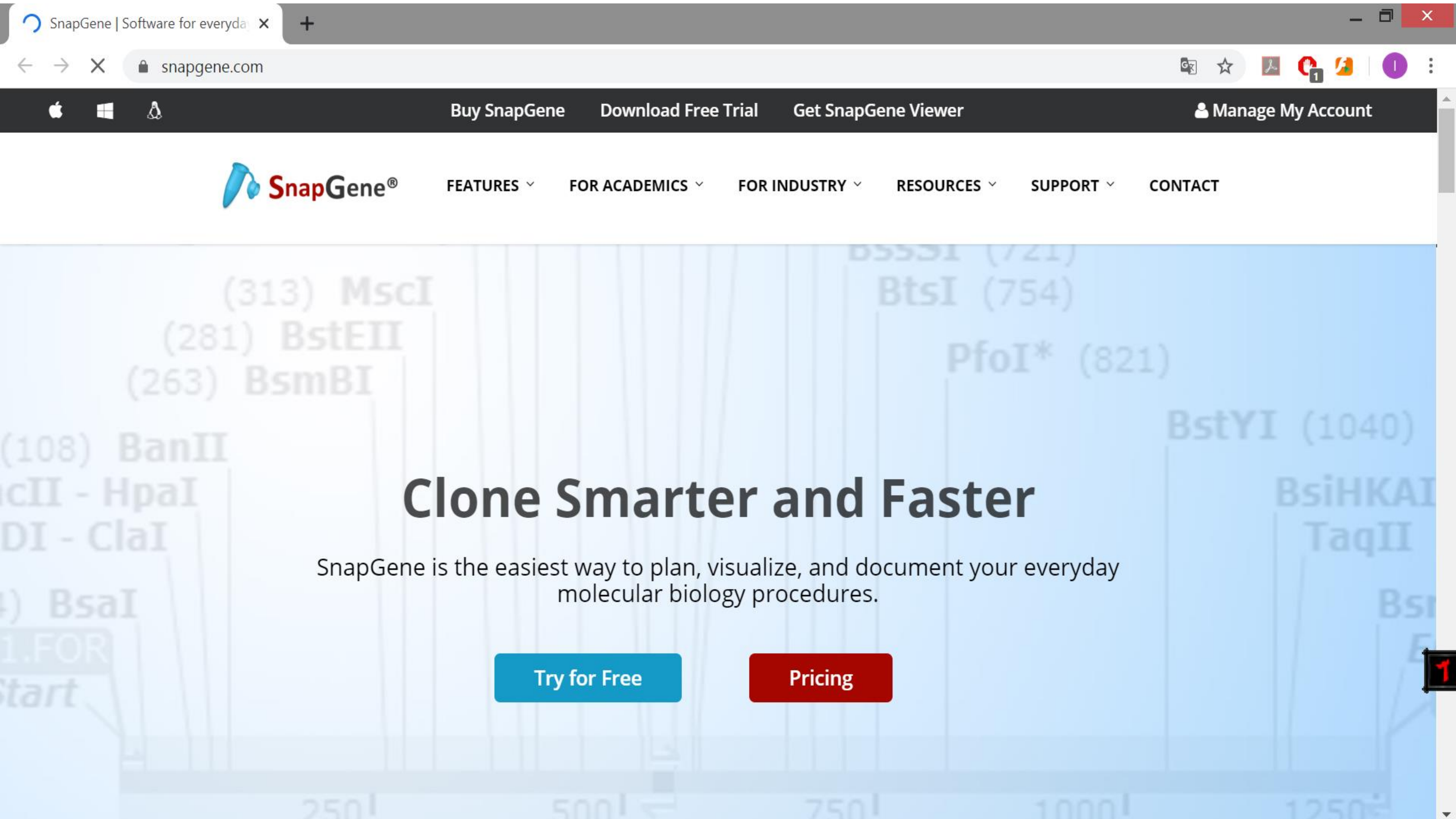
Ключевые слова: *анализ нуклеотидных последовательностей, SnapGene, GeneRunner, Vector NTI 11, CLC Sequence Viewer 8, аминокислотные последовательности, визуализация последовательностей*

SnapGENE – клонируй умнее и быстрее

- это самый простой способ планирования, визуализирования и документирования ваших повседневных процедур молекулярной биологии.

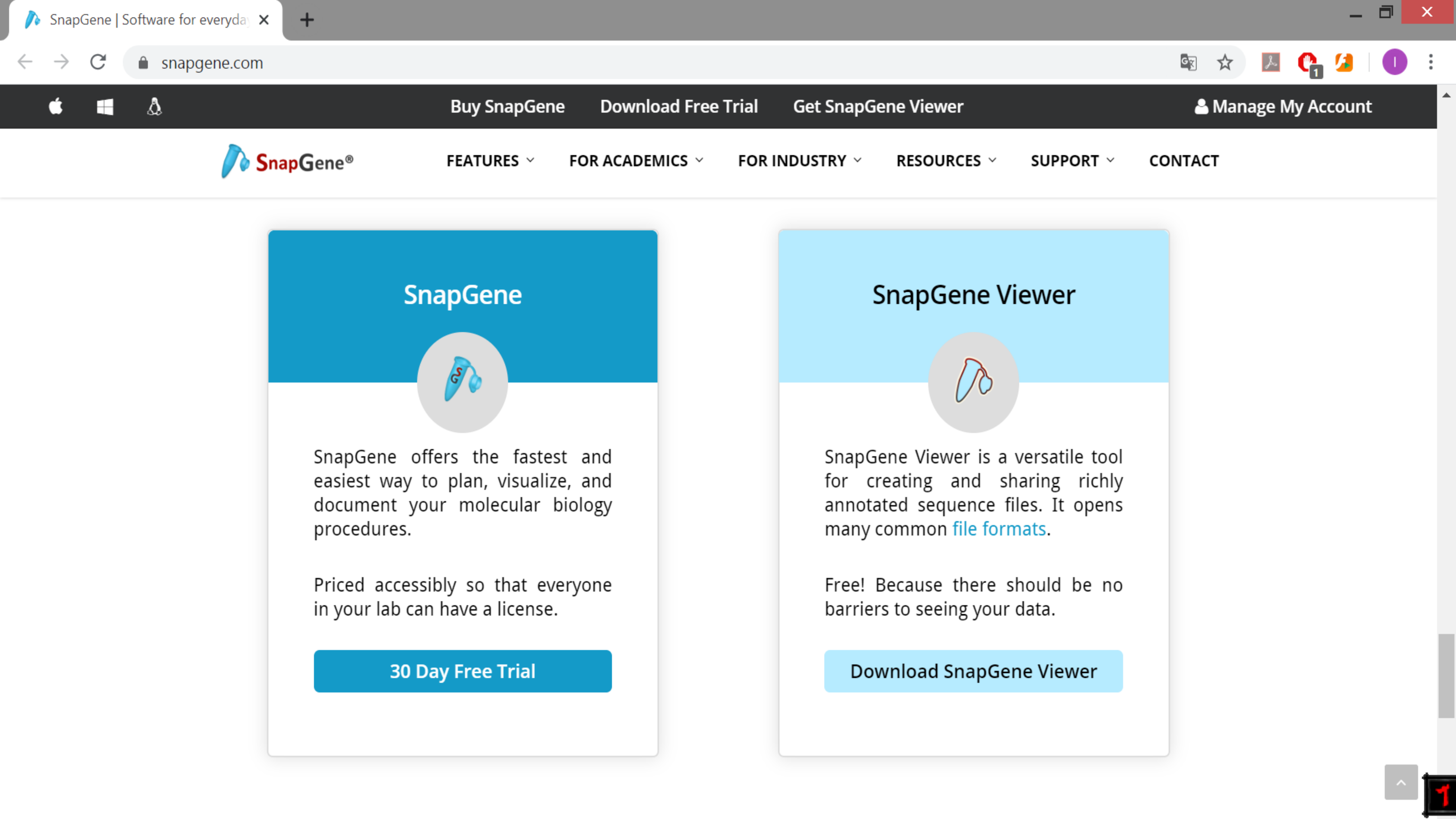
SnapGene®

Software for molecular biology



Clone Smarter and Faster

SnapGene is the easiest way to plan, visualize, and document your everyday molecular biology procedures.



SnapGene

SnapGene offers the fastest and easiest way to plan, visualize, and document your molecular biology procedures.

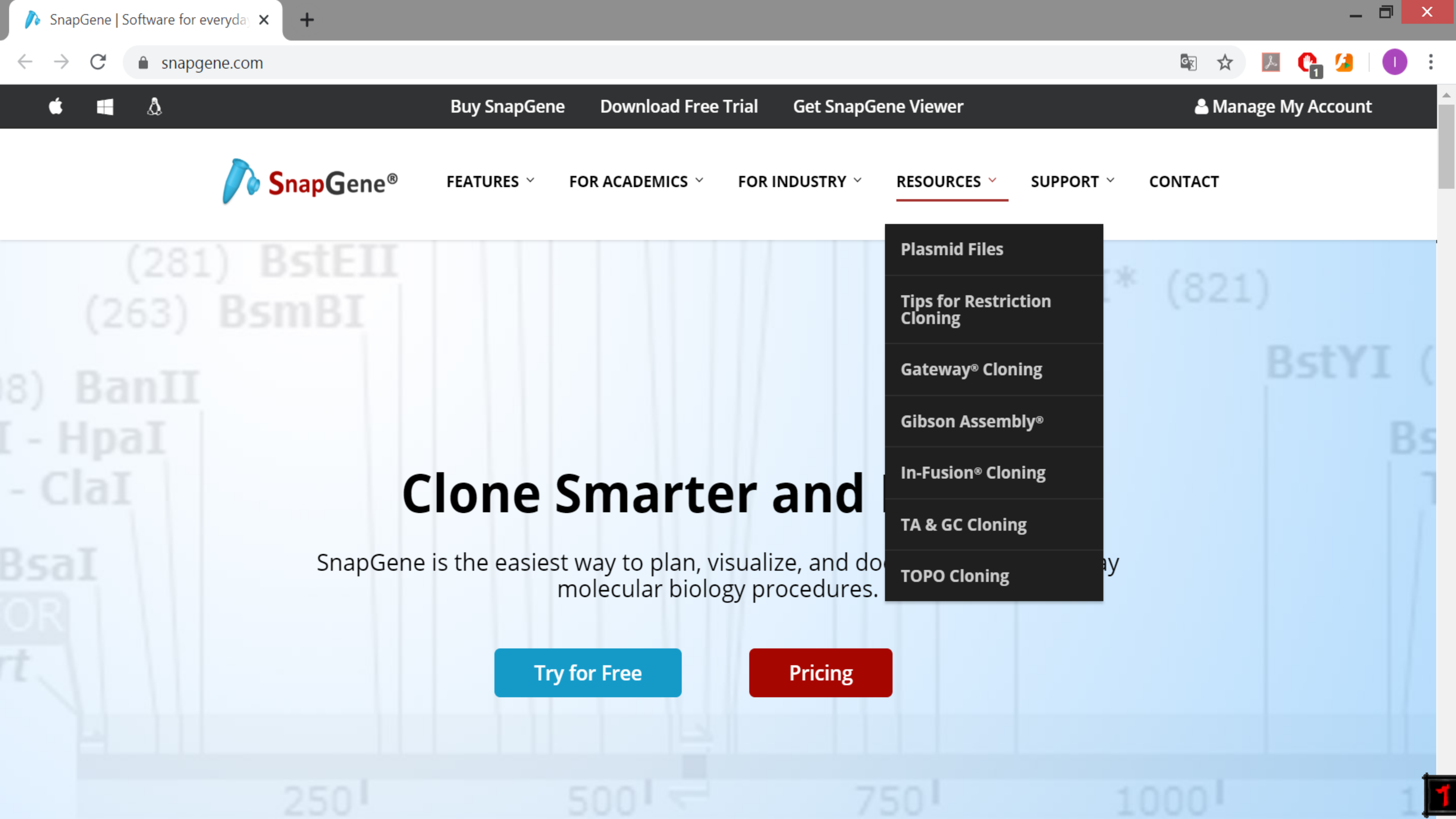
Priced accessibly so that everyone in your lab can have a license.

SnapGene Viewer

SnapGene Viewer is a versatile tool for creating and sharing richly annotated sequence files. It opens many common file formats.

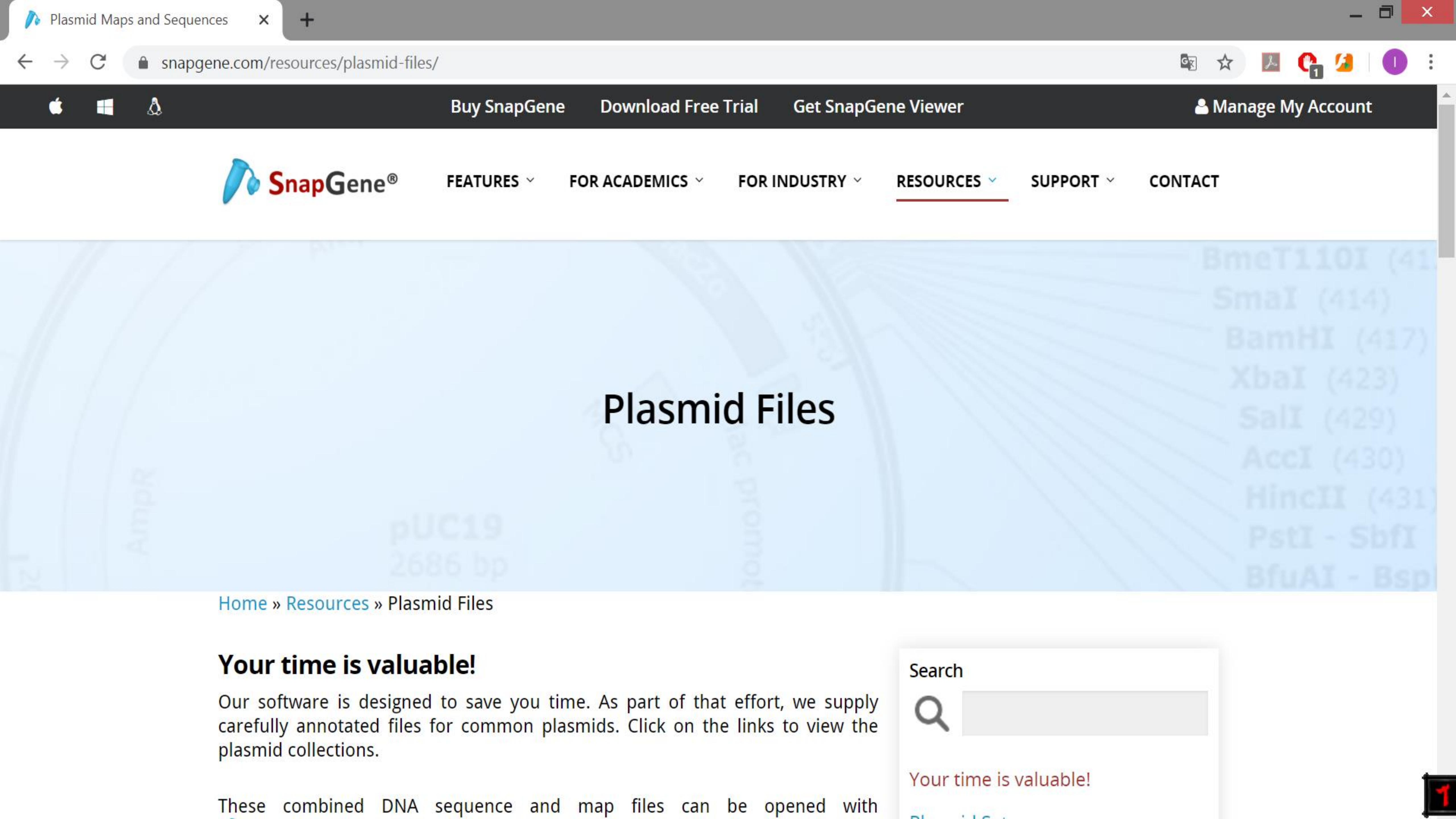
Free! Because there should be no barriers to seeing your data.


Этот компьютер
Новая папка
Корзина
График оплаты 20...
ЭЦП Жанар пароль Аа...
Ахметова Жанар Нұр...
Темірғали Иманали И...
жанар перевод
4x_1172_pl...
SnapGene
SnapGene™ 1.1.3
New DNA File...
Open...
Open Recent
Import from GenBank...
Reference
Help
Exit



Clone Smarter and

SnapGene is the easiest way to plan, visualize, and do … ay
molecular biology procedures.



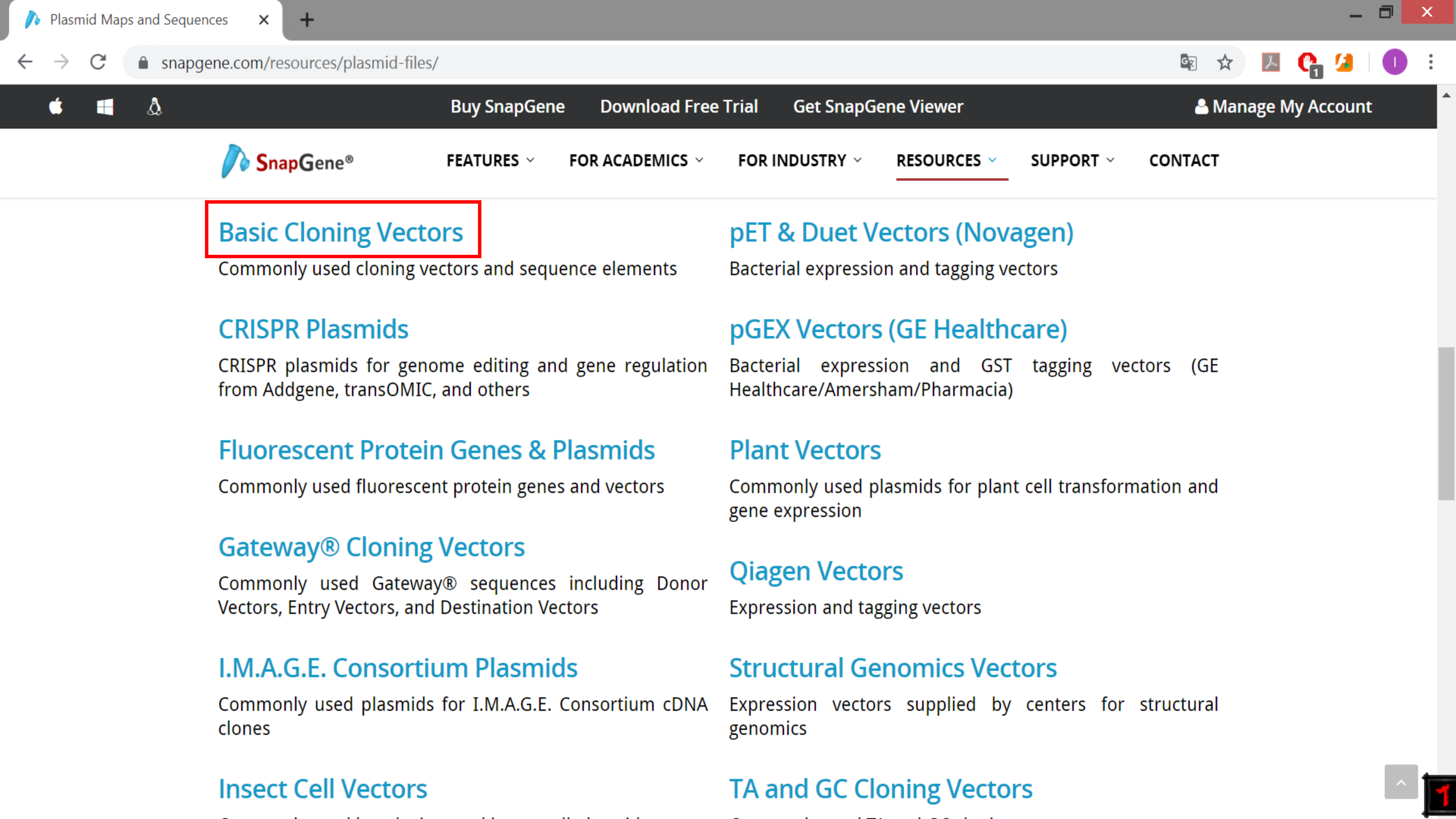
Plasmid Files

Home » Resources » Plasmid Files

Your time is valuable!

Our software is designed to save you time. As part of that effort, we supply carefully annotated files for common plasmids. Click on the links to view the plasmid collections.

These combined DNA sequence and map files can be opened with



Basic Cloning Vectors

Commonly used cloning vectors and sequence elements

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CRISPR plasmids for genome editing and gene regulation from Addgene, transOMIC, and others

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Commonly used fluorescent protein genes and vectors

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Commonly used plasmids for I.M.A.G.E. Consortium cDNA clones

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Commonly used plasmids for plant cell transformation and gene expression

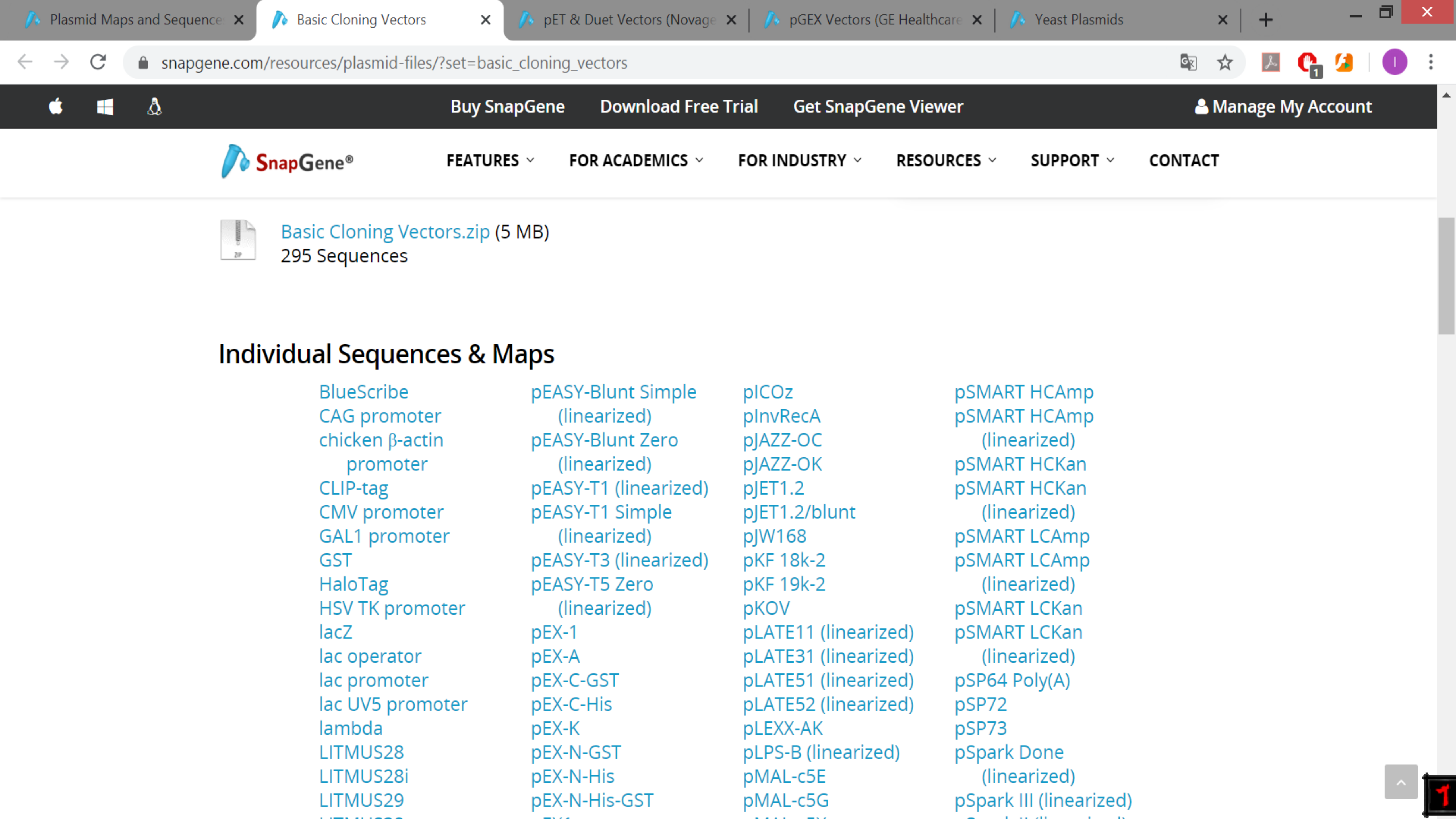
Qiagen Vectors

Expression and tagging vectors

Structural Genomics Vectors

Expression vectors supplied by centers for structural genomics

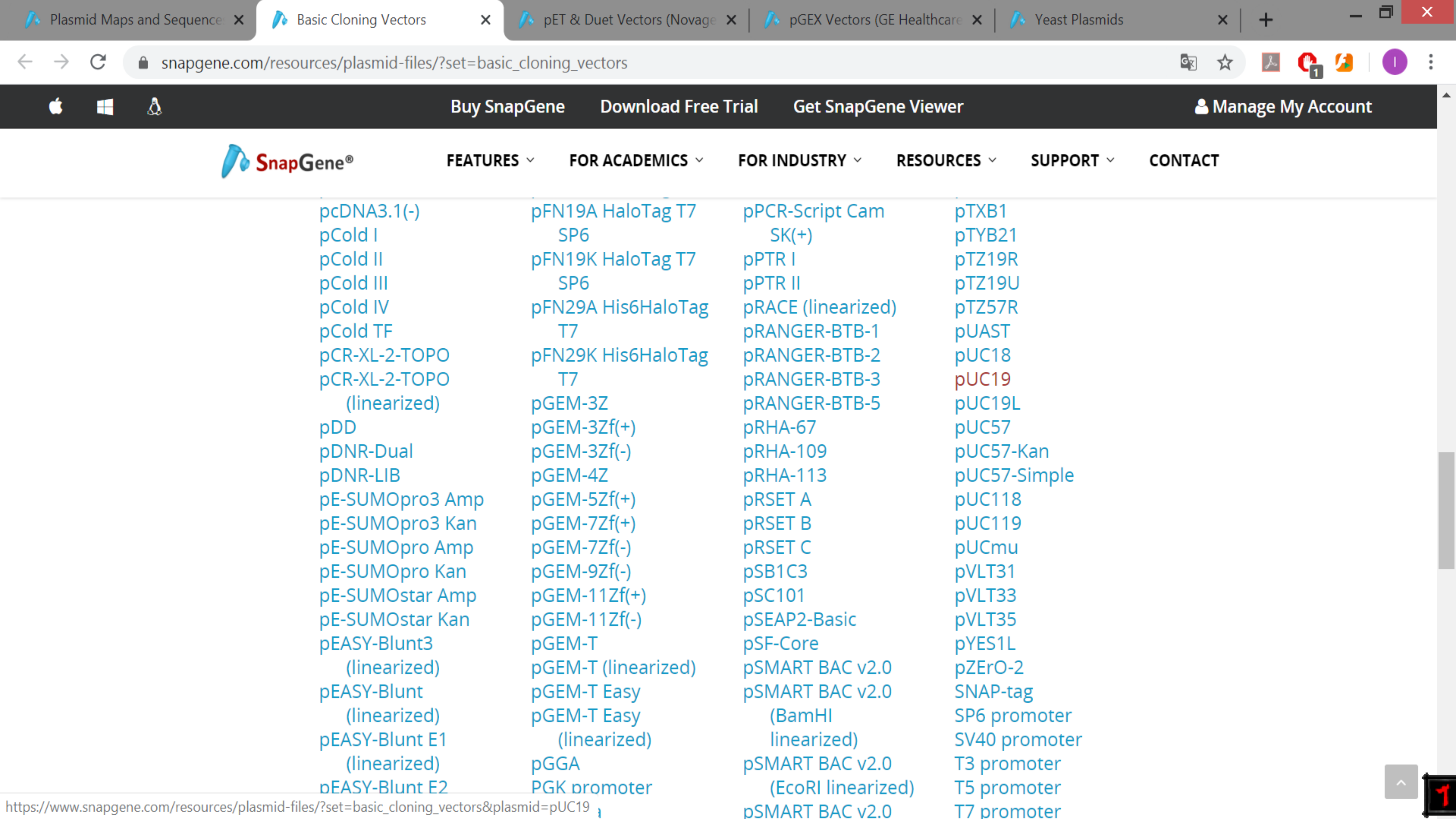
TA and GC Cloning Vectors



Basic Cloning Vectors.zip (5 MB)
295 Sequences

Individual Sequences & Maps

- BlueScribe
- CAG promoter
- chicken β-actin promoter
- CLIP-tag
- CMV promoter
- GAL1 promoter
- GST
- HaloTag
- HSV TK promoter
- lacZ
- lac operator
- lac promoter
- lac UV5 promoter
- lambda
- LITMUS28
- LITMUS28i
- LITMUS29
- pEASY-Blunt Simple (linearized)
- pEASY-Blunt Zero (linearized)
- pEASY-T1 (linearized)
- pEASY-T1 Simple (linearized)
- pEASY-T3 (linearized)
- pEASY-T5 Zero (linearized)
- pEX-1
- pEX-A
- pEX-C-GST
- pEX-C-His
- pEX-K
- pEX-N-GST
- pEX-N-His
- pEX-N-His-GST
- pICOz
- pInvRecA
- pJAZZ-OC
- pJAZZ-OK
- pJET1.2
- pJET1.2/blunt
- pJW168
- pKF 18k-2
- pKF 19k-2
- pKOV
- pLATE11 (linearized)
- pLATE31 (linearized)
- pLATE51 (linearized)
- pLATE52 (linearized)
- pLEXX-AK
- pLPS-B (linearized)
- pMAL-c5E
- pMAL-c5G
- pSMART HCAmp
- pSMART HCAmp (linearized)
- pSMART HCKan
- pSMART HCKan (linearized)
- pSMART LCAmp
- pSMART LCAmp (linearized)
- pSMART LCKan
- pSMART LCKan (linearized)
- pSP64 Poly(A)
- pSP72
- pSP73
- pSpark Done (linearized)
- pSpark III (linearized)



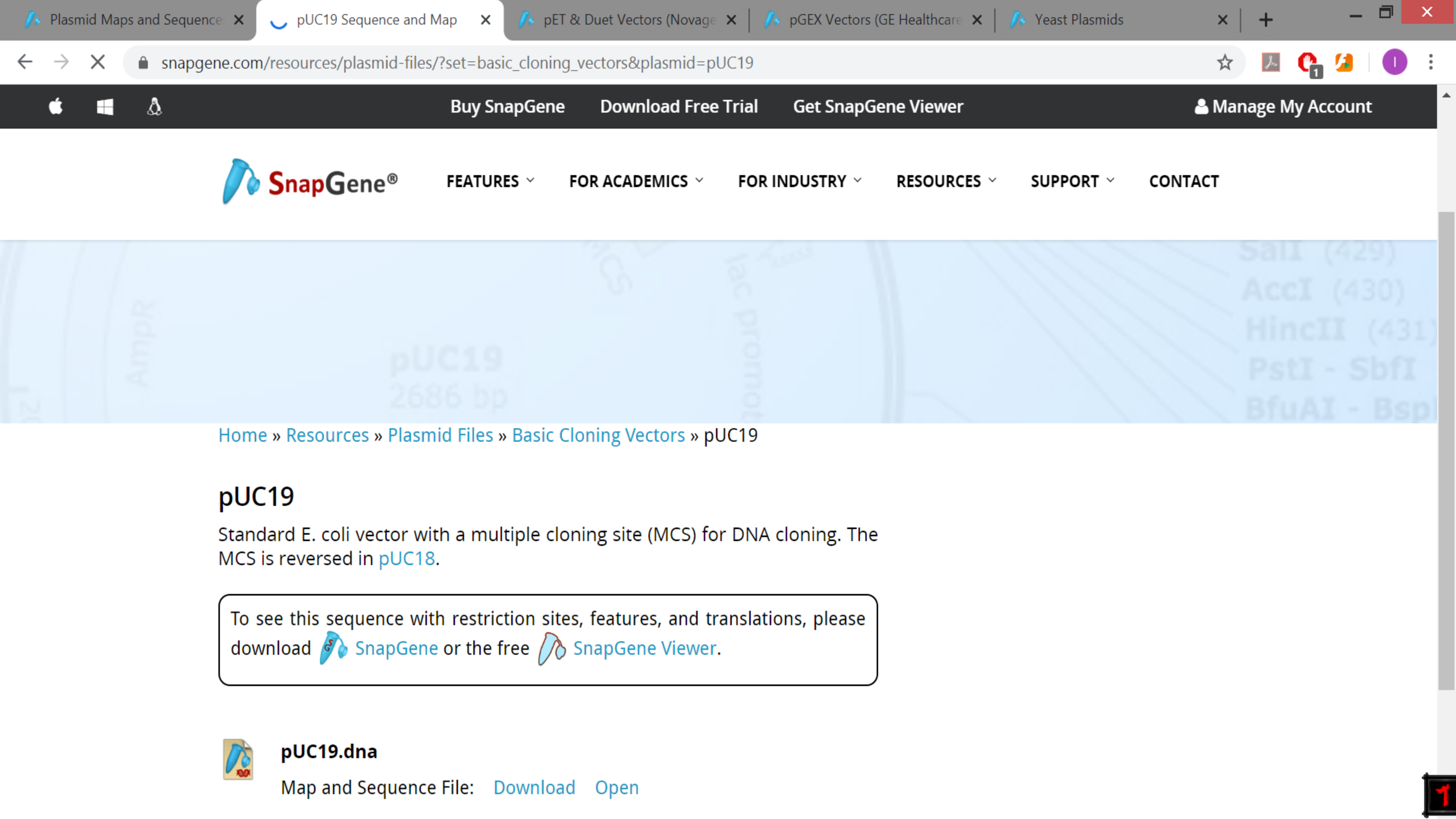
pcDNA3.1(-)
pCold I
pCold II
pCold III
pCold IV
pCold TF
pCR-XL-2-TOPO
pCR-XL-2-TOPO (linearized)
pDD
pDNR-Dual
pDNR-LIB
pE-SUMOpro3 Amp
pE-SUMOpro3 Kan
pE-SUMOpro Amp
pE-SUMOpro Kan
pE-SUMOstar Amp
pE-SUMOstar Kan
pEASY-Blunt3 (linearized)
pEASY-Blunt (linearized)
pEASY-Blunt E1 (linearized)
pEASY-Blunt E2

pFN19A HaloTag T7 SP6
pFN19K HaloTag T7 SP6
pFN29A His6HaloTag T7
pFN29K His6HaloTag T7
pGEM-3Z
pGEM-3Zf(+)
pGEM-3Zf(-)
pGEM-4Z
pGEM-5Zf(+)
pGEM-7Zf(+)
pGEM-7Zf(-)
pGEM-9Zf(-)
pGEM-11Zf(+)
pGEM-11Zf(-)
pGEM-T
pGEM-T (linearized)
pGEM-T Easy
pGEM-T Easy (linearized)
pGGA
PGK promoter

pPCR-Script Cam SK(+)
pPTR I
pPTR II
pRACE (linearized)
pRANGER-BTB-1
pRANGER-BTB-2
pRANGER-BTB-3
pRANGER-BTB-5
pRHA-67
pRHA-109
pRHA-113
pRSET A
pRSET B
pRSET C
pSB1C3
pSC101
pSEAP2-Basic
pSF-Core
pSMART BAC v2.0
pSMART BAC v2.0 (BamHI linearized)
pSMART BAC v2.0 (EcoRI linearized)
pSMART BAC v2.0

pTXB1
pTYB21
pTZ19R
pTZ19U
pTZ57R
pUAST
pUC18
pUC19
pUC19L
pUC57
pUC57-Kan
pUC57-Simple
pUC118
pUC119
pUCmu
pVLT31
pVLT33
pVLT35
pYES1L
pZErO-2
SNAP-tag
SP6 promoter
SV40 promoter
T3 promoter
T5 promoter
T7 promoter

https://www.snapgene.com/resources/plasmid-files/?set=basic_cloning_vectors&plasmid=pUC19



Home » Resources » Plasmid Files » Basic Cloning Vectors » pUC19

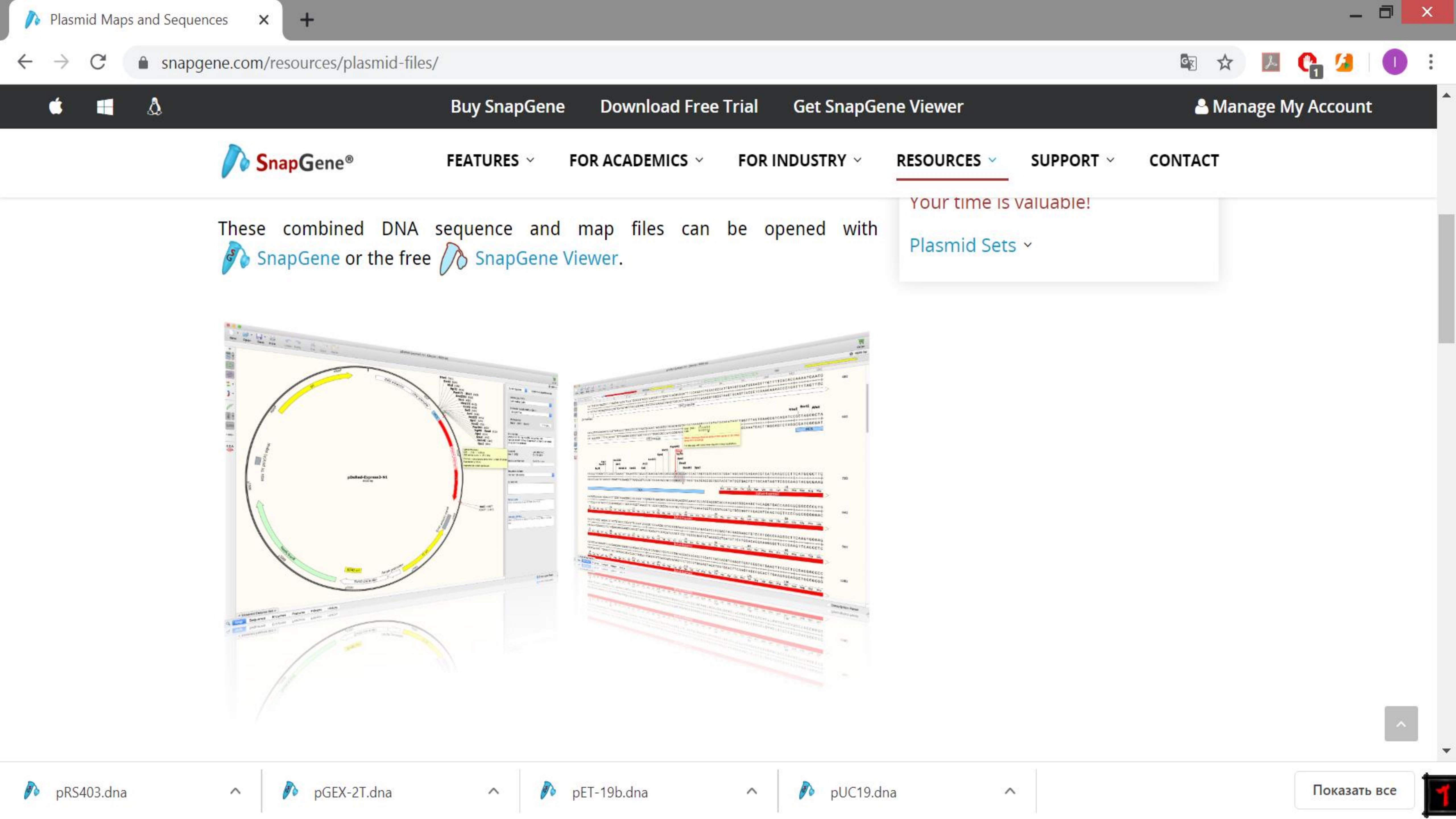
pUC19

Standard E. coli vector with a multiple cloning site (MCS) for DNA cloning. The MCS is reversed in pUC18.

To see this sequence with restriction sites, features, and translations, please download SnapGene or the free SnapGene Viewer.

pUC19.dna

Map and Sequence File: Download Open



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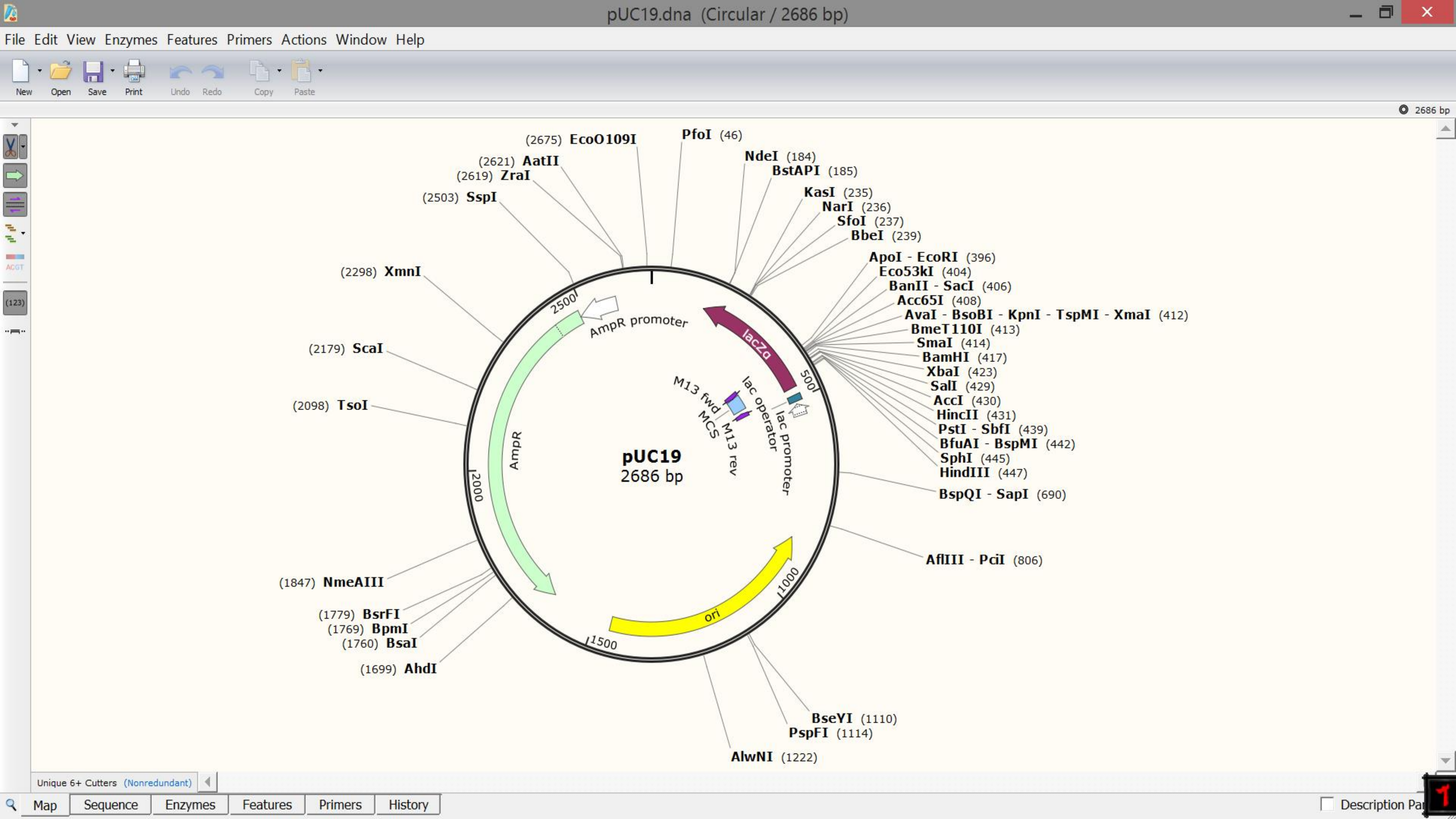
pUC19.dna (Circular / 2686 bp)
File Edit View Enzymes Features Primers Actions Window Help
New
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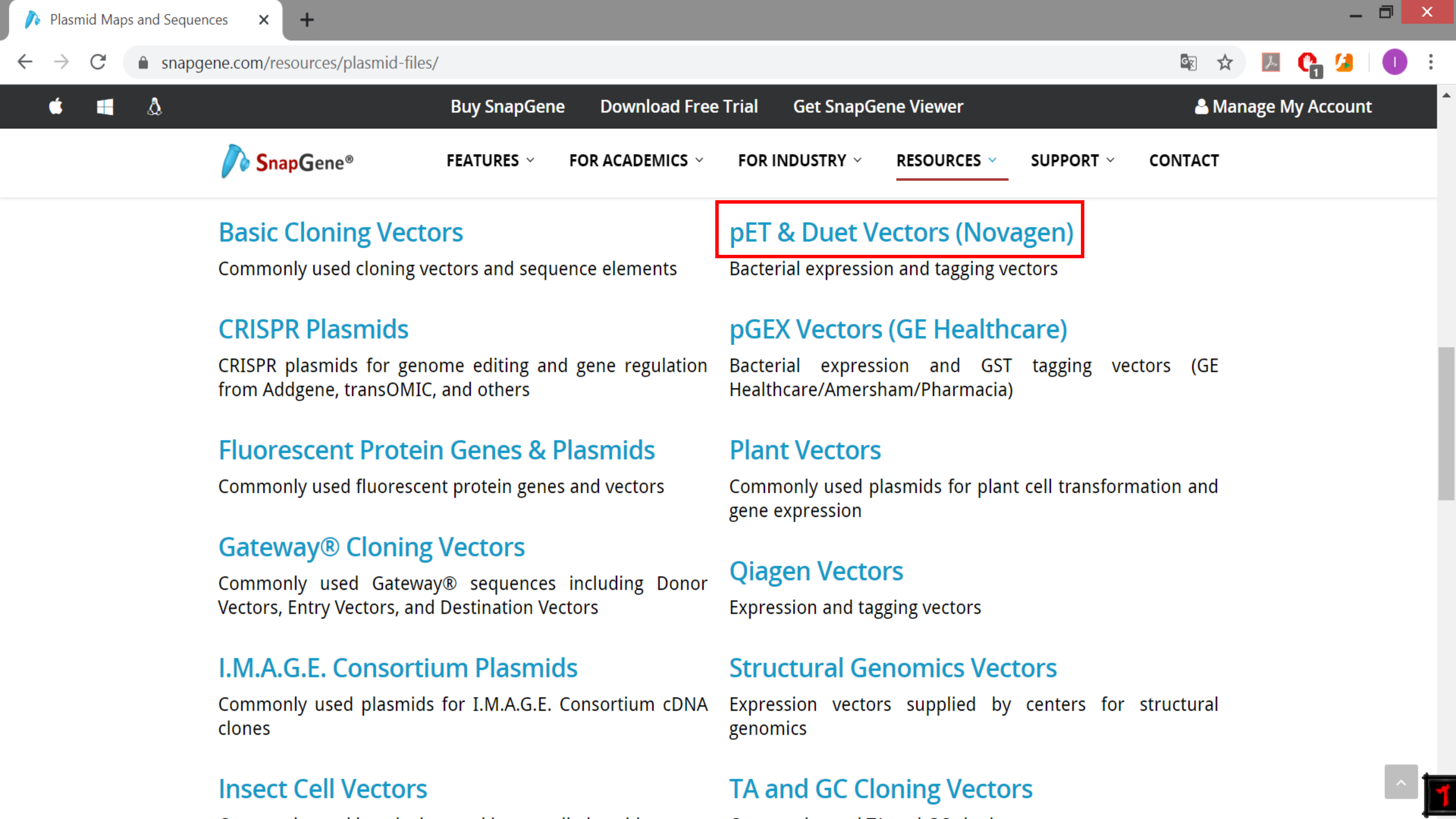
Save
Print
Undo
Redo
Copy
Paste
2686 bp
(123)
(2675) EcoO109I
PfoI (46)
NdeI (184)
BstAPI (185)
(2621) AatII
(2619) ZraI
(2503) SspI
KasI (235)
NarI (236)
SfoI (237)
BbeI (239)
ApoI - EcoRI (396)
Eco53kI (404)
BanII - SacI (406)
Acc65I (408)
AvaI - BsoBI - KpnI - TspMI - XmaI (412)
BmeT110I (413)
SmaI (414)
BamHI (417)
XbaI (423)
SalI (429)
AccI (430)
HincII (431)
PstI - SbfI (439)
BfuAI - BspMI (442)
SphI (445)
HindIII (447)
BspQI - SapI (690)
AflIII - PciI (806)
(2298) XmnI
(2179) ScaI
(2098) TsoI
(1847) NmeAIII
(1779) BsrFI
(1769) BpmI
(1760) BsaI
(1699) AhdI
BseYI (1110)
PspFI (1114)
AlwNI (1222)
AmpR promoter
lacZα
M13 fwd
MCS
M13 rev
lac operator
lac promoter
AmpR
ori
pUC19
2686 bp
2500
500
2000
1000
1500
Unique 6+ Cutters (Nonredundant)
Map
Sequence
Enzymes
Features
Primers
History
Description Pa



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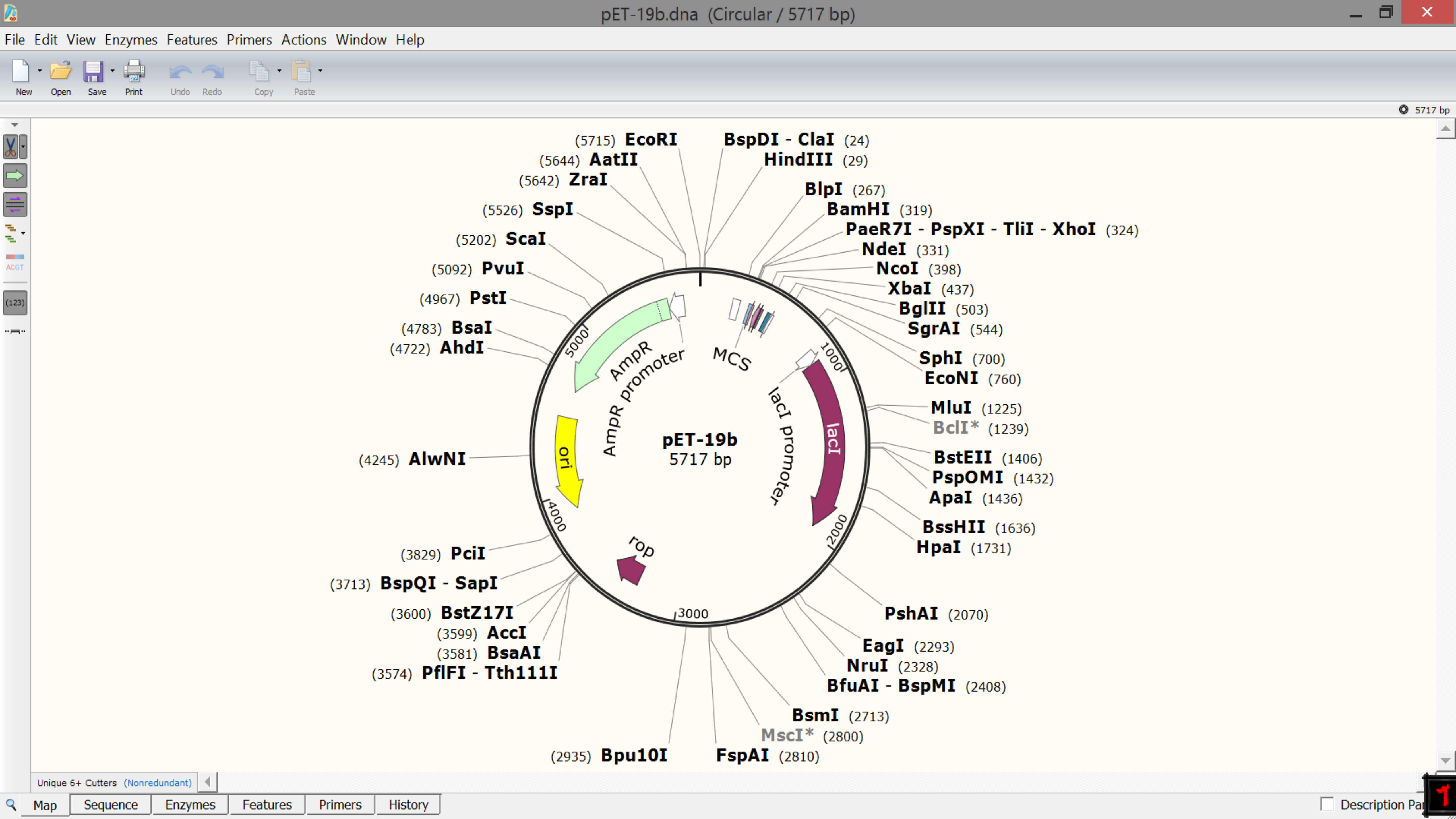
pET-19b.dna (Circular / 5717 bp)
File Edit View Enzymes Features Primers Actions Window Help
New Open Save Print Undo Redo Copy Paste
5717 bp
(5715) EcoRI
(5644) AatII
(5642) ZraI
(5526) SspI
(5202) ScaI
(5092) PvuI
(4967) PstI
(4783) BsaI
(4722) AhdI
(4245) AlwNI
(3829) PciI
(3713) BspQI - SapI
(3600) BstZ17I
(3599) AccI
(3581) BsaAI
(3574) PflFI - Tth111I
(2935) Bpu10I
BspDI - ClaI (24)
HindIII (29)
BlpI (267)
BamHI (319)
PaeR7I - PspXI - TliI - XhoI (324)
NdeI (331)
NcoI (398)
XbaI (437)
BglII (503)
SgrAI (544)
SphI (700)
EcoNI (760)
MluI (1225)
BclI* (1239)
BstEII (1406)
PspOMI (1432)
ApaI (1436)
BssHII (1636)
HpaI (1731)
PshAI (2070)
EagI (2293)
NruI (2328)
BfuAI - BspMI (2408)
BsmI (2713)
MscI* (2800)
FspAI (2810)
pET-19b
5717 bp
AmpR
AmpR promoter
MCS
lacI
lacI promoter
ori
rop
1000
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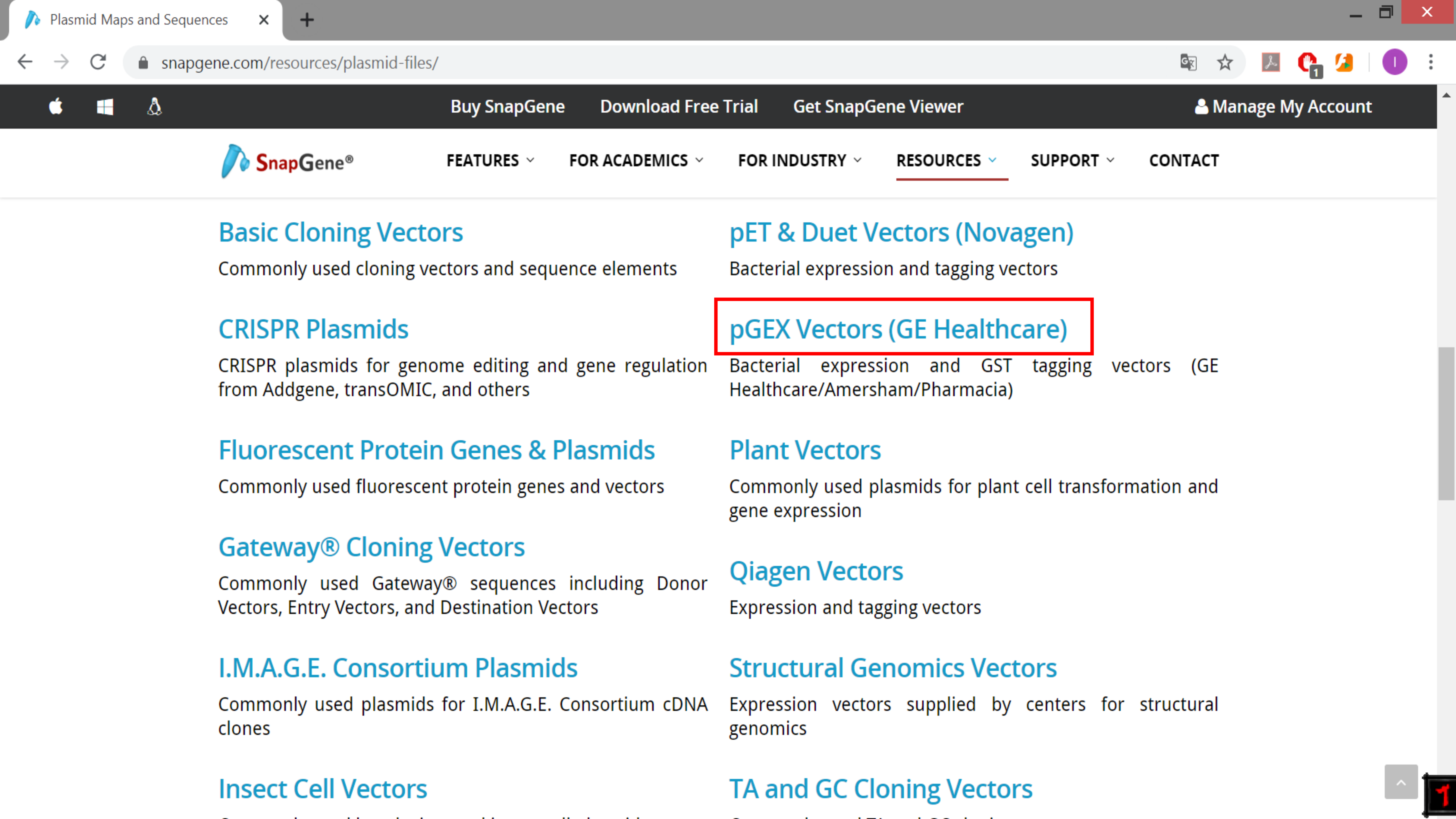
4000
5000
Unique 6+ Cutters (Nonredundant)
Map Sequence Enzymes Features Primers History
Description Pa



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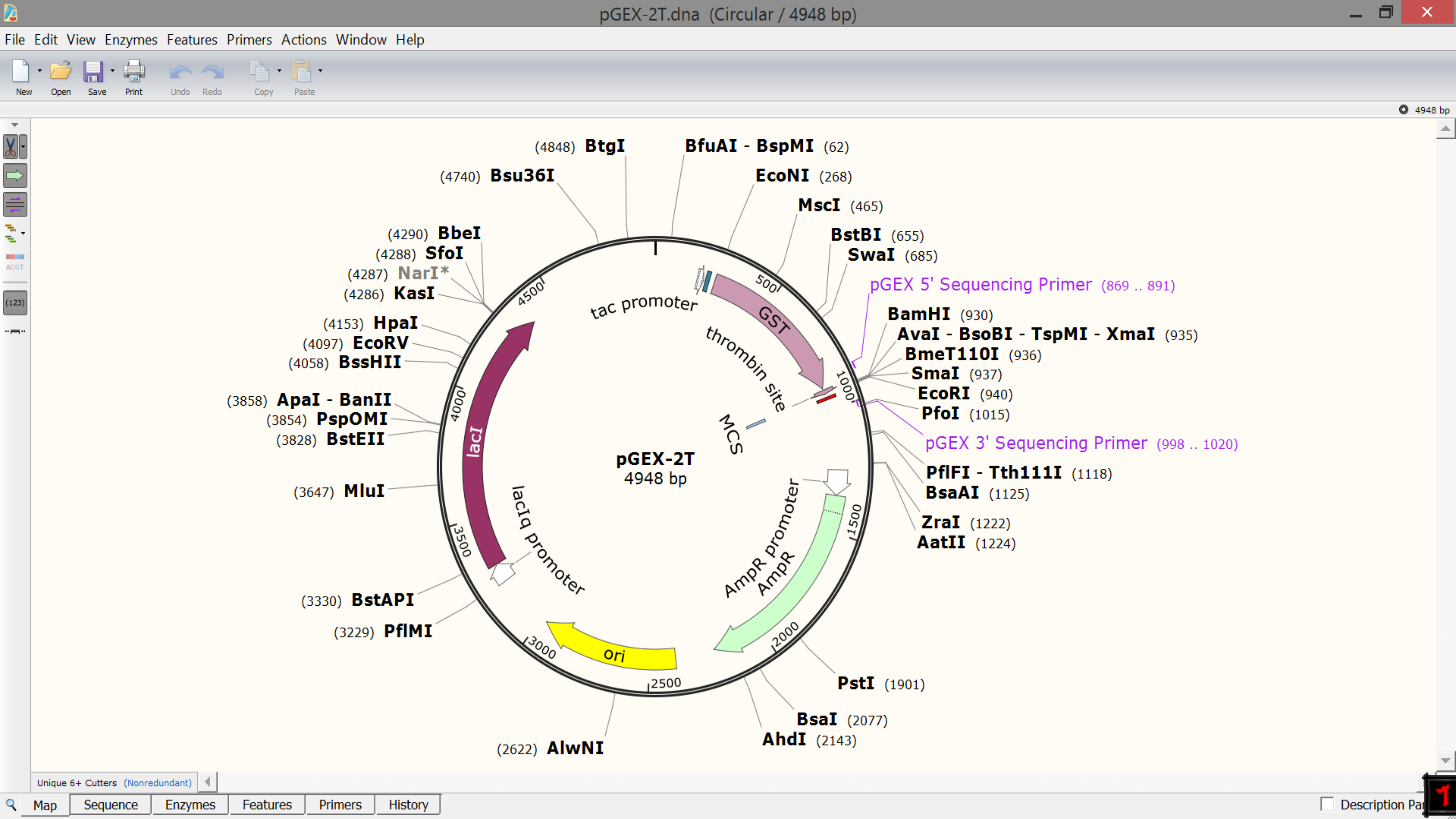
pGEX-2T.dna (Circular / 4948 bp)
File Edit View Enzymes Features Primers Actions Window Help
New Open Save Print Undo Redo Copy Paste
4948 bp
(123)
ACGT
(4848) BtgI
BfuAI - BspMI (62)
(4740) Bsu36I
EcoNI (268)
MscI (465)
BstBI (655)
SwaI (685)
(4290) BbeI
(4288) SfoI
(4287) NarI*
(4286) KasI
pGEX 5' Sequencing Primer (869 .. 891)
BamHI (930)
AvaI - BsoBI - TspMI - XmaI (935)
BmeT110I (936)
SmaI (937)
EcoRI (940)
PfoI (1015)
pGEX 3' Sequencing Primer (998 .. 1020)
(4153) HpaI
(4097) EcoRV
(4058) BssHII
(3858) ApaI - BanII
(3854) PspOMI
(3828) BstEII
(3647) MluI
PflFI - Tth111I (1118)
BsaAI (1125)
ZraI (1222)
AatII (1224)
(3330) BstAPI
(3229) PflMI
PstI (1901)
BsaI (2077)
AhdI (2143)
(2622) AlwNI
tac promoter
GST
thrombin site
MCS
lacI
lacIq promoter
AmpR promoter
AmpR
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pGEX-2T
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4500
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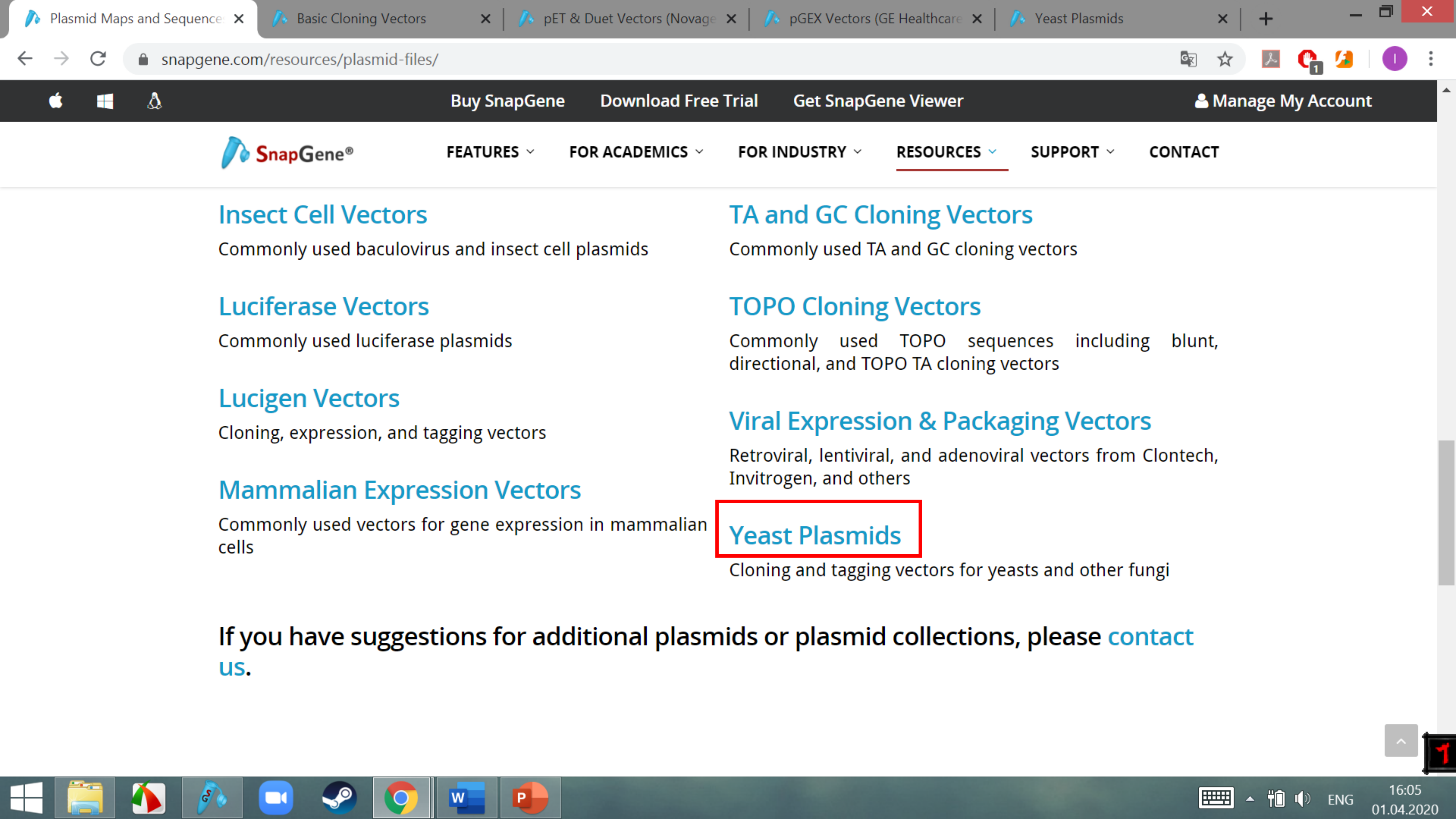


Insect Cell Vectors

Commonly used baculovirus and insect cell plasmids

Luciferase Vectors

Commonly used luciferase plasmids

Lucigen Vectors

Cloning, expression, and tagging vectors

Mammalian Expression Vectors

Commonly used vectors for gene expression in mammalian cells

TA and GC Cloning Vectors

Commonly used TA and GC cloning vectors

TOPO Cloning Vectors

Commonly used TOPO sequences including blunt, directional, and TOPO TA cloning vectors

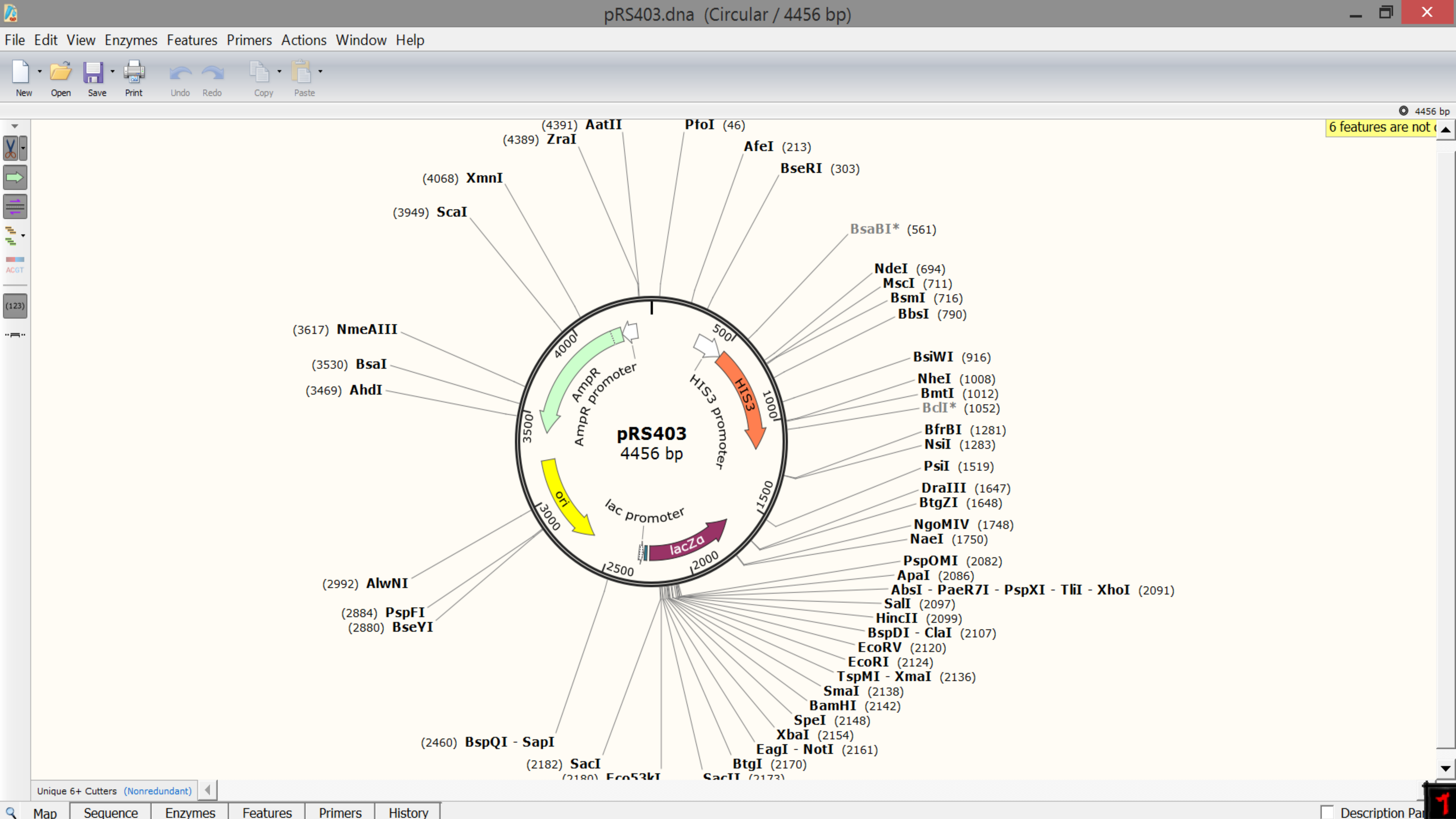
Viral Expression & Packaging Vectors

Retroviral, lentiviral, and adenoviral vectors from Clontech, Invitrogen, and others

Yeast Plasmids

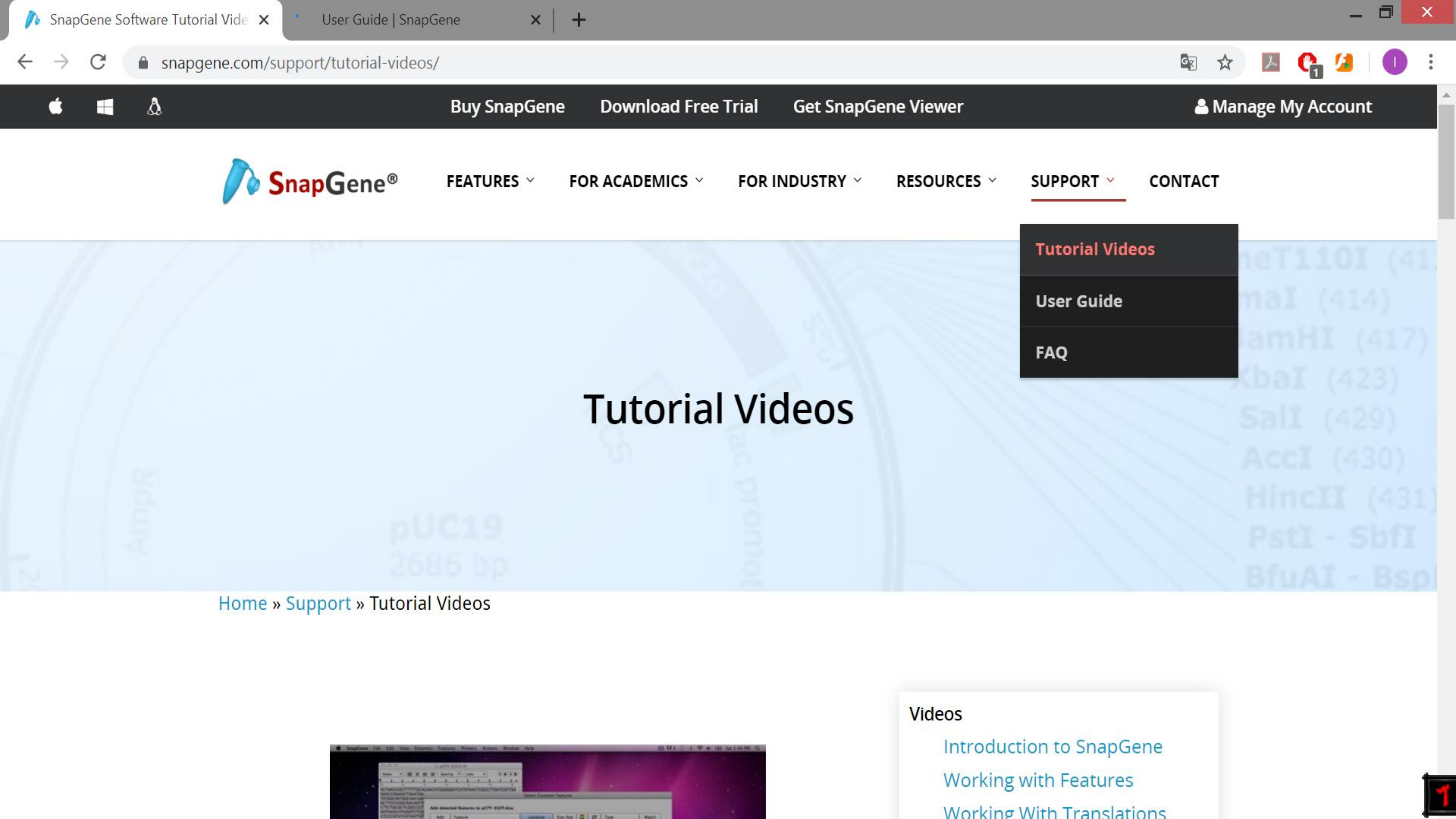
Cloning and tagging vectors for yeasts and other fungi

If you have suggestions for additional plasmids or plasmid collections, please contact us.



pRS403.dna (Circular / 4456 bp)

6 features are not

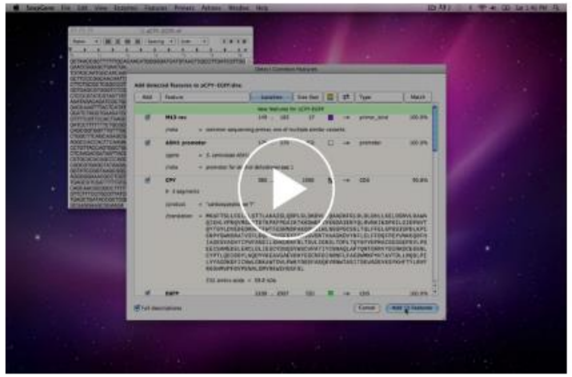


Tutorial Videos

Home » Support » Tutorial Videos

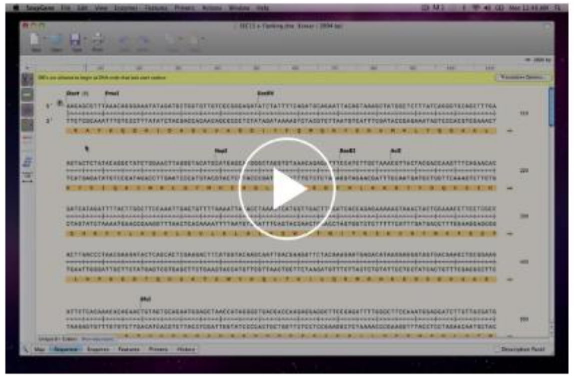
Videos

- Introduction to SnapGene
- Working with Features
- Working With Translations



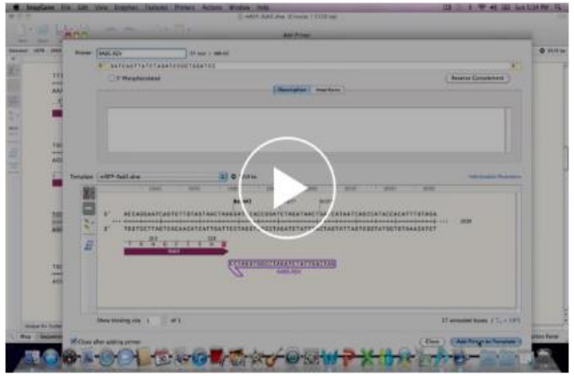
Working with Features

Learn how to create and edit DNA features with SnapGene or SnapGene Viewer, and how to customize the automatic annotation of common features.



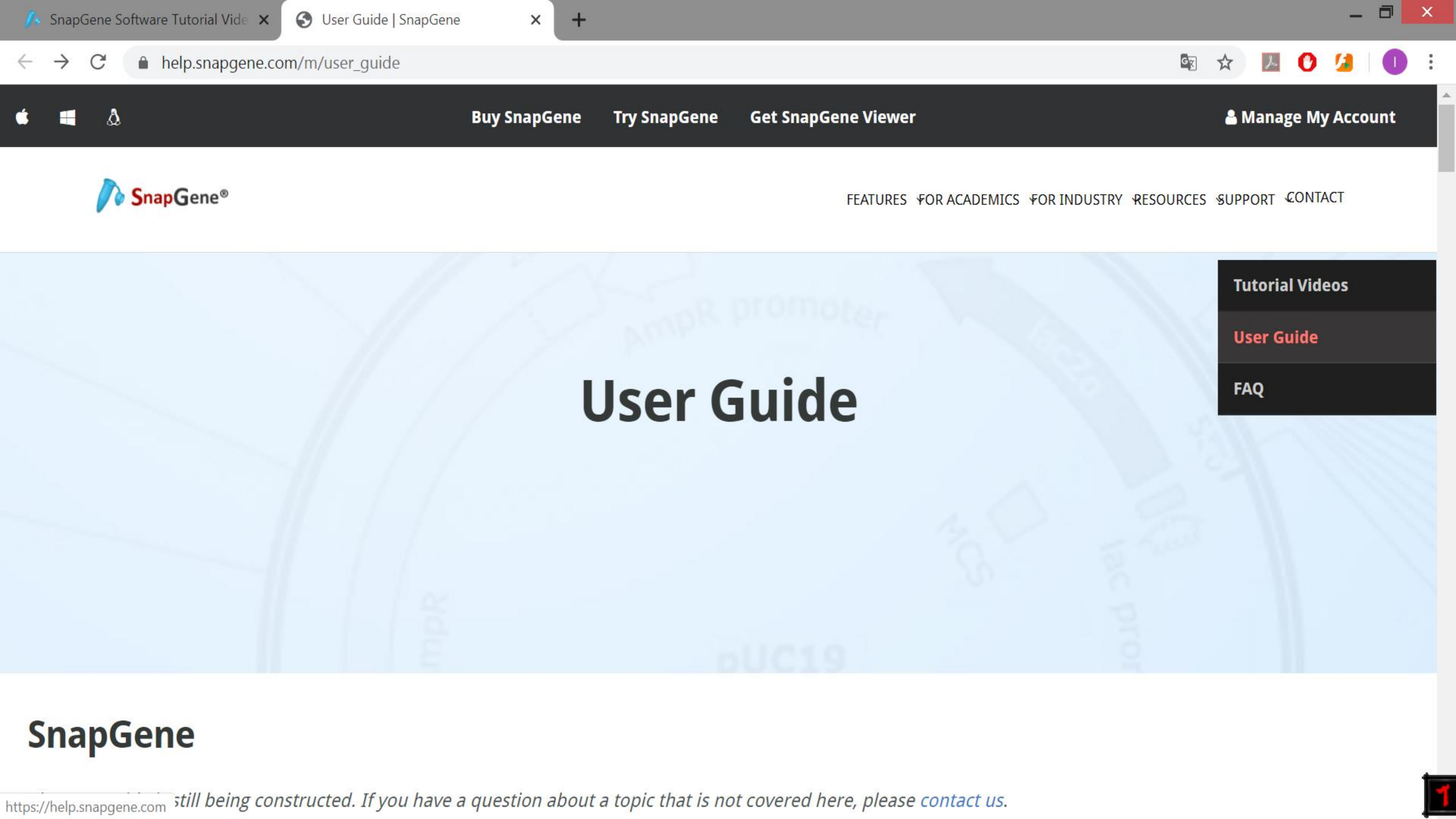
Working with Translations

Learn how SnapGene or SnapGene Viewer can help you to view and edit translated features, open reading frames (ORFs), and whole-sequence translations.



Primers, PCR, and Mutagenesis

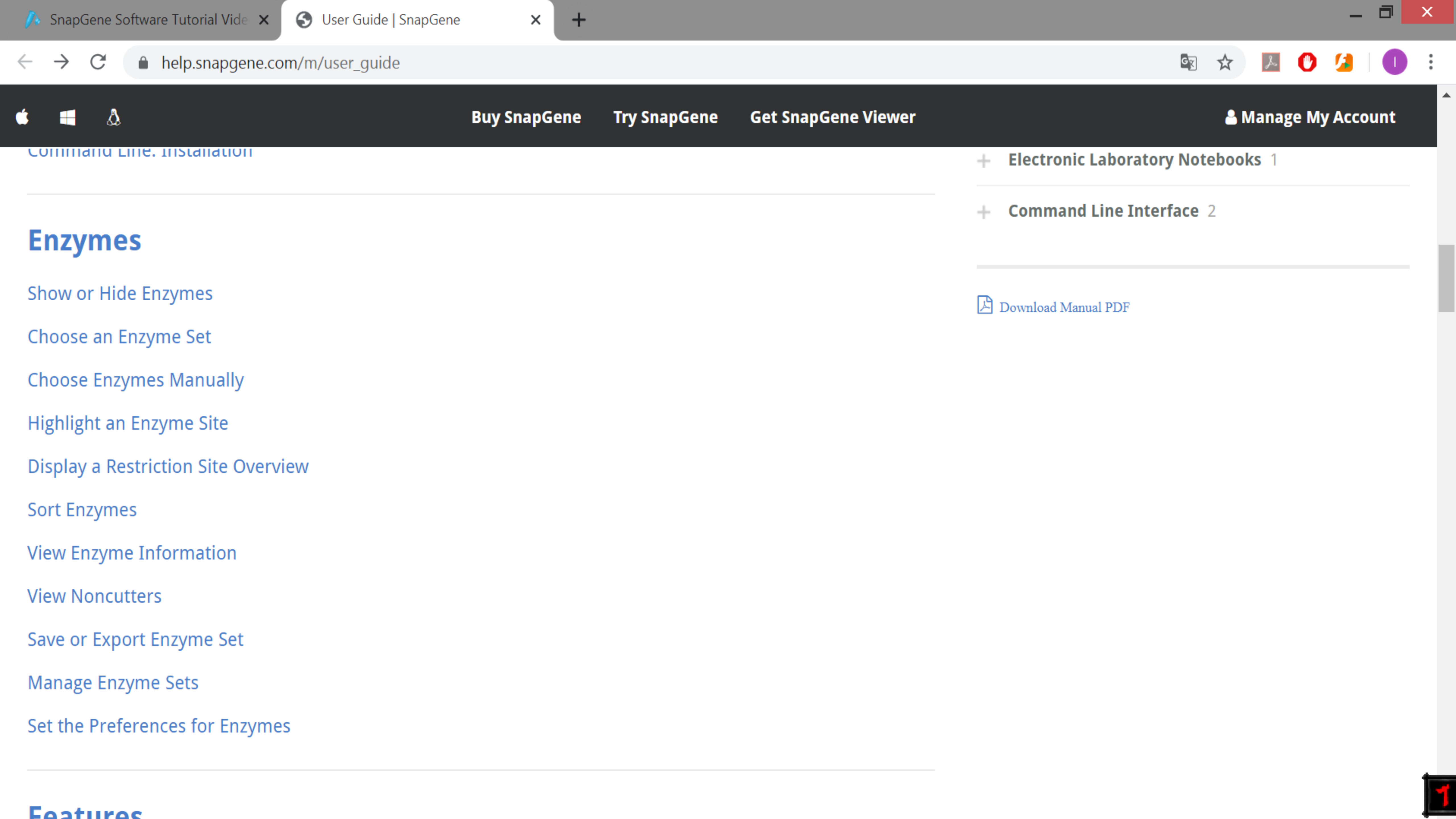
Learn how to make primers, and to simulate PCR and primer-directed mutagenesis.



User Guide

SnapGene

still being constructed. If you have a question about a topic that is not covered here, please contact us.



Command Line: Installation

Enzymes

Show or Hide Enzymes

Choose an Enzyme Set

Choose Enzymes Manually

Highlight an Enzyme Site

Display a Restriction Site Overview

Sort Enzymes

View Enzyme Information

View Noncutters

Save or Export Enzyme Set

Manage Enzyme Sets

Set the Preferences for Enzymes

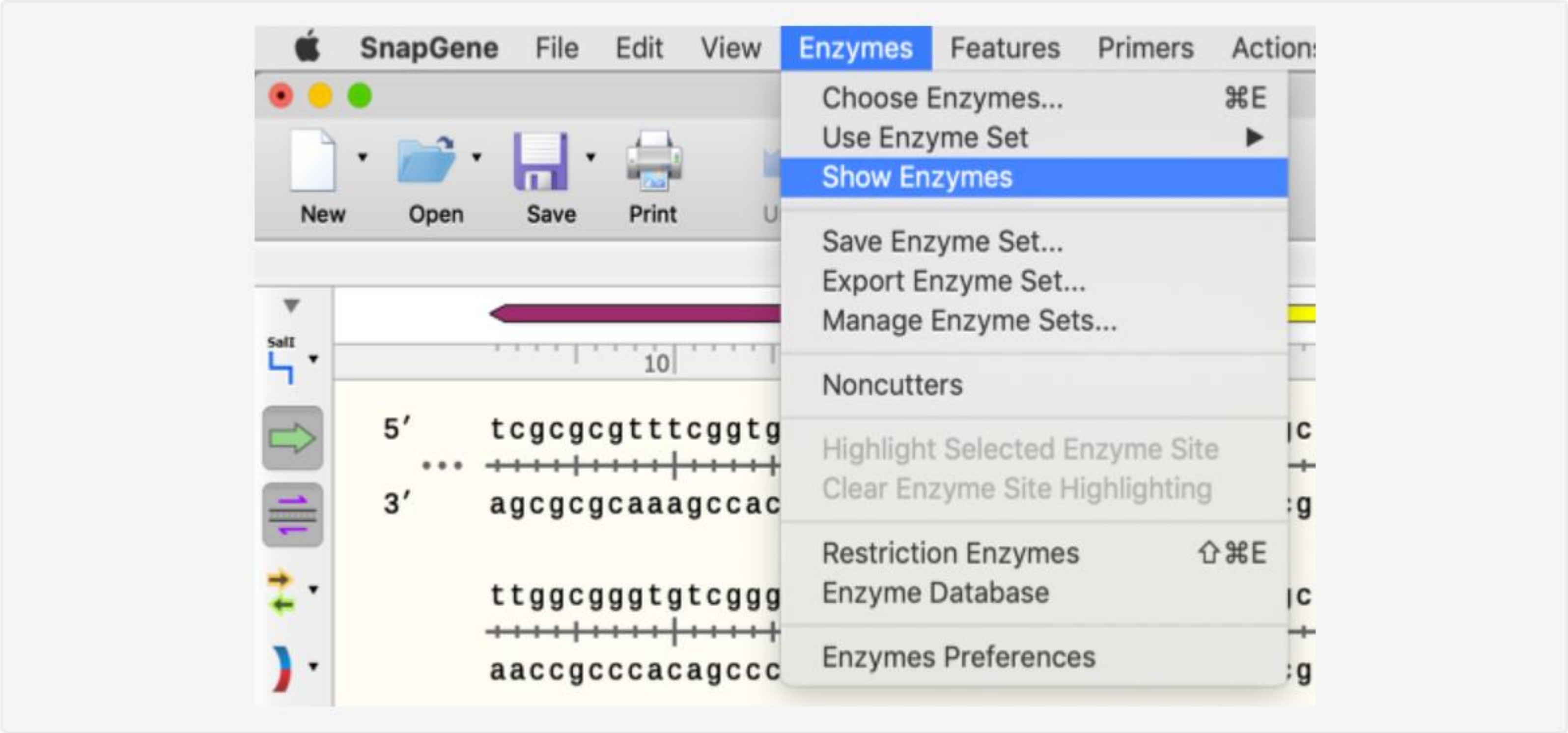
+ **Electronic Laboratory Notebooks** 1

+ **Command Line Interface** 2

Download Manual PDF

Features

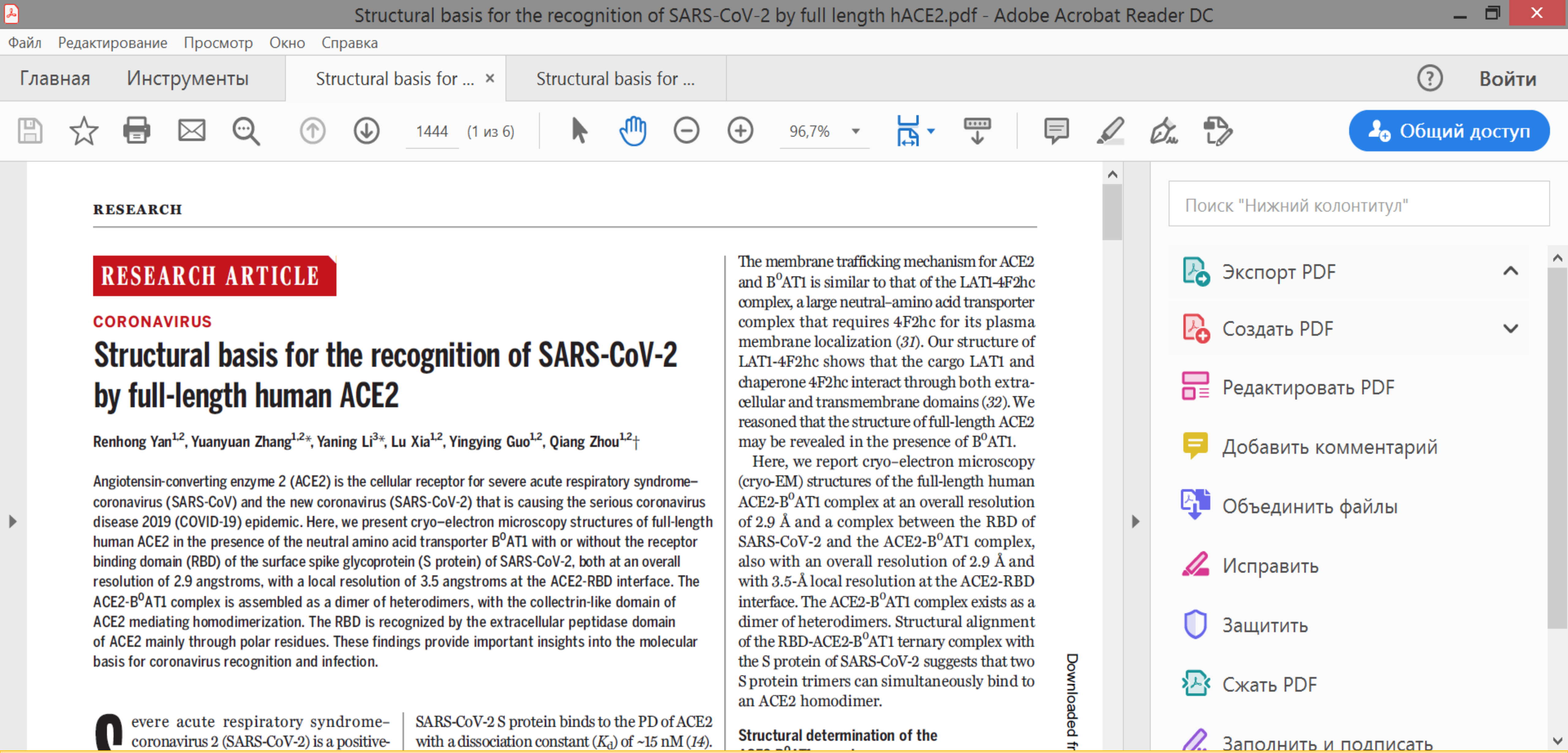
Show the Enzymes



To show the enzymes, click **Enzymes** → **Show Enzymes**.

Hide the Enzymes

Highlight an Enzyme Site
Display a Restriction Site Overview
Sort Enzymes
View Enzyme Information
View Noncutters
Save or Export Enzyme Set
Manage Enzyme Sets
Set the Preferences for Enzymes
+ Features 21
+ Primers 7
+ Translations 6
+ Colors 4
+ Searching 3



RESEARCH

RESEARCH ARTICLE

CORONAVIRUS

Structural basis for the recognition of SARS-CoV-2 by full-length human ACE2

Renhong Yan[1,2], Yuanyuan Zhang[1,2]*, Yaning Li[3]*, Lu Xia[1,2], Yingying Guo[1,2], Qiang Zhou[1,2]†

Angiotensin-converting enzyme 2 (ACE2) is the cellular receptor for severe acute respiratory syndrome–coronavirus (SARS-CoV) and the new coronavirus (SARS-CoV-2) that is causing the serious coronavirus disease 2019 (COVID-19) epidemic. Here, we present cryo–electron microscopy structures of full-length human ACE2 in the presence of the neutral amino acid transporter B^{0}AT1 with or without the receptor binding domain (RBD) of the surface spike glycoprotein (S protein) of SARS-CoV-2, both at an overall resolution of 2.9 angstroms, with a local resolution of 3.5 angstroms at the ACE2-RBD interface. The ACE2-B^{0}AT1 complex is assembled as a dimer of heterodimers, with the collectrin-like domain of ACE2 mediating homodimerization. The RBD is recognized by the extracellular peptidase domain of ACE2 mainly through polar residues. These findings provide important insights into the molecular basis for coronavirus recognition and infection.

Severe acute respiratory syndrome–coronavirus 2 (SARS-CoV-2) is a positive-

SARS-CoV-2 S protein binds to the PD of ACE2 with a dissociation constant (K_d) of ~15 nM (14).

The membrane trafficking mechanism for ACE2 and B^{0}AT1 is similar to that of the LAT1-4F2hc complex, a large neutral–amino acid transporter complex that requires 4F2hc for its plasma membrane localization (31). Our structure of LAT1-4F2hc shows that the cargo LAT1 and chaperone 4F2hc interact through both extracellular and transmembrane domains (32). We reasoned that the structure of full-length ACE2 may be revealed in the presence of B^{0}AT1.

Here, we report cryo–electron microscopy (cryo-EM) structures of the full-length human ACE2-B^{0}AT1 complex at an overall resolution of 2.9 Å and a complex between the RBD of SARS-CoV-2 and the ACE2-B^{0}AT1 complex, also with an overall resolution of 2.9 Å and with 3.5-Å local resolution at the ACE2-RBD interface. The ACE2-B^{0}AT1 complex exists as a dimer of heterodimers. Structural alignment of the RBD-ACE2-B^{0}AT1 ternary complex with the S protein of SARS-CoV-2 suggests that two S protein trimers can simultaneously bind to an ACE2 homodimer.

Structural determination of the

Ангиотензин-превращающий фермент 2 (ACE2) является клеточным рецептором для тяжелого острого респираторного синдрома - коронавируса (SARS-CoV) и нового коронавируса (SARS-CoV-2), который вызывает серьезную эпидемию коронавирусной болезни 2019 (COVID-19).

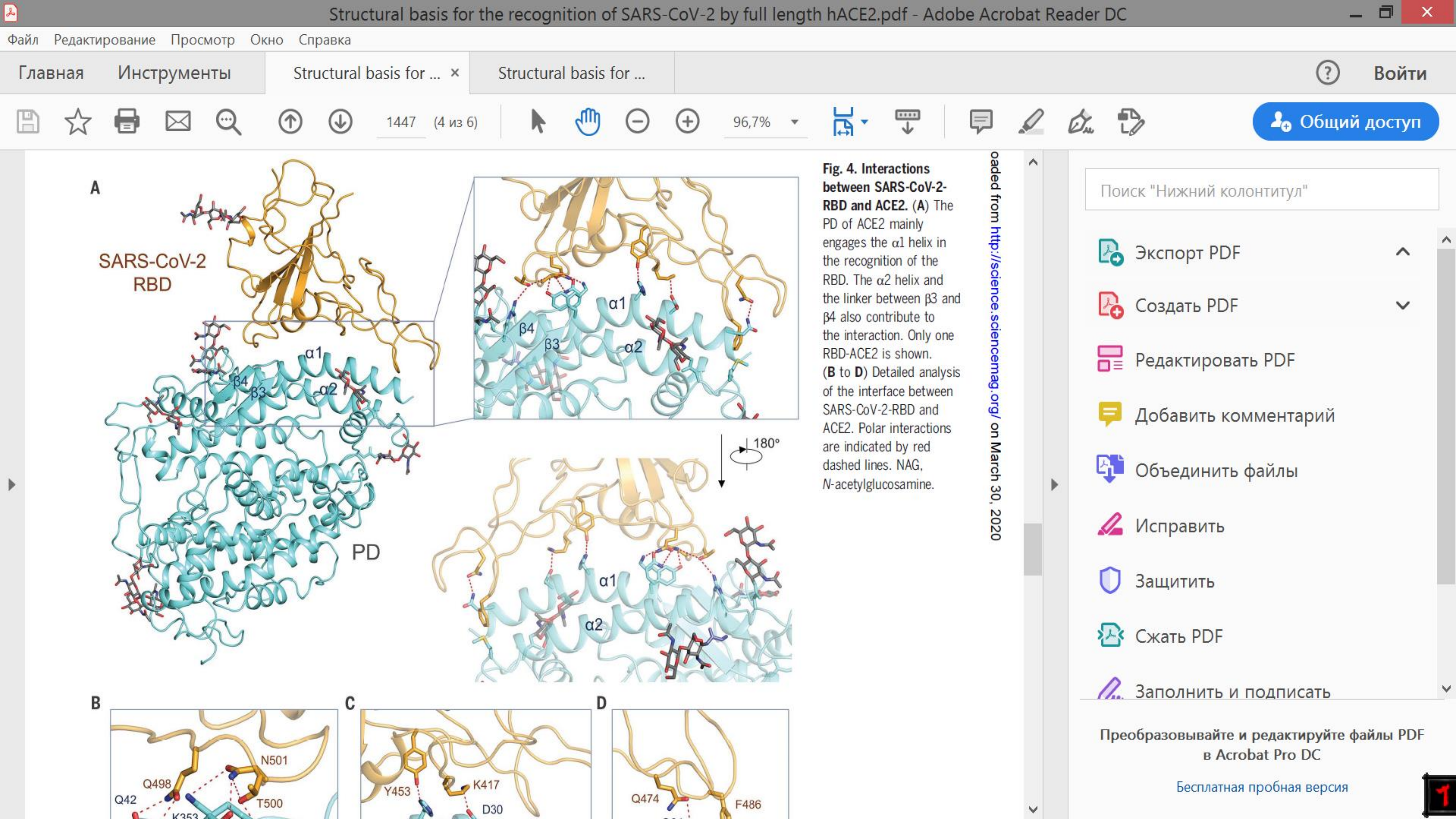


Fig. 4. Interactions between SARS-CoV-2-RBD and ACE2. (**A**) The PD of ACE2 mainly engages the α1 helix in the recognition of the RBD. The α2 helix and the linker between β3 and β4 also contribute to the interaction. Only one RBD-ACE2 is shown. (**B** to **D**) Detailed analysis of the interface between SARS-CoV-2-RBD and ACE2. Polar interactions are indicated by red dashed lines. NAG, *N*-acetylglucosamine.

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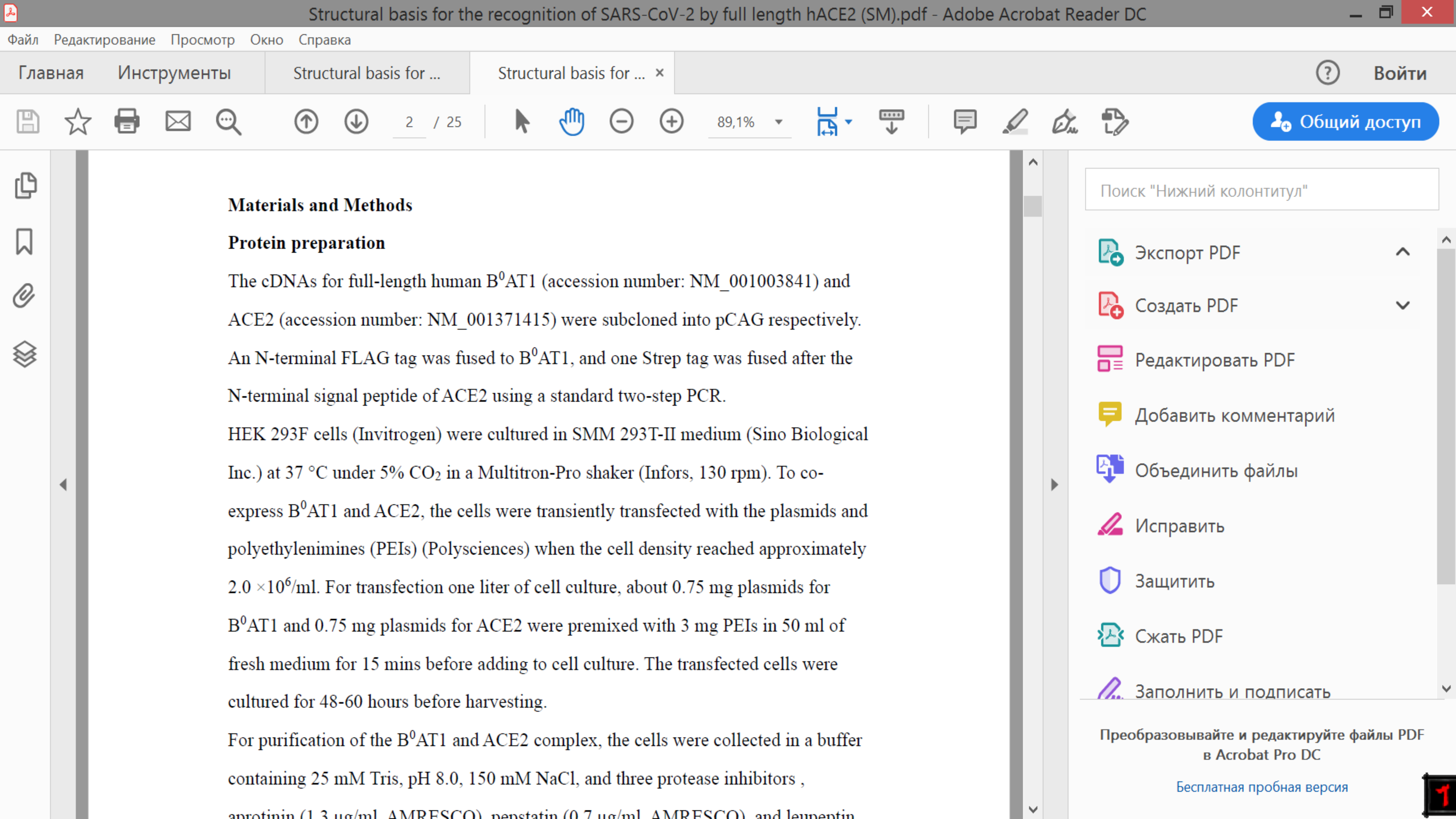


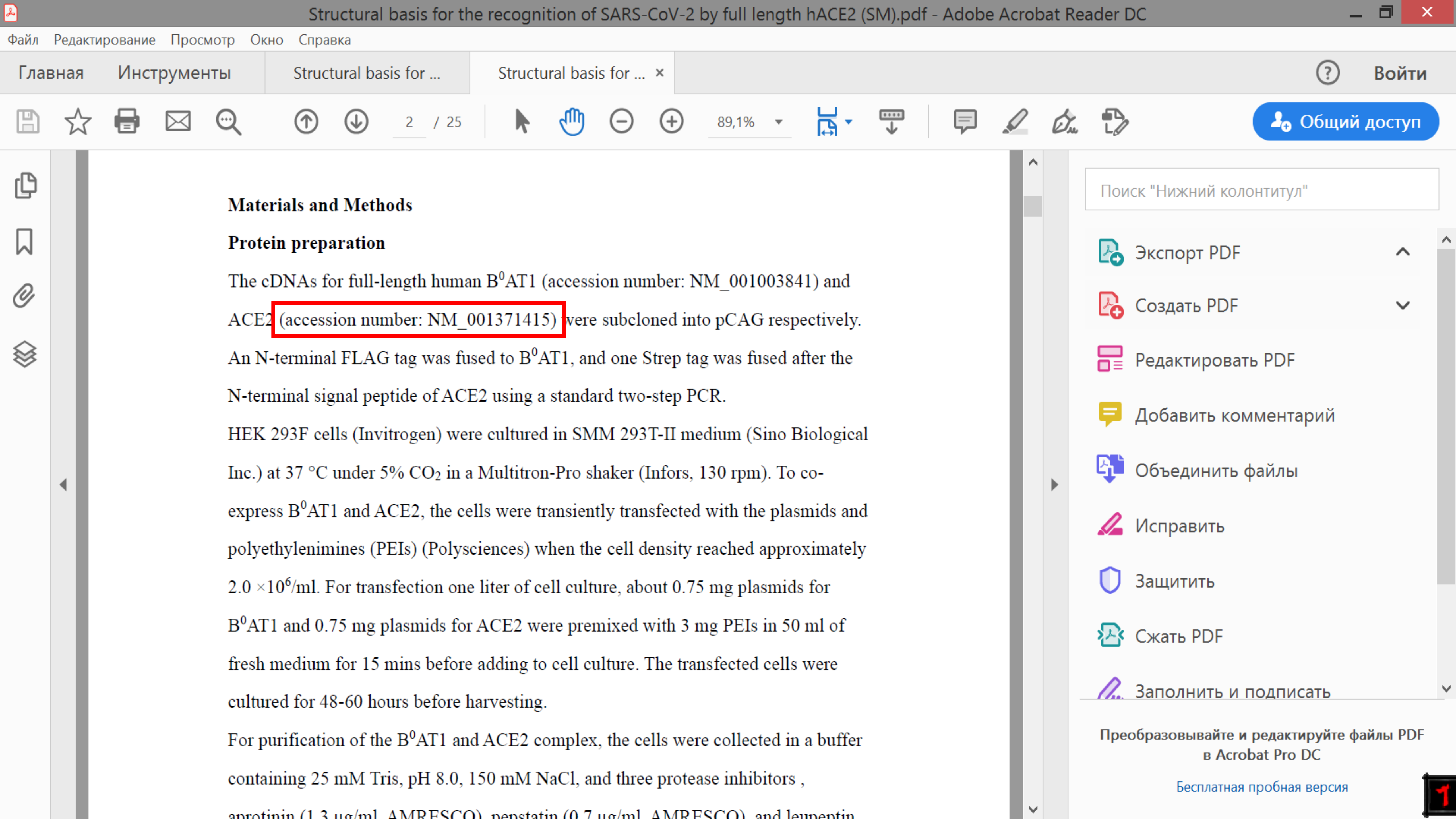
Materials and Methods

Protein preparation

The cDNAs for full-length human B^0AT1 (accession number: NM_001003841) and ACE2 (accession number: NM_001371415) were subcloned into pCAG respectively. An N-terminal FLAG tag was fused to B^0AT1, and one Strep tag was fused after the N-terminal signal peptide of ACE2 using a standard two-step PCR.

HEK 293F cells (Invitrogen) were cultured in SMM 293T-II medium (Sino Biological Inc.) at 37 °C under 5% CO_2 in a Multitron-Pro shaker (Infors, 130 rpm). To co-express B^0AT1 and ACE2, the cells were transiently transfected with the plasmids and polyethylenimines (PEIs) (Polysciences) when the cell density reached approximately 2.0×10^6/ml. For transfection one liter of cell culture, about 0.75 mg plasmids for B^0AT1 and 0.75 mg plasmids for ACE2 were premixed with 3 mg PEIs in 50 ml of fresh medium for 15 mins before adding to cell culture. The transfected cells were cultured for 48-60 hours before harvesting.

For purification of the B^0AT1 and ACE2 complex, the cells were collected in a buffer containing 25 mM Tris, pH 8.0, 150 mM NaCl, and three protease inhibitors , aprotinin (1.3 μg/ml, AMRESCO), pepstatin (0.7 μg/ml, AMRESCO), and leupeptin



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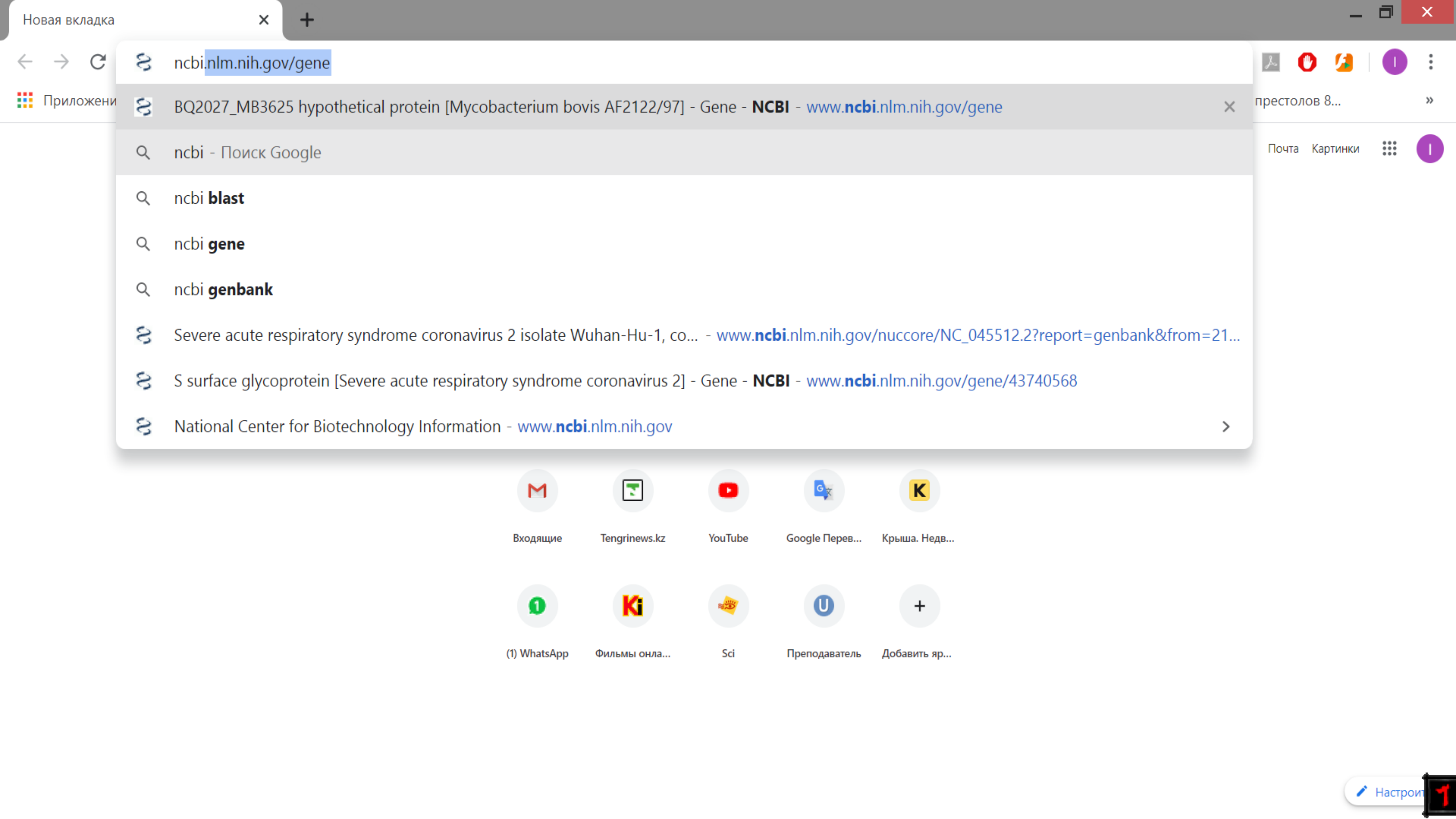

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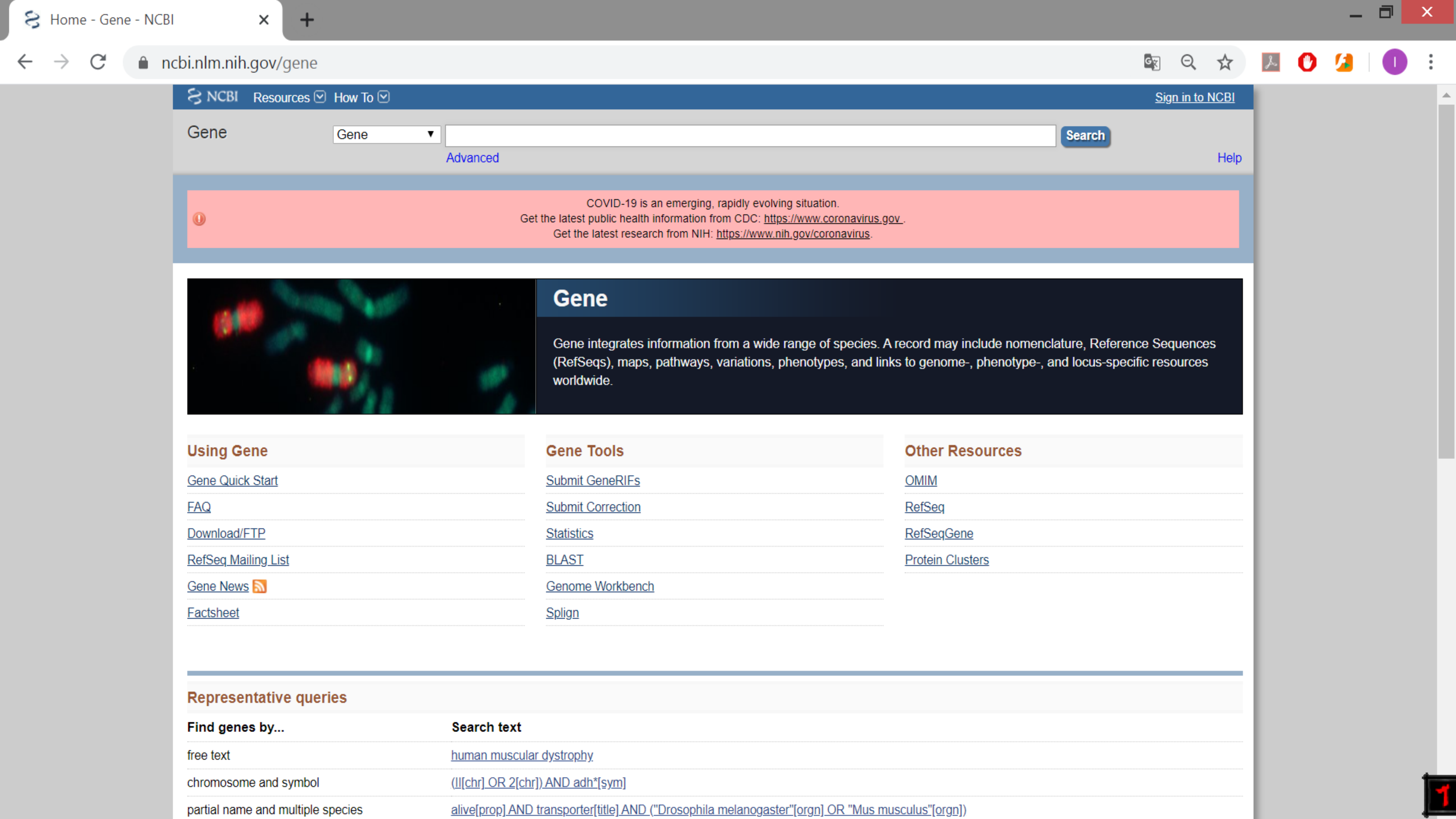

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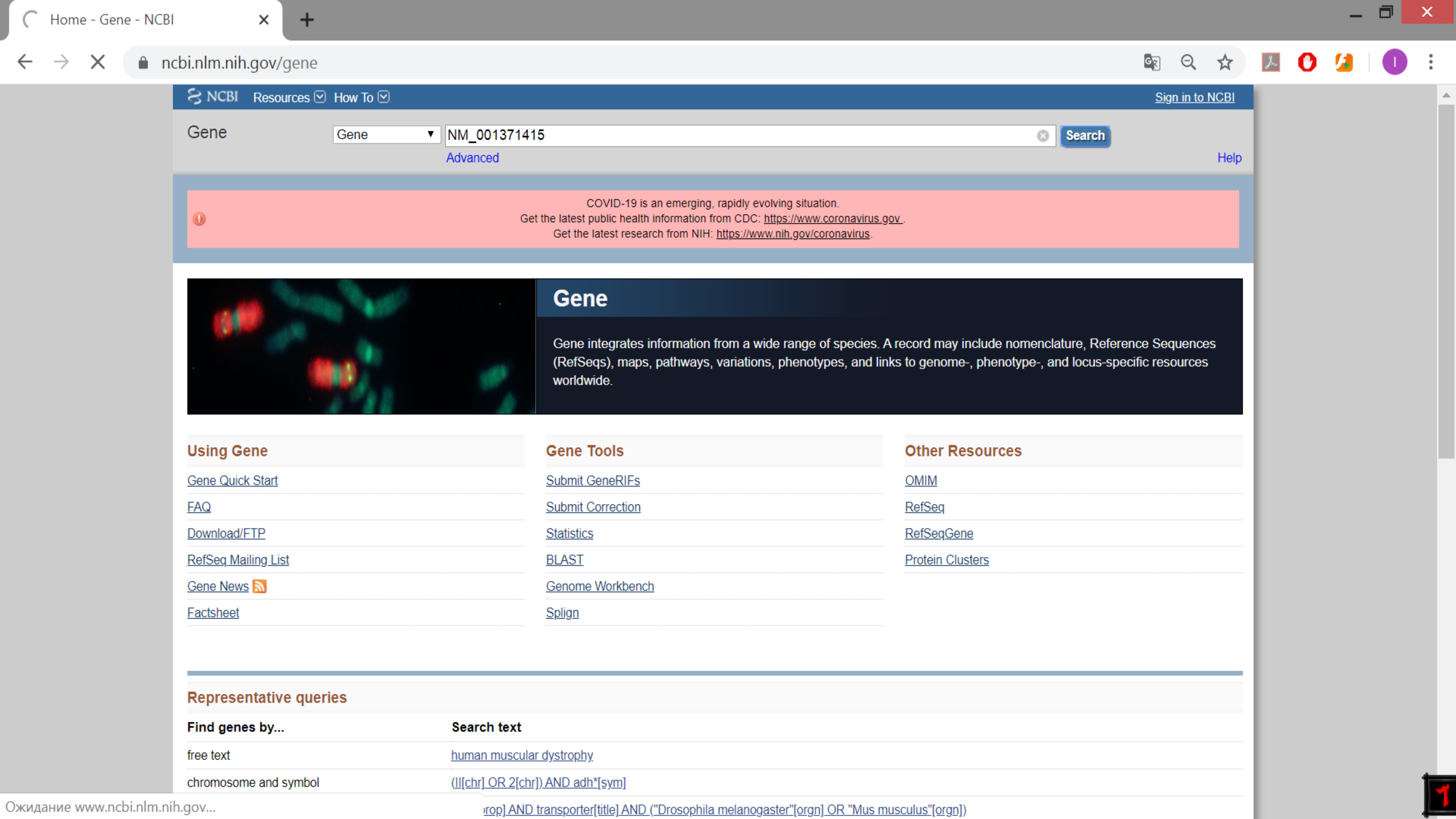
free text	human muscular dystrophy
chromosome and symbol	(II[chr] OR 2[chr]) AND adh*[sym]
partial name and multiple species	alive[prop] AND transporter[title] AND ("Drosophila melanogaster"[orgn] OR "Mus musculus"[orgn])



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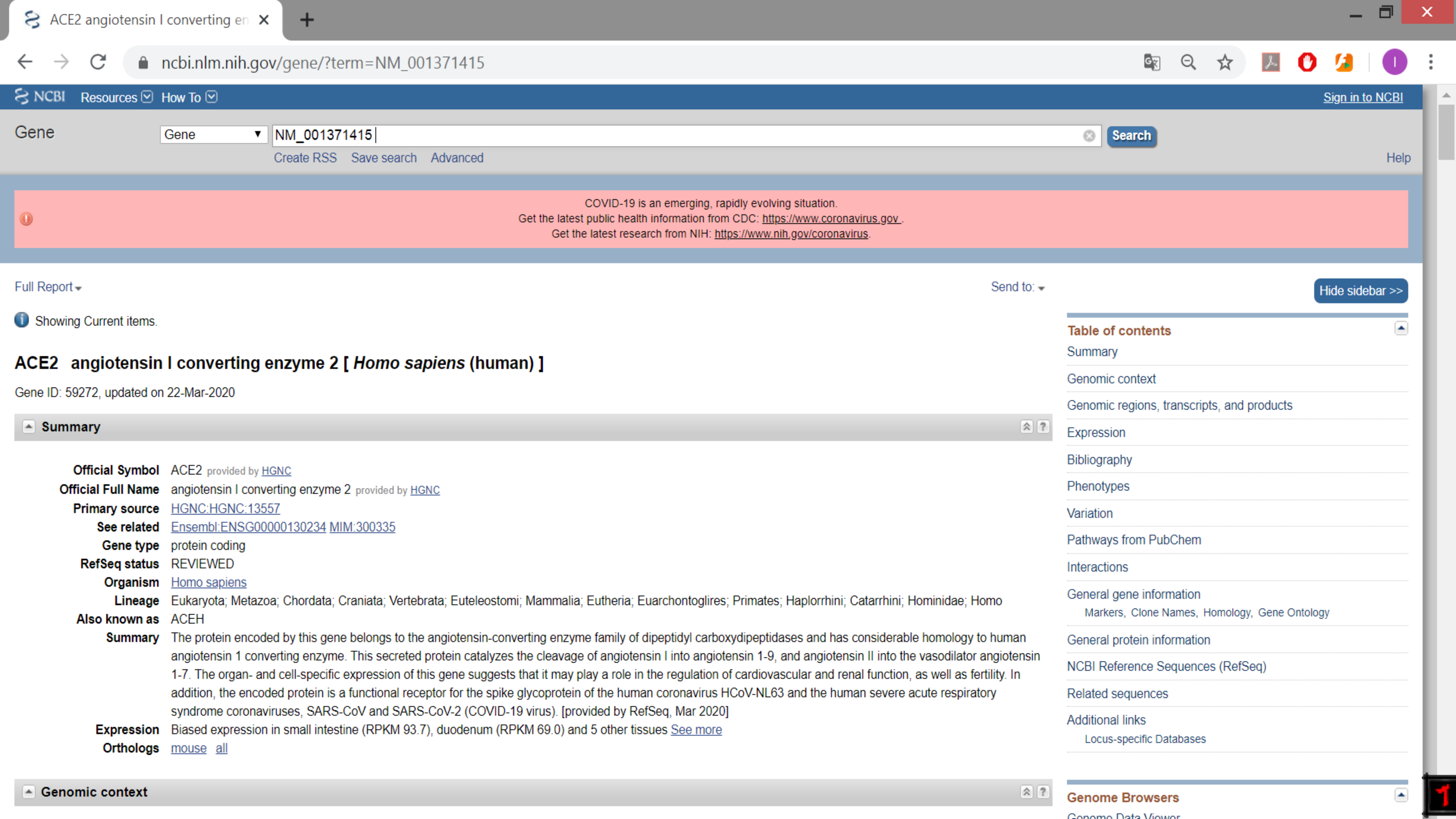

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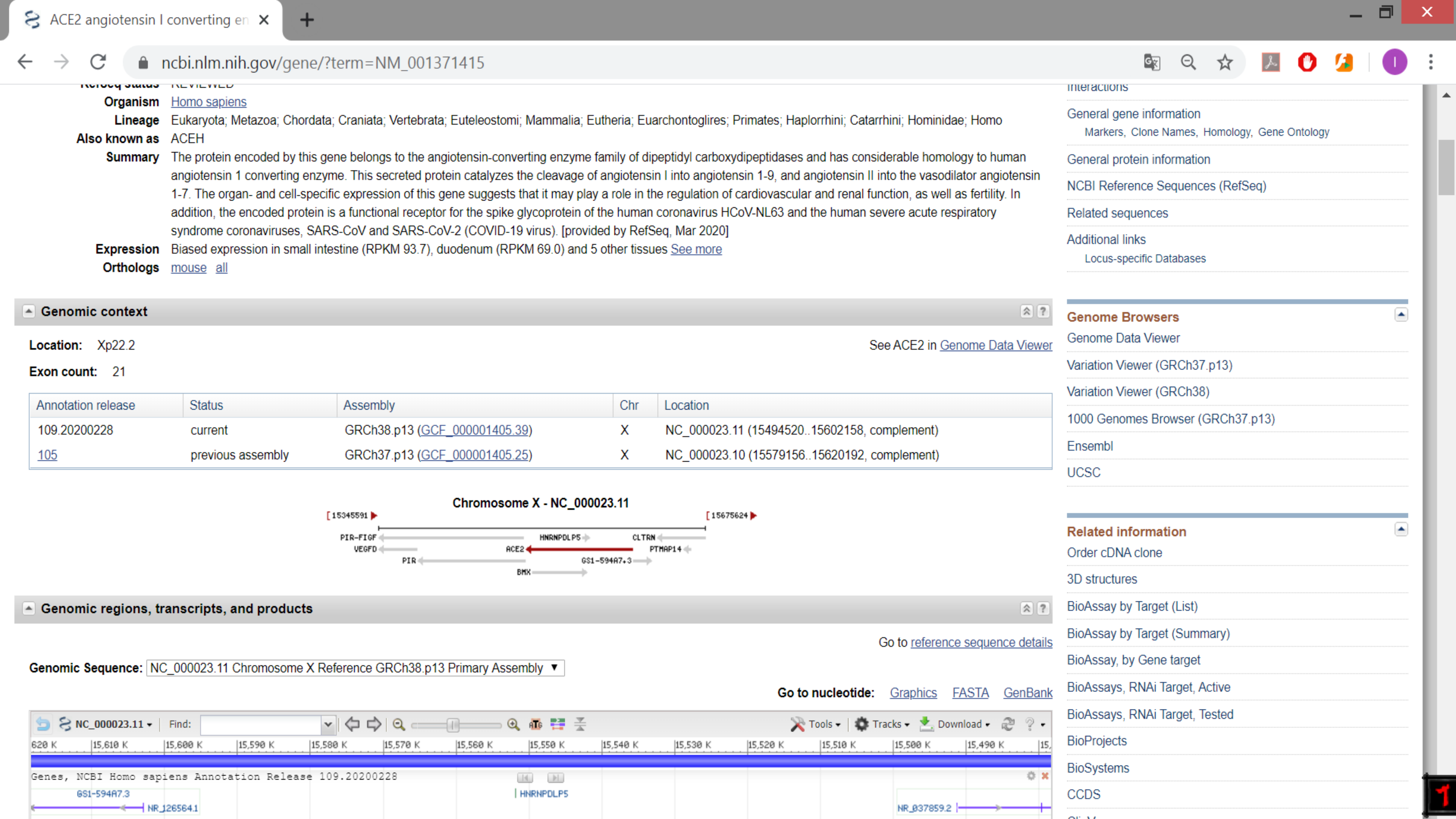
ACE2 angiotensin I converting enzyme 2 [*Homo sapiens* (human)]

Gene ID: 59272, updated on 22-Mar-2020

Summary

Official Symbol	ACE2 provided by HGNC
Official Full Name	angiotensin I converting enzyme 2 provided by HGNC
Primary source	HGNC:HGNC:13557
See related	Ensembl:ENSG00000130234 MIM:300335
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as	ACEH
Summary	The protein encoded by this gene belongs to the angiotensin-converting enzyme family of dipeptidyl carboxydipeptidases and has considerable homology to human angiotensin 1 converting enzyme. This secreted protein catalyzes the cleavage of angiotensin I into angiotensin 1-9, and angiotensin II into the vasodilator angiotensin 1-7. The organ- and cell-specific expression of this gene suggests that it may play a role in the regulation of cardiovascular and renal function, as well as fertility. In addition, the encoded protein is a functional receptor for the spike glycoprotein of the human coronavirus HCoV-NL63 and the human severe acute respiratory syndrome coronaviruses, SARS-CoV and SARS-CoV-2 (COVID-19 virus). [provided by RefSeq, Mar 2020]
Expression	Biased expression in small intestine (RPKM 93.7), duodenum (RPKM 69.0) and 5 other tissues See more
Orthologs	mouse all

Genomic context



Organism Homo sapiens

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

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Genomic context

Location: Xp22.2

See ACE2 in Genome Data Viewer

Exon count: 21

Annotation release	Status	Assembly	Chr	Location
109.20200228	current	GRCh38.p13 (GCF_000001405.39)	X	NC_000023.11 (15494520..15602158, complement)
105	previous assembly	GRCh37.p13 (GCF_000001405.25)	X	NC_000023.10 (15579156..15620192, complement)

Chromosome X - NC_000023.11

Genomic regions, transcripts, and products

Go to reference sequence details

Genomic Sequence: NC_000023.11 Chromosome X Reference GRCh38.p13 Primary Assembly

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Interactions

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Markers, Clone Names, Homology, Gene Ontology

General protein information

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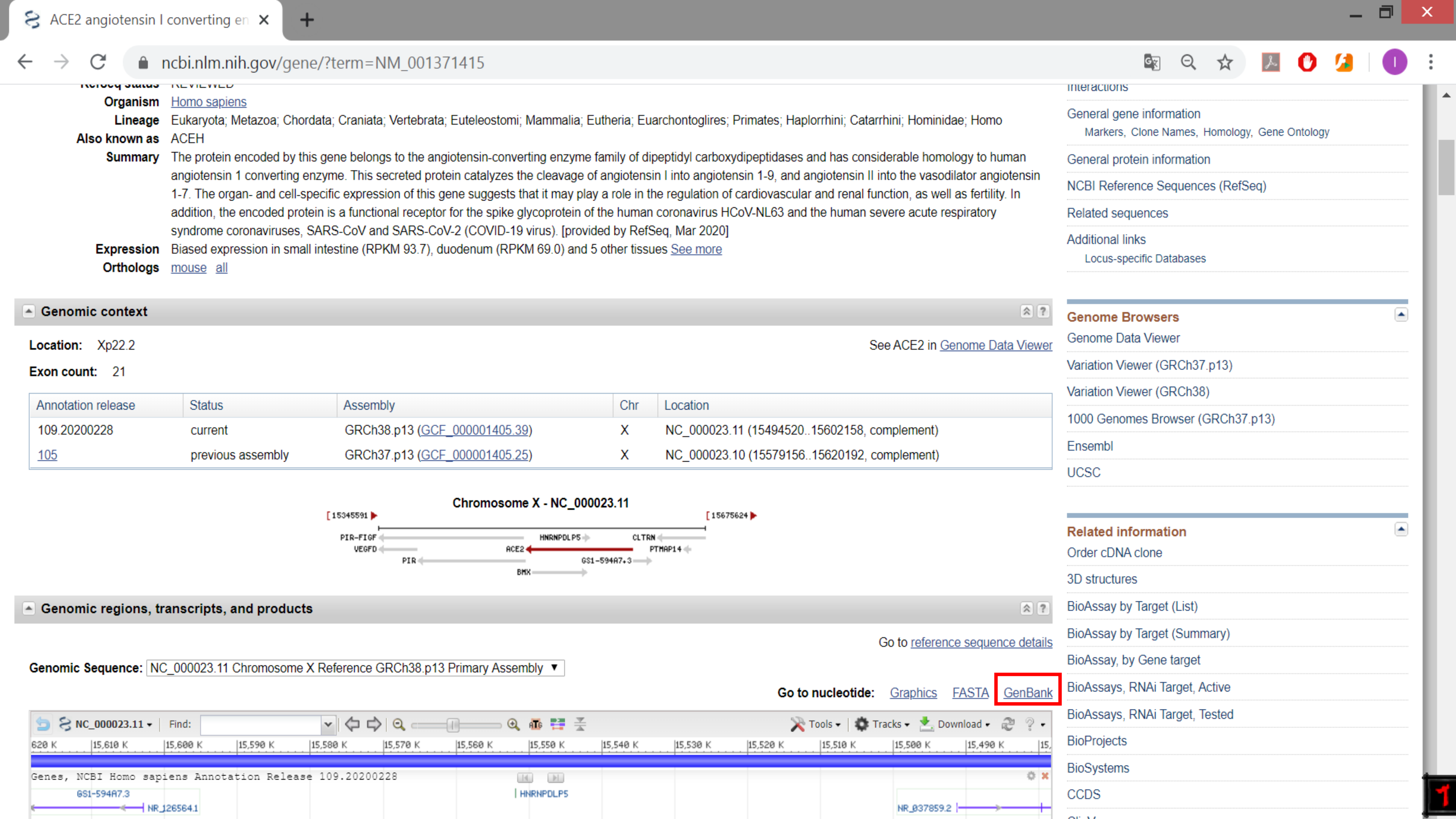

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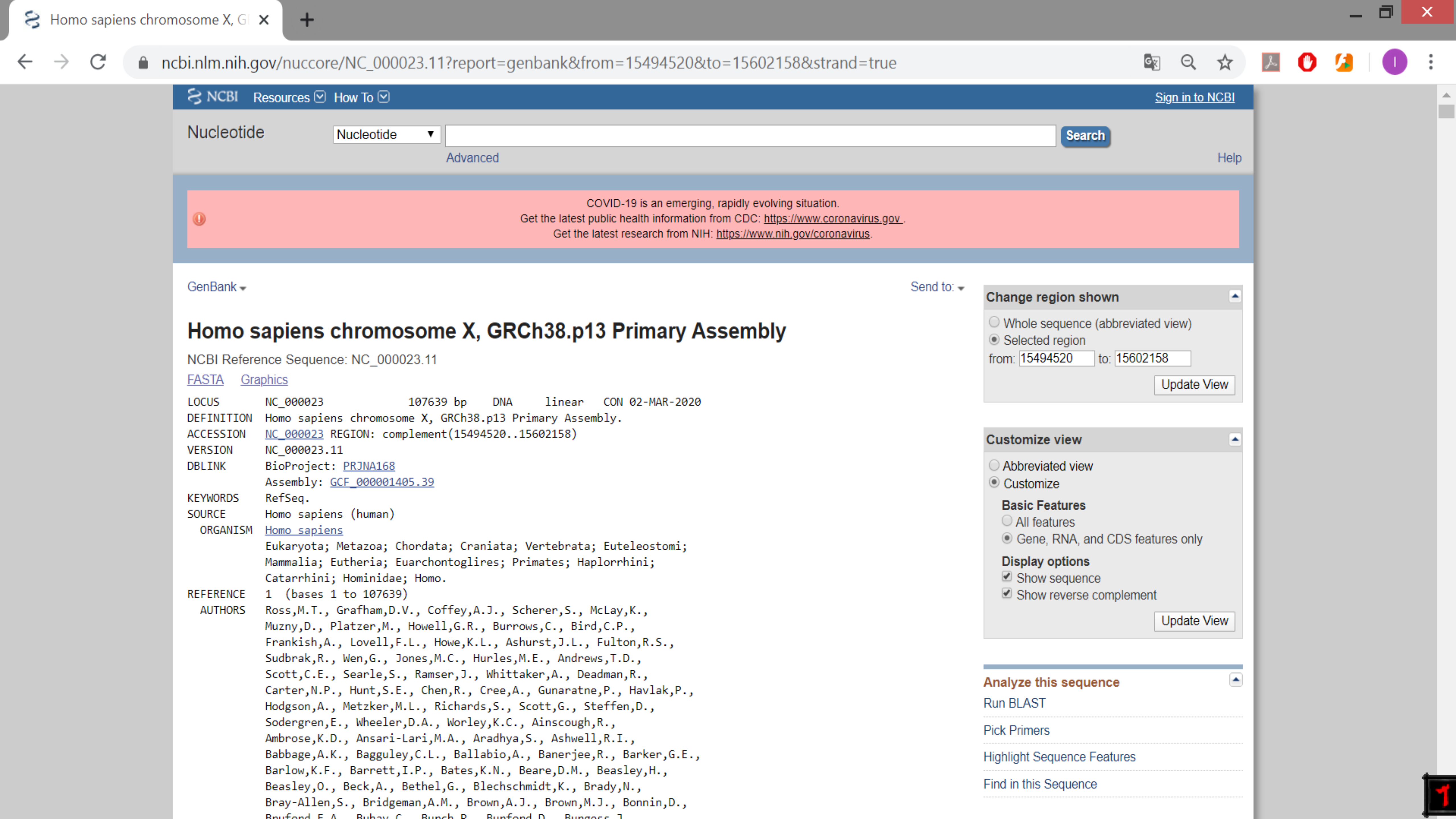

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Homo sapiens chromosome X, GRCh38.p13 Primary Assembly

NCBI Reference Sequence: NC_000023.11

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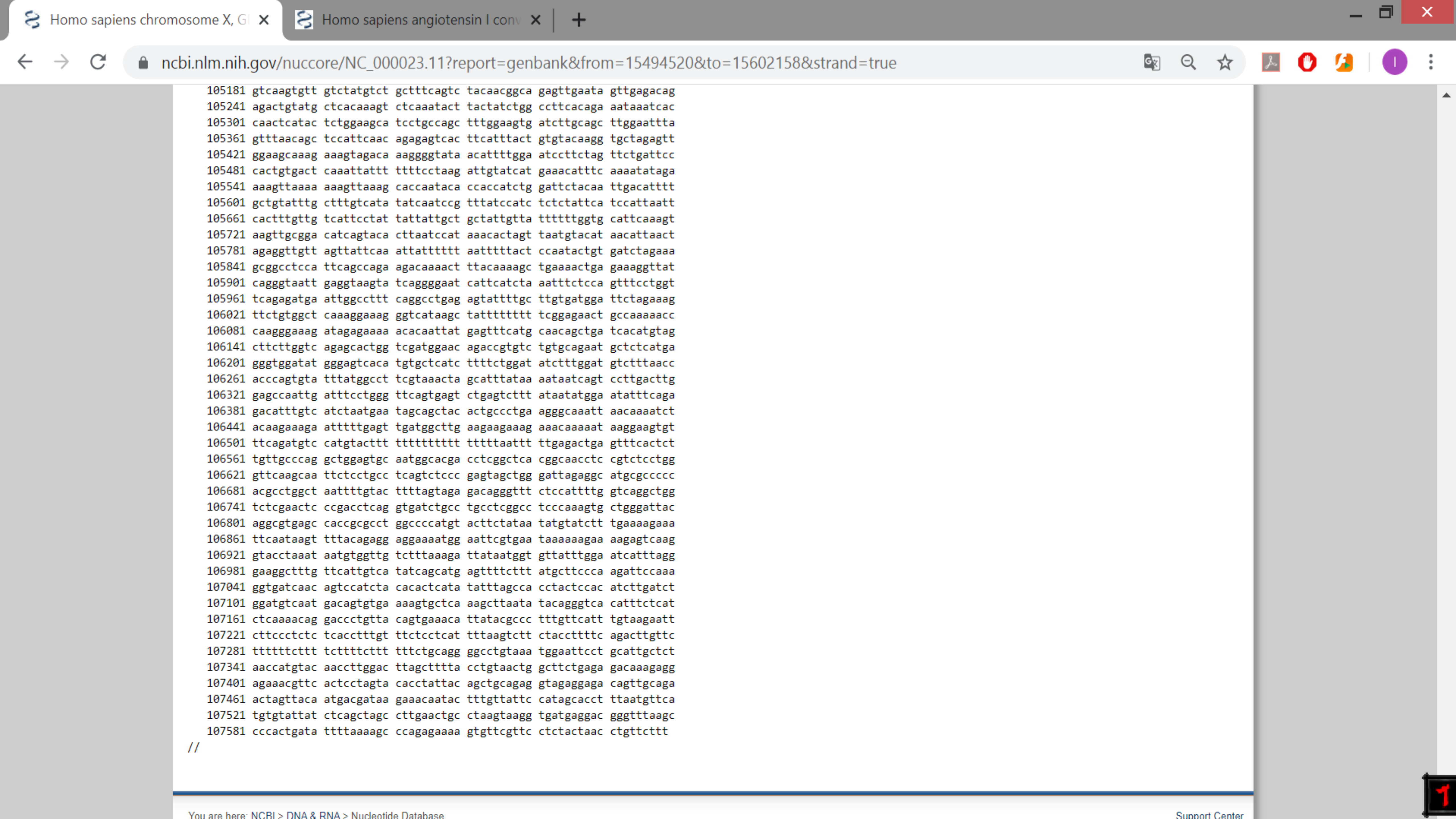

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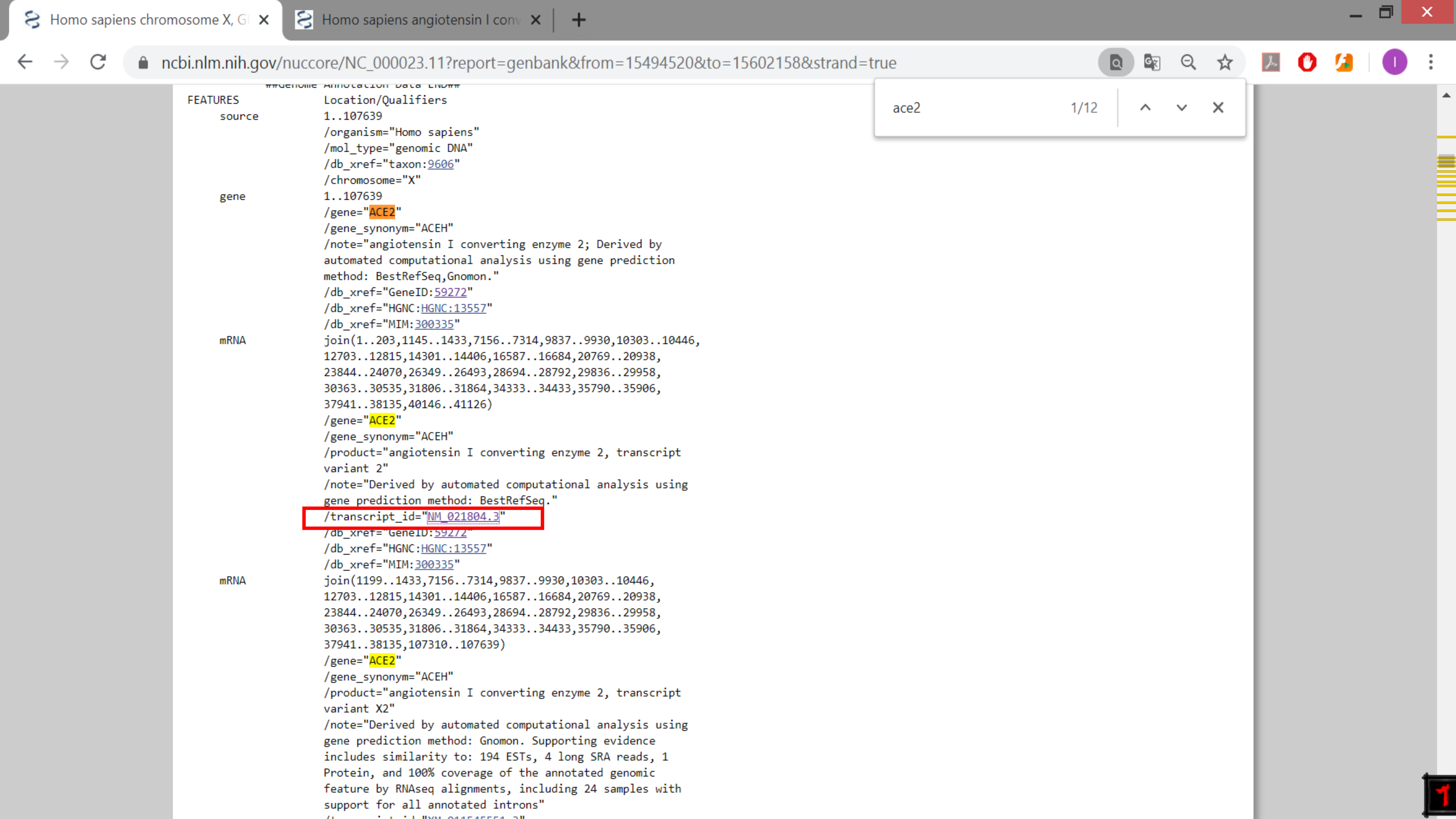

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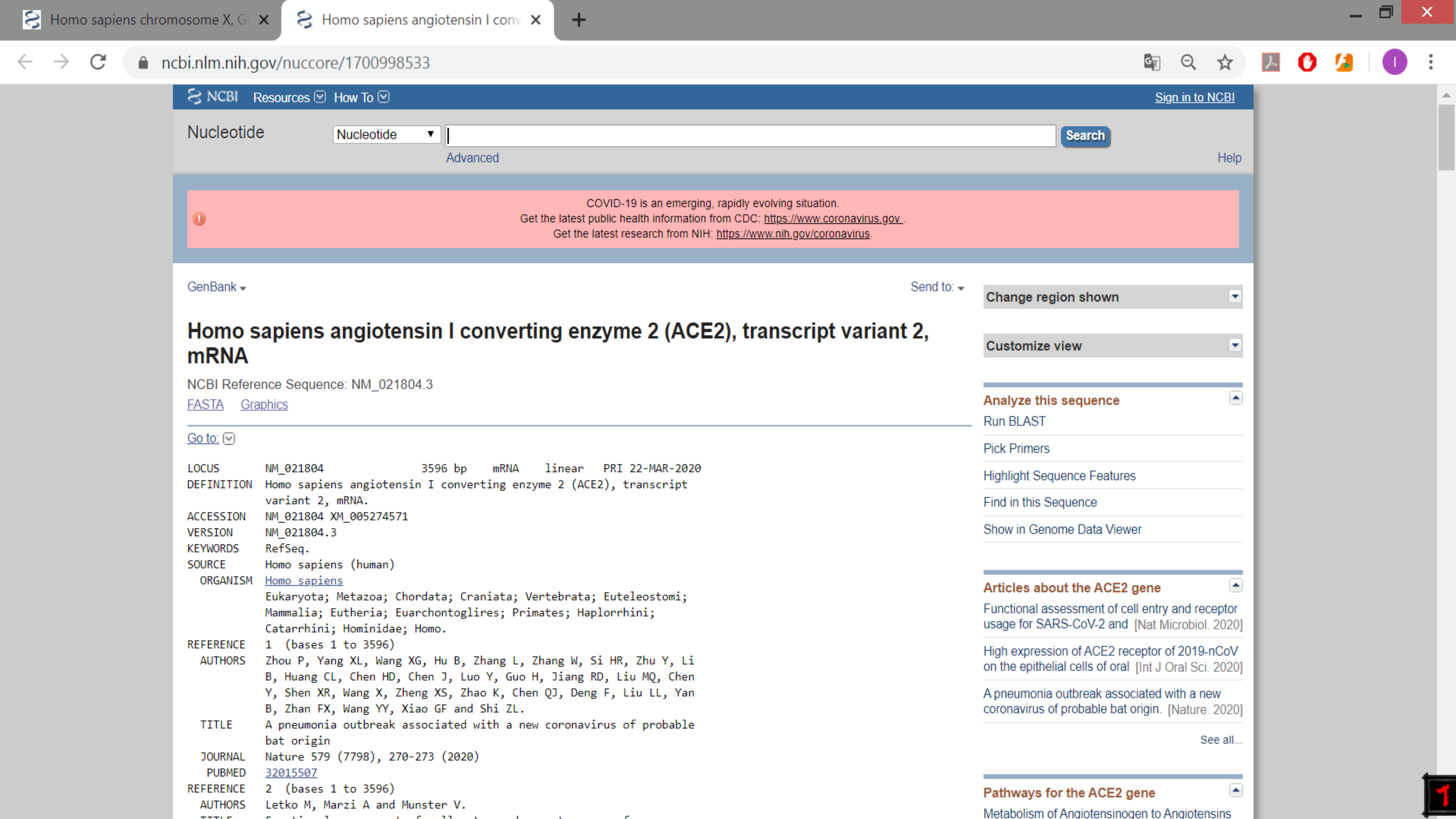

COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: https://www.coronavirus.gov .
Get the latest research from NIH: https://www.nih.gov/coronavirus.

Homo sapiens angiotensin I converting enzyme 2 (ACE2), transcript variant 2, mRNA

NCBI Reference Sequence: NM_021804.3

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  AUTHORS   Zhou P, Yang XL, Wang XG, Hu B, Zhang L, Zhang W, Si HR, Zhu Y, Li
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            Y, Shen XR, Wang X, Zheng XS, Zhao K, Chen QJ, Deng F, Liu LL, Yan
            B, Zhan FX, Wang YY, Xiao GF and Shi ZL.
  TITLE     A pneumonia outbreak associated with a new coronavirus of probable
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  JOURNAL   Nature 579 (7798), 270-273 (2020)
   PUBMED   32015507
REFERENCE   2  (bases 1 to 3596)
  AUTHORS   Letko M, Marzi A and Munster V.
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Analyze this sequence

Articles about the ACE2 gene

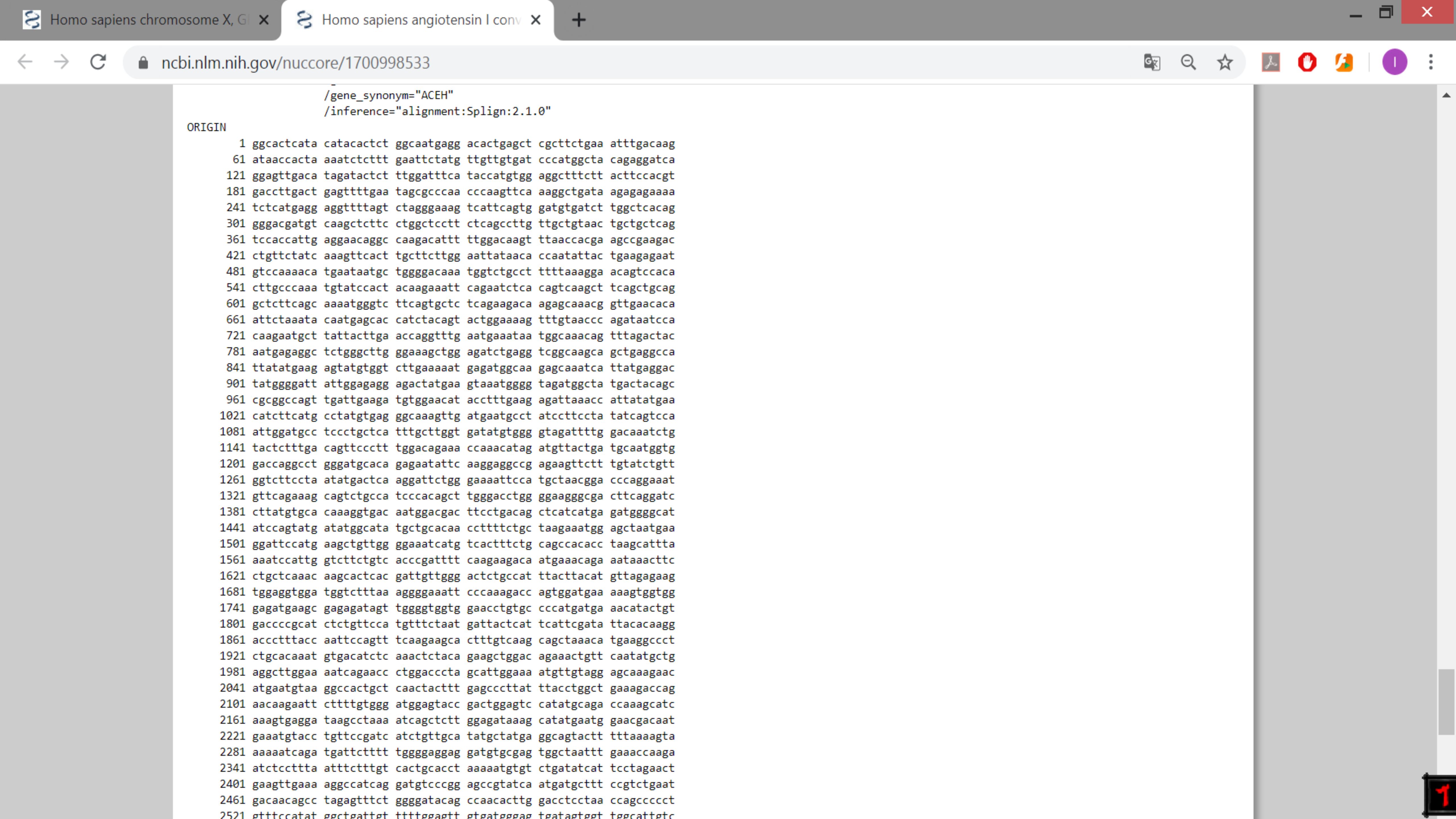
Functional assessment of cell entry and receptor usage for SARS-CoV-2 and [Nat Microbiol. 2020]

High expression of ACE2 receptor of 2019-nCoV on the epithelial cells of oral [Int J Oral Sci. 2020]

A pneumonia outbreak associated with a new coronavirus of probable bat origin. [Nature. 2020]

Pathways for the ACE2 gene

Metabolism of Angiotensinogen to Angiotensins



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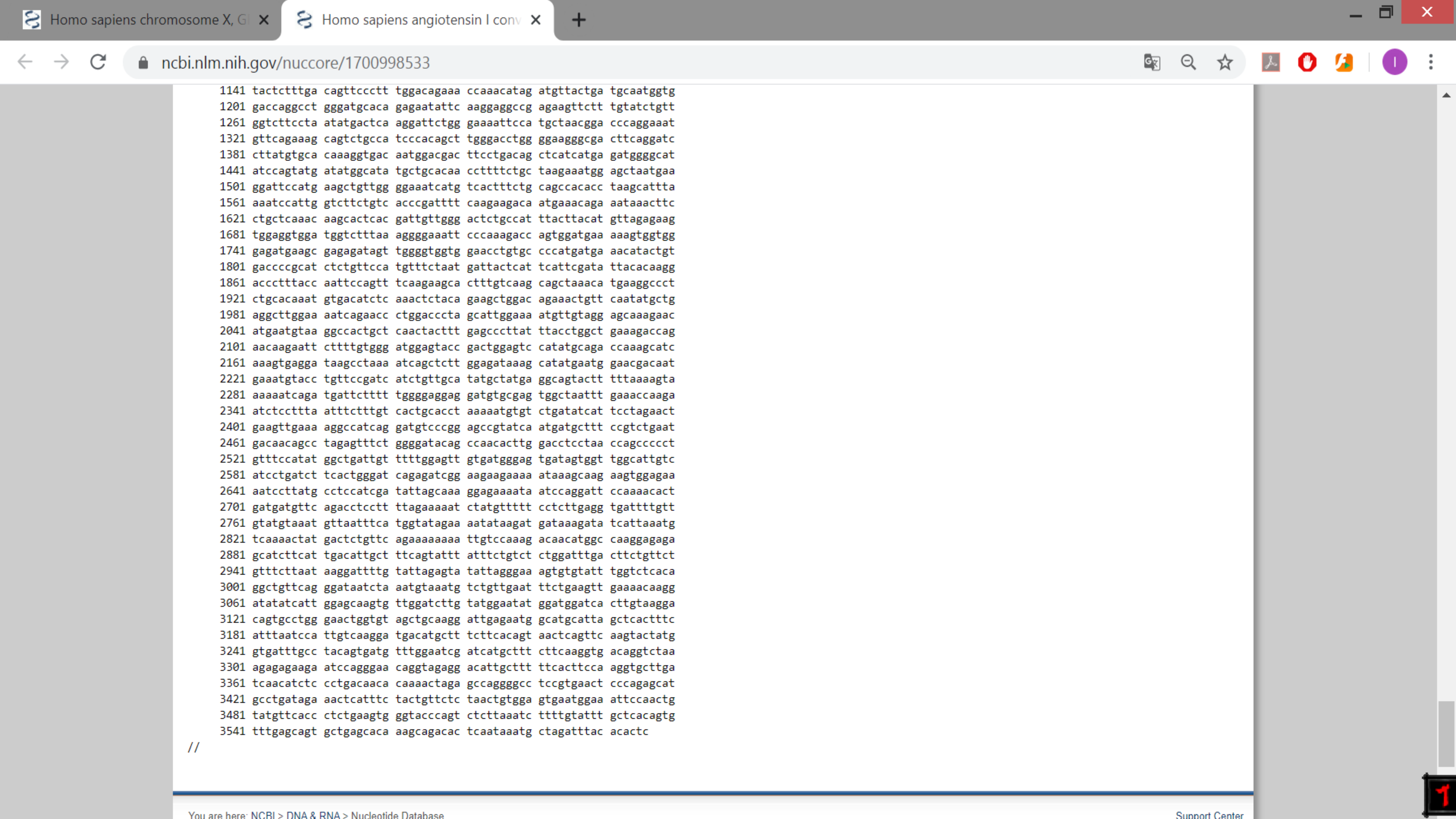

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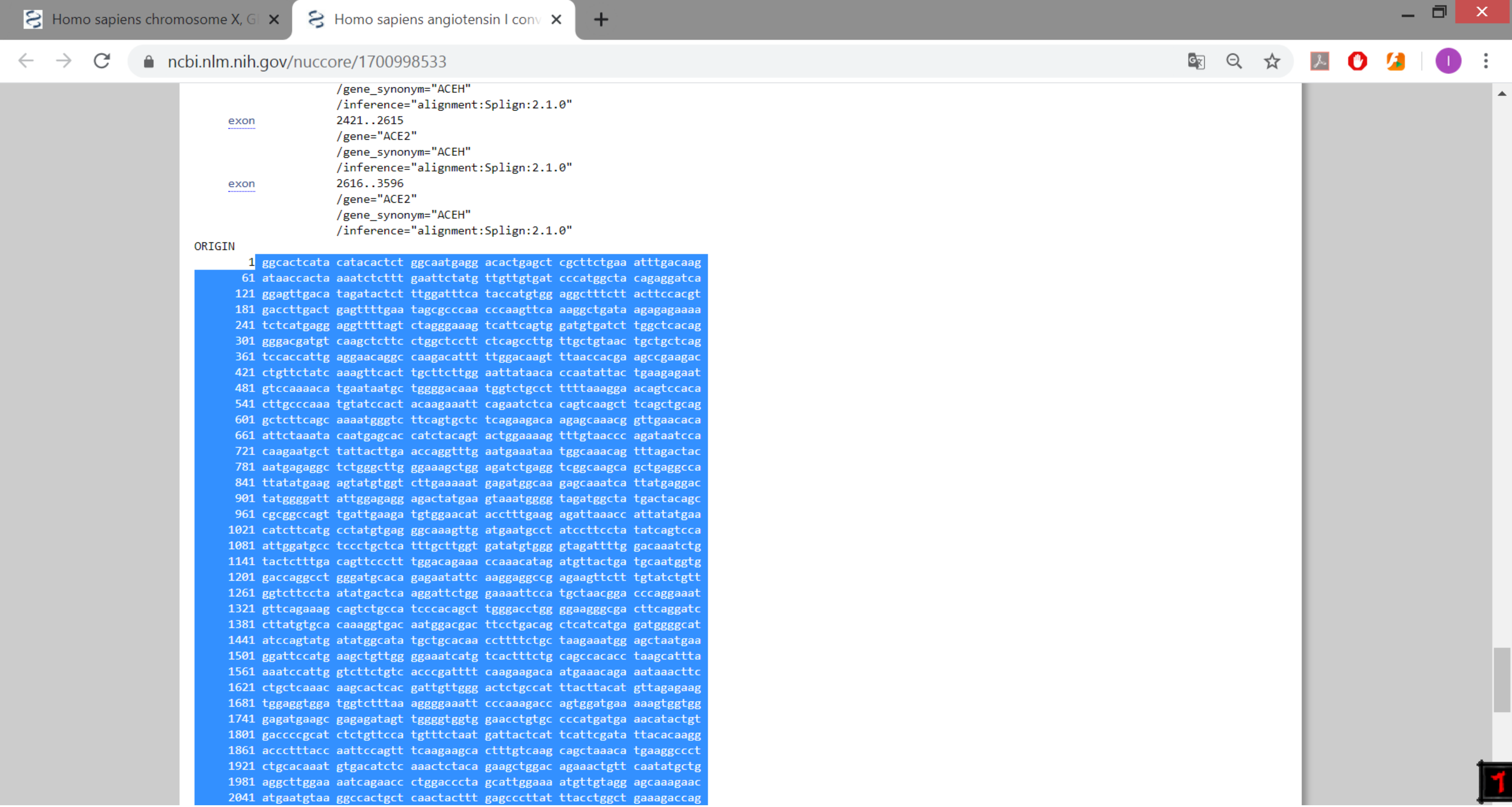

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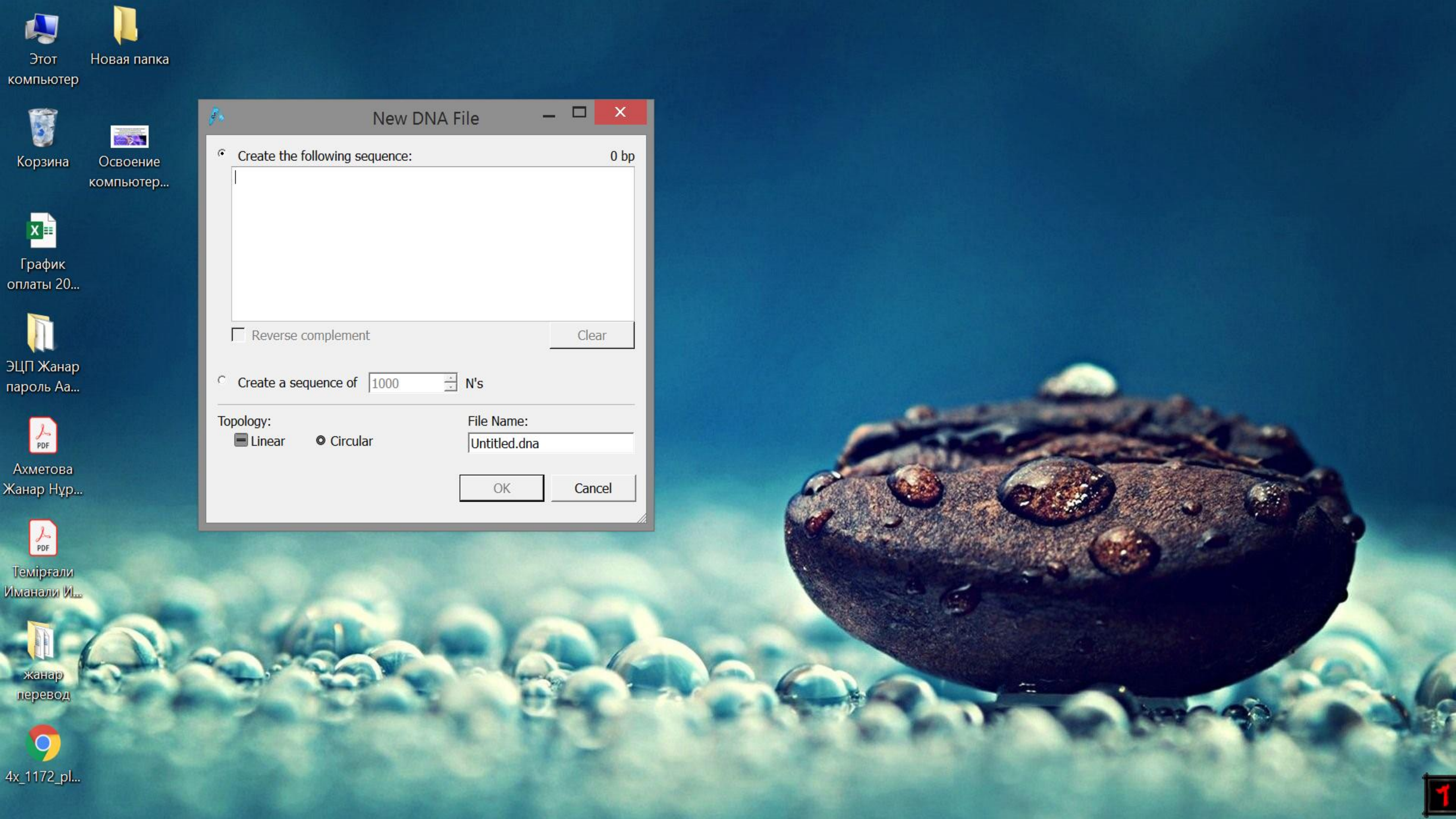

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☐ Reverse complement

○ Create a sequence of 1000 N's

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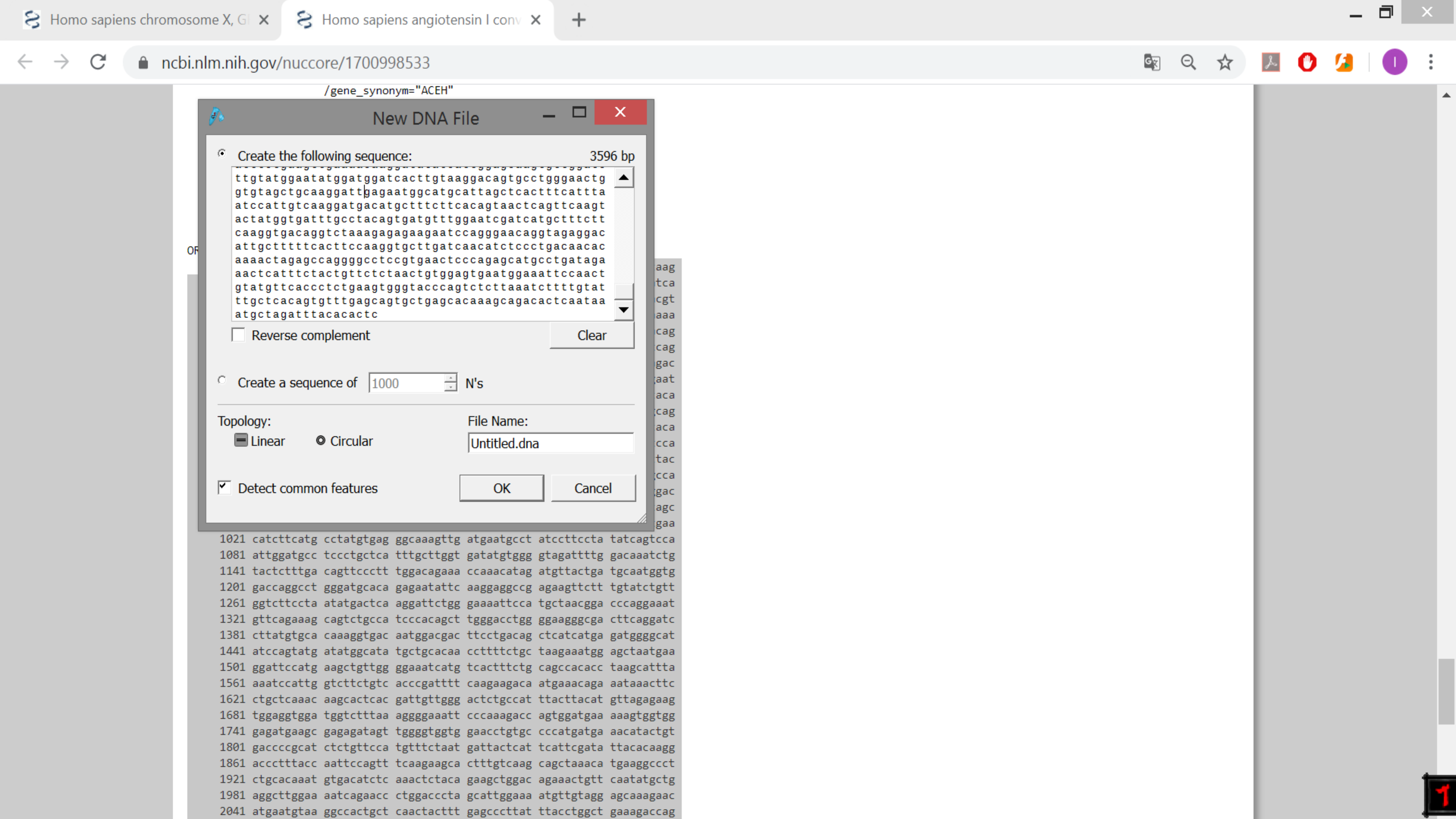

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☐ Reverse complement

○ Create a sequence of 1000 N's

Topology: ☐ Linear ● Circular

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☑ Detect common features

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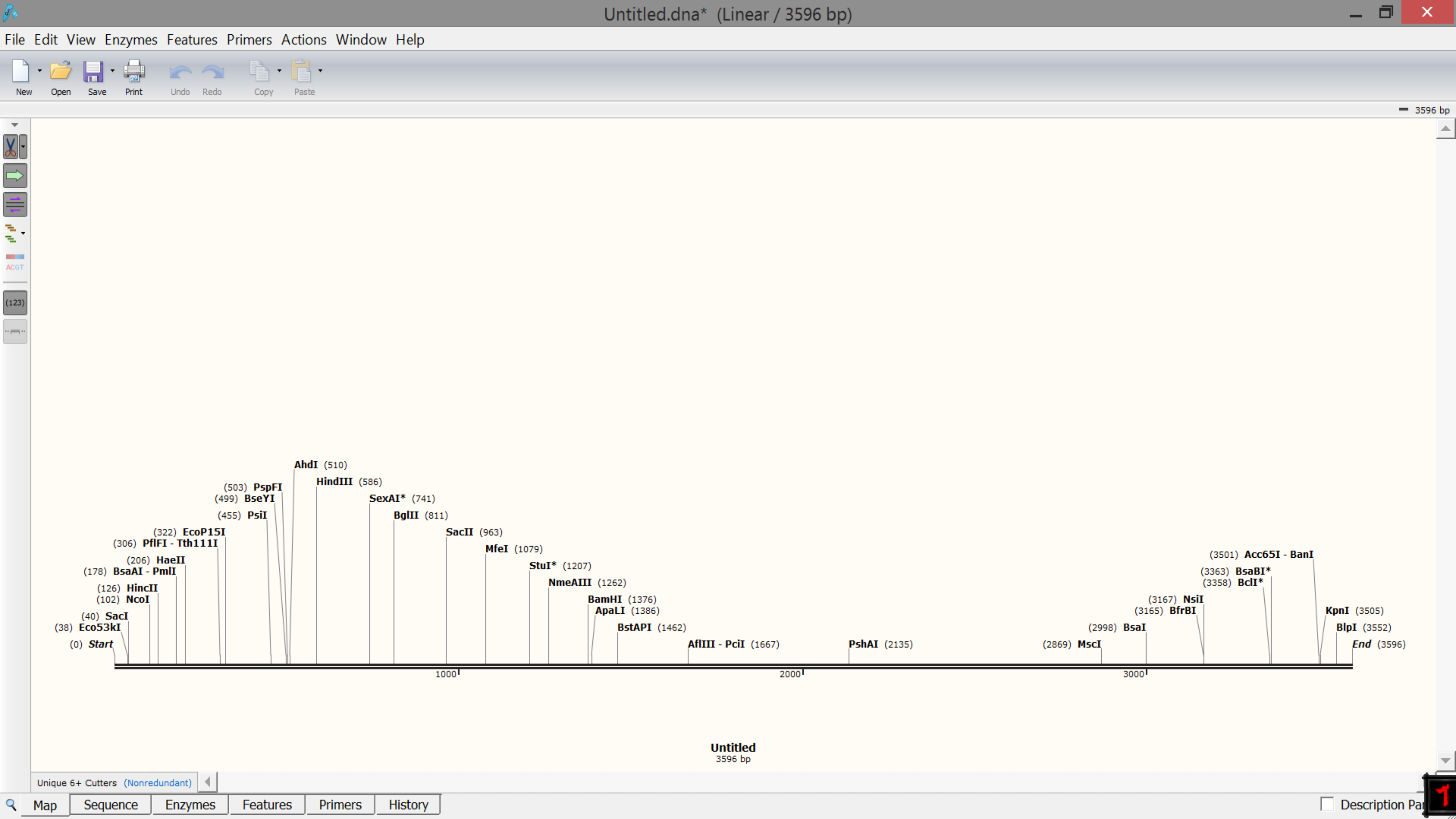
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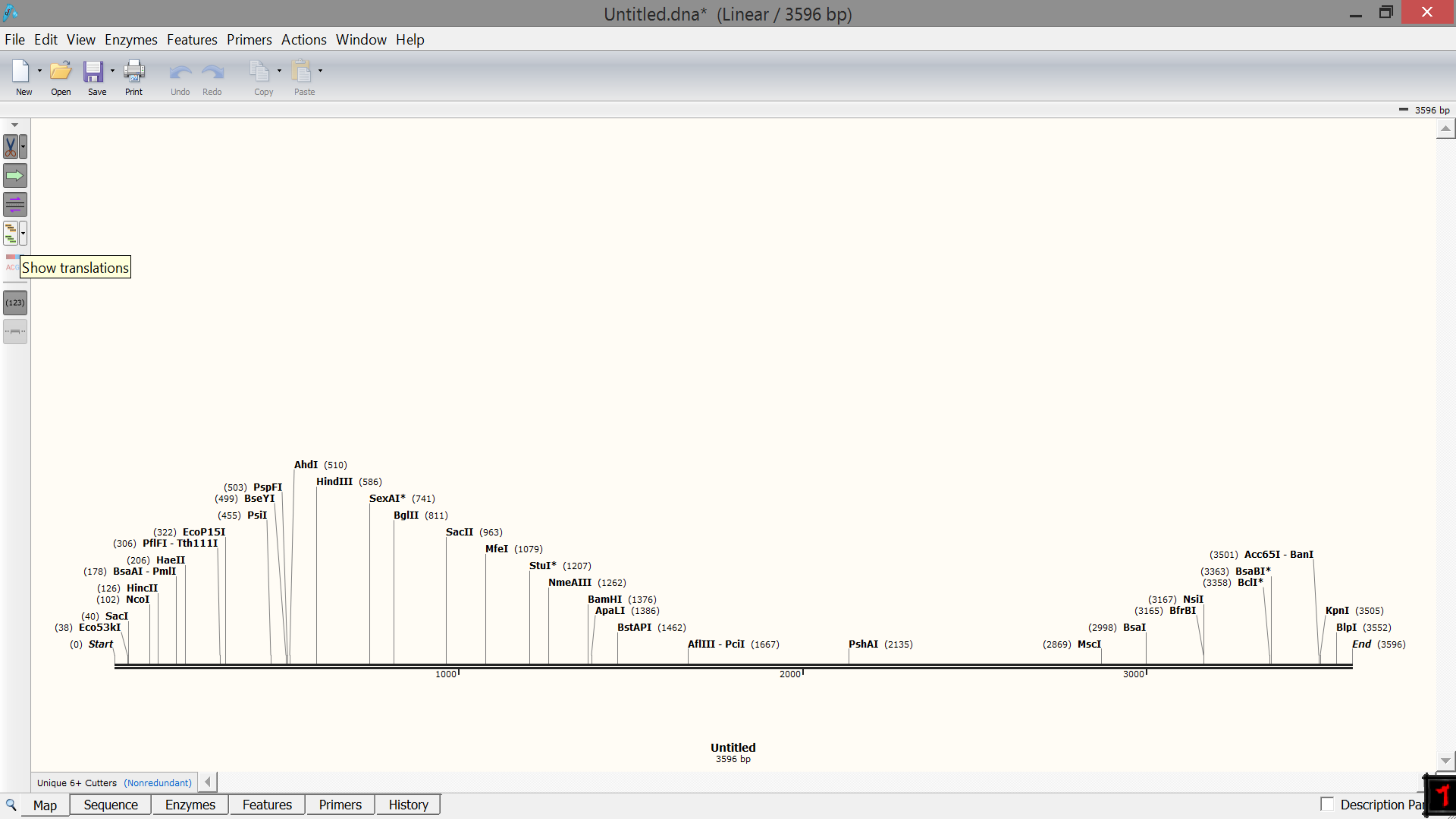
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Show translations
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HindIII (586)
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SacII (963)
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MfeI (1079)
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(178) BsaAI - PmlI
NmeAIII (1262)
(126) HincII
BamHI (1376)
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(40) SacI
BstAPI (1462)
(38) Eco53kI
(0) Start
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PshAI (2135)
(2869) MscI
(2998) BsaI
(3167) NsiI
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End (3596)
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Map
Sequence
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History
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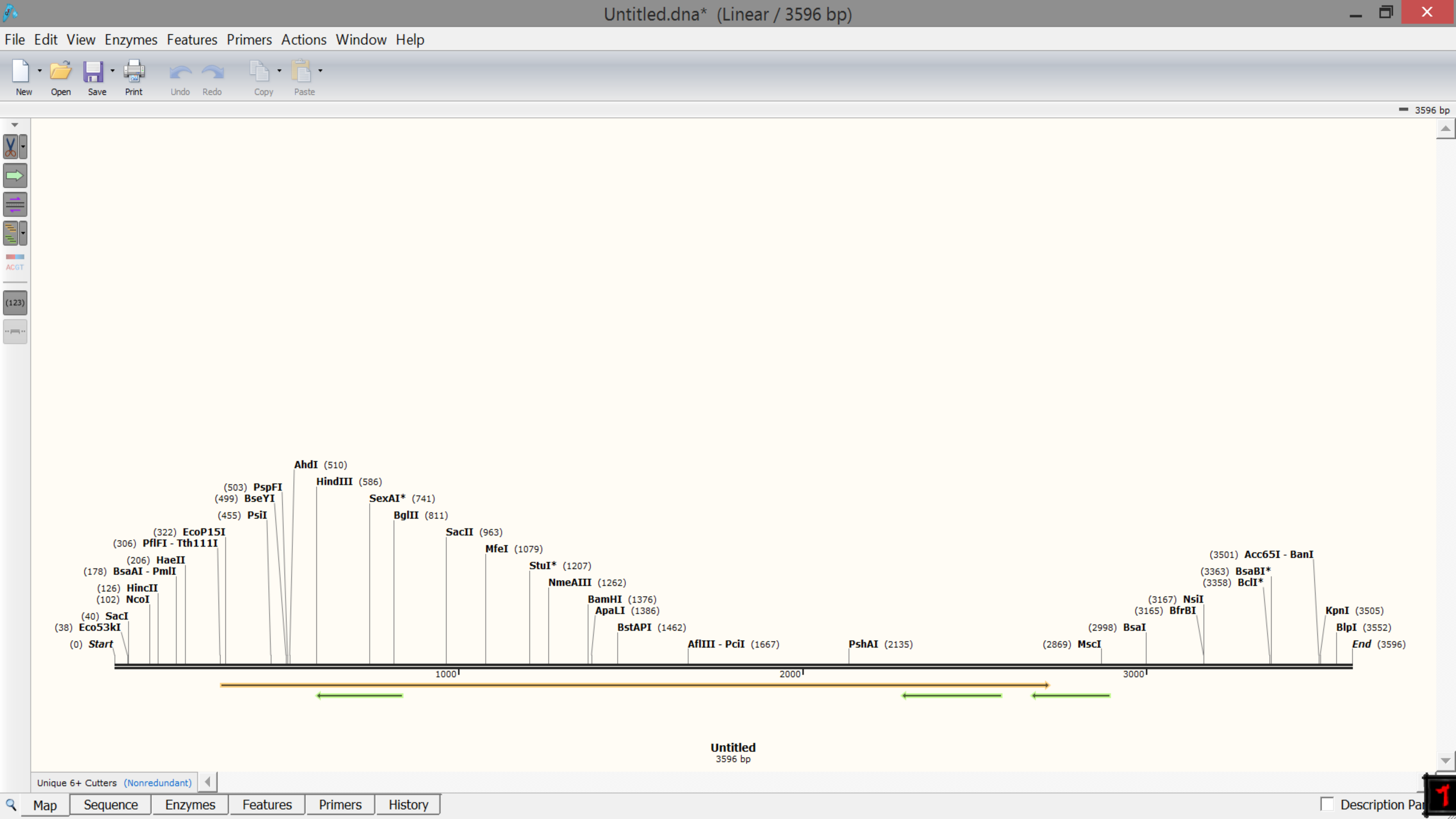
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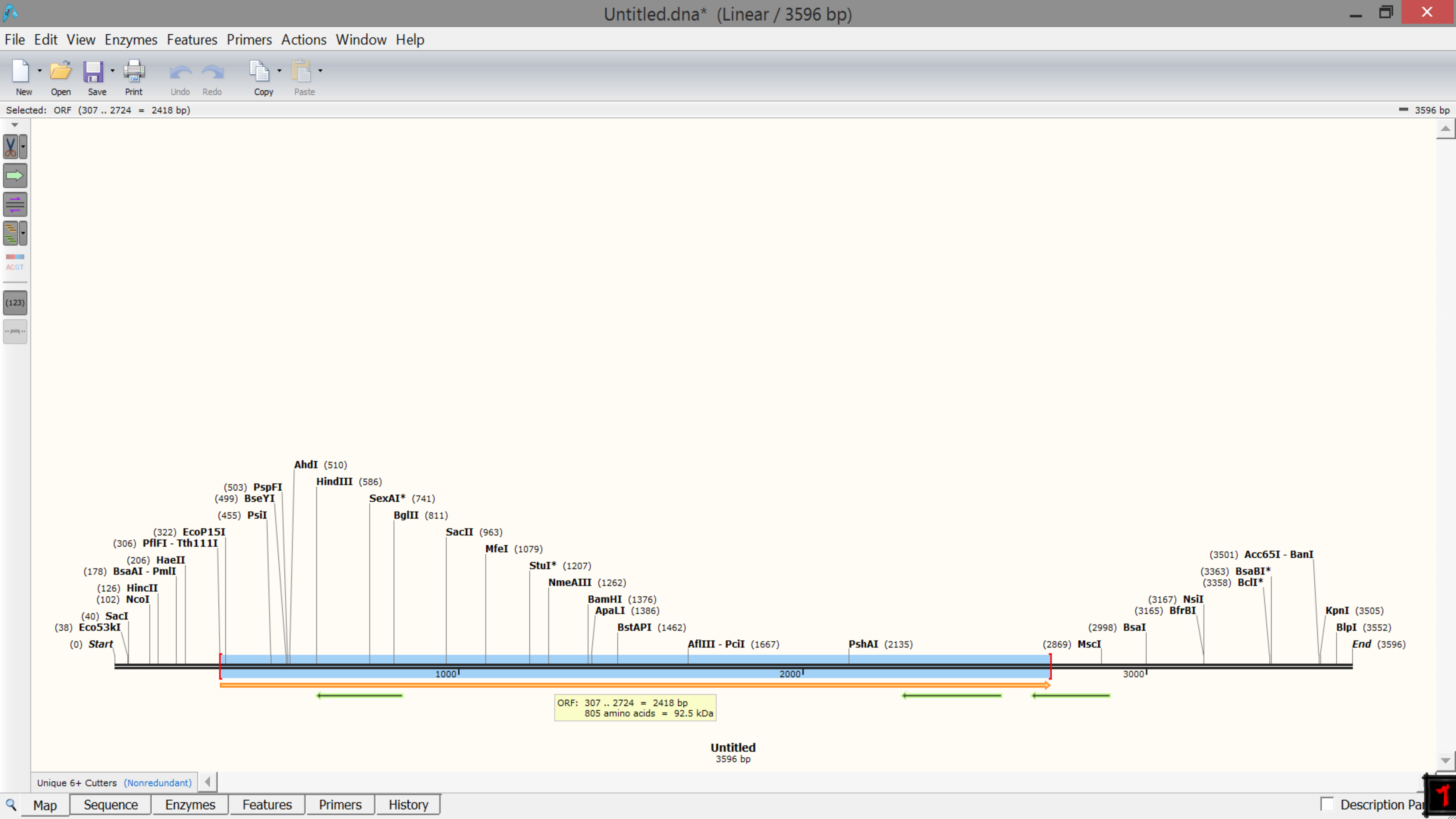

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ORF: 307 .. 2724 = 2418 bp
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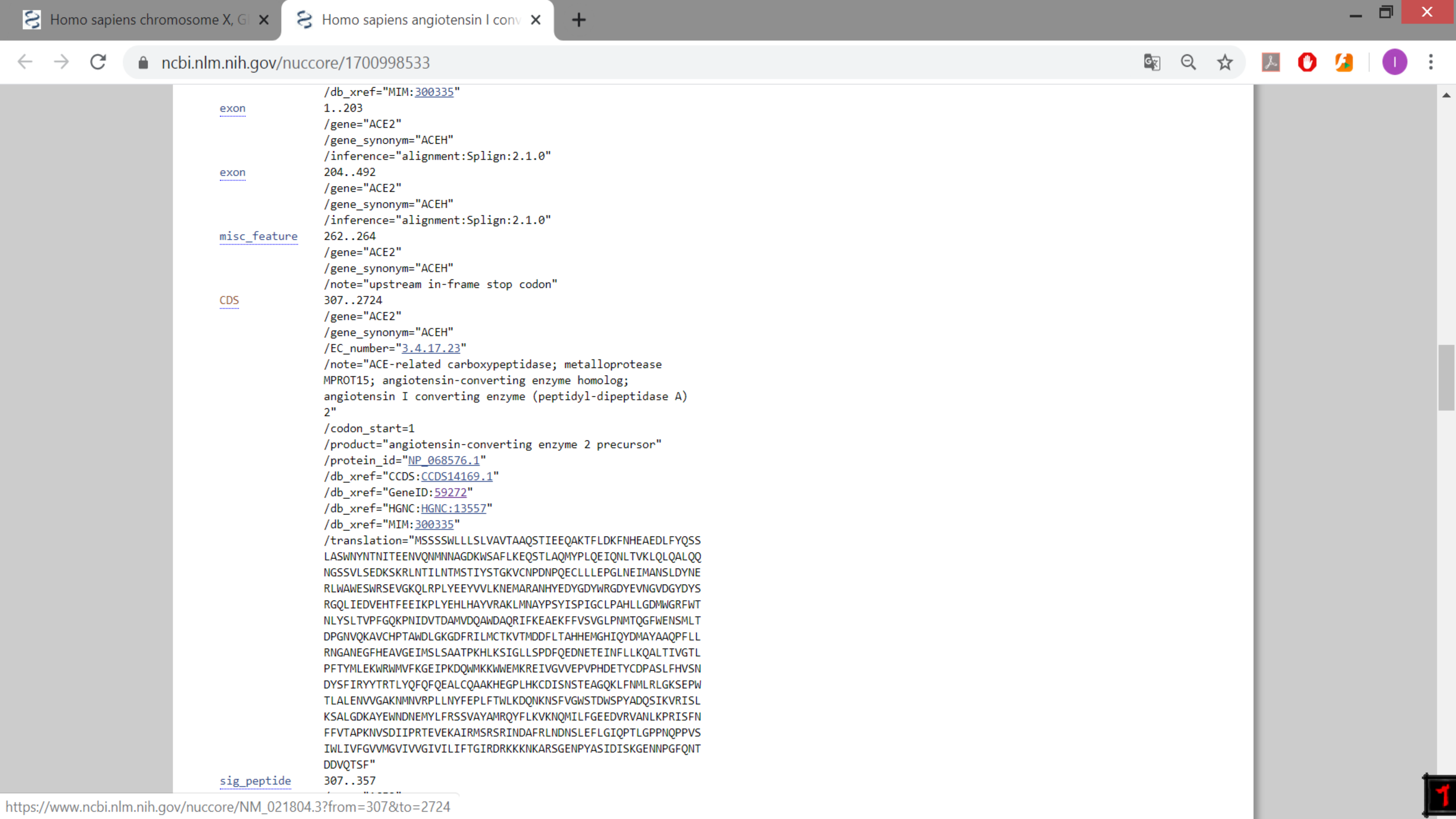

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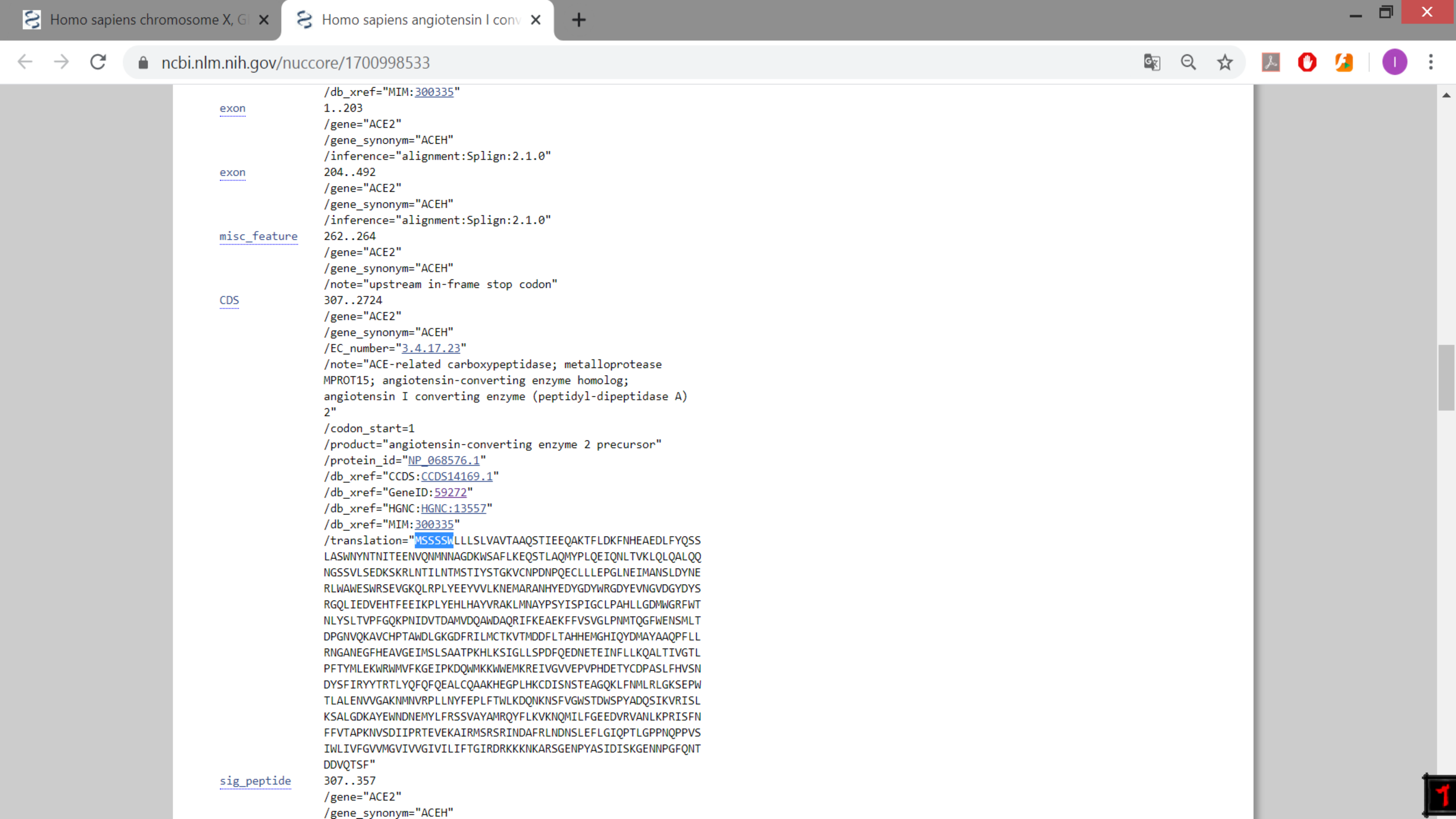

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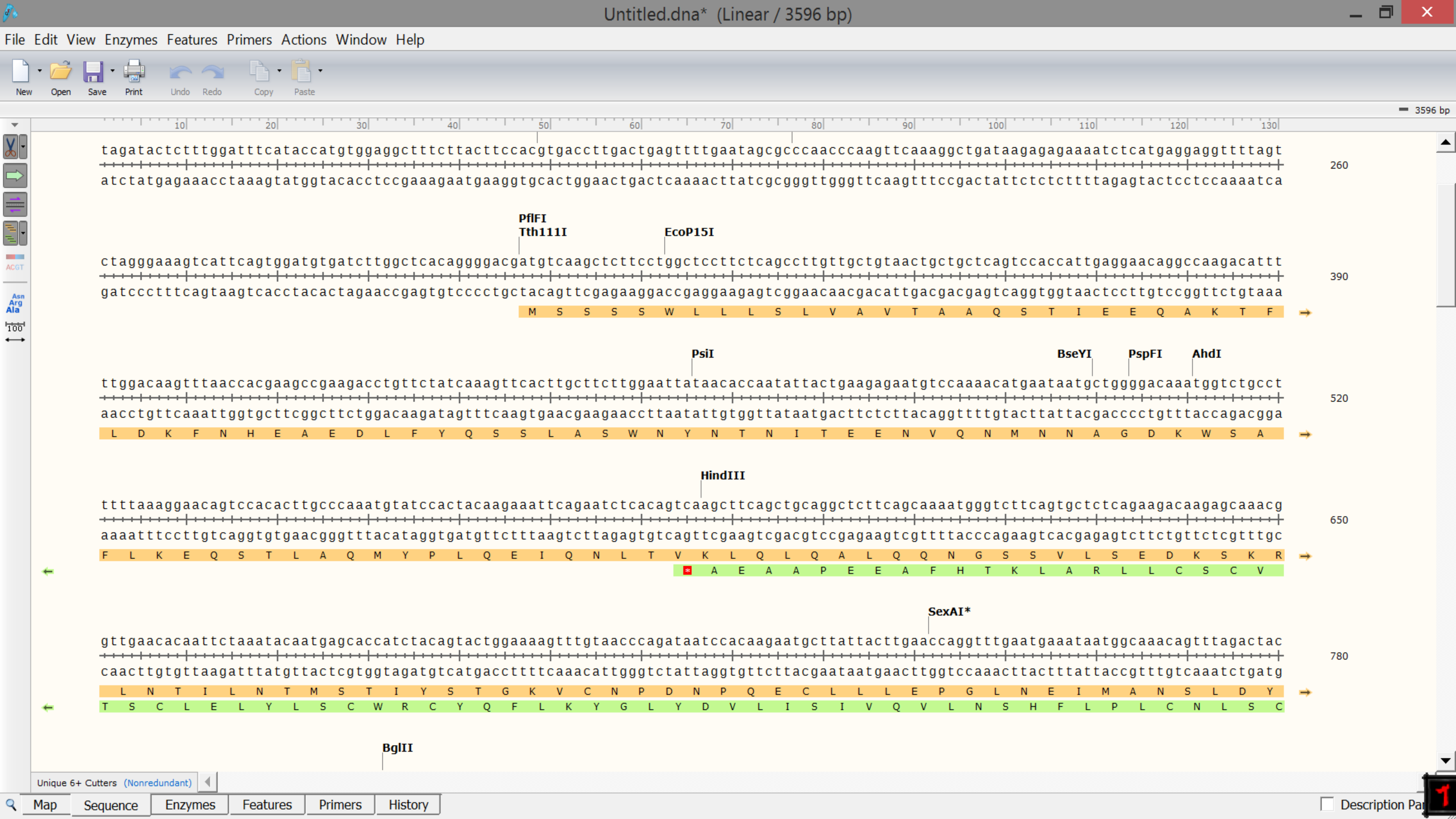

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                                              PflFI
                                              Tth111I                     EcoP15I
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                                              M  S  S  S  S  W  L  L  L  S  L  V  A  V  T  A  A  Q  S  T  I  E  E  Q  A  K  T  F  →

                                                                            PsiI                                       BseYI       PspFI      AhdI
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 L  D  K  F  N  H  E  A  E  D  L  F  Y  Q  S  S  L  A  S  W  N  Y  N  T  N  I  T  E  E  N  V  Q  N  M  N  N  A  G  D  K  W  S  A  →

                                                                             HindIII
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F  L  K  E  Q  S  T  L  A  Q  M  Y  P  L  Q  E  I  Q  N  L  T  V  K  L  Q  L  Q  A  L  Q  Q  N  G  S  S  V  L  S  E  D  K  S  K  R  →
←                                                                  *  A  E  A  A  P  E  E  A  F  H  T  K  L  A  R  L  L  C  S  C  V

                                                                                                       SexAI*
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  L  N  T  I  L  N  T  M  S  T  I  Y  S  T  G  K  V  C  N  P  D  N  P  Q  E  C  L  L  L  E  P  G  L  N  E  I  M  A  N  S  L  D  Y  →
← T  S  C  L  E  L  Y  L  S  C  W  R  C  Y  Q  F  L  K  Y  G  L  Y  D  V  L  I  S  I  V  Q  V  L  N  S  H  F  L  P  L  C  N  L  S  C

                              BglII
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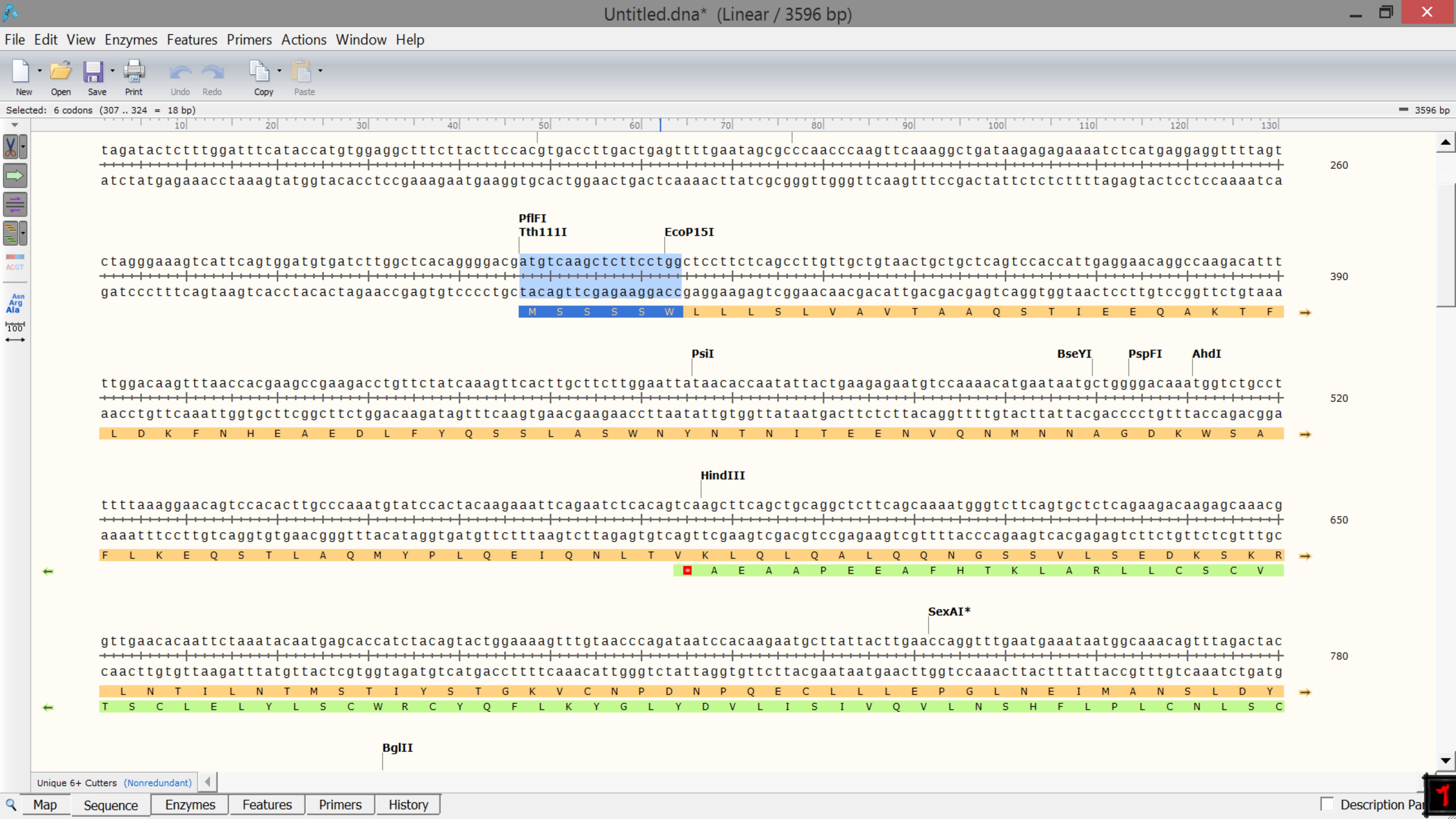

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3596 bp

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PflFI
Tth111I                                                  EcoP15I
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M  S  S  S  S  W  L  L  L  S  L  V  A  V  T  A  A  Q  S  T  I  E  E  Q  A  K  T  F

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                                                                   *  A  E  A  A  P  E  E  A  F  H  T  K  L  A  R  L  L  C  S  C  V

SexAI*
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BglII
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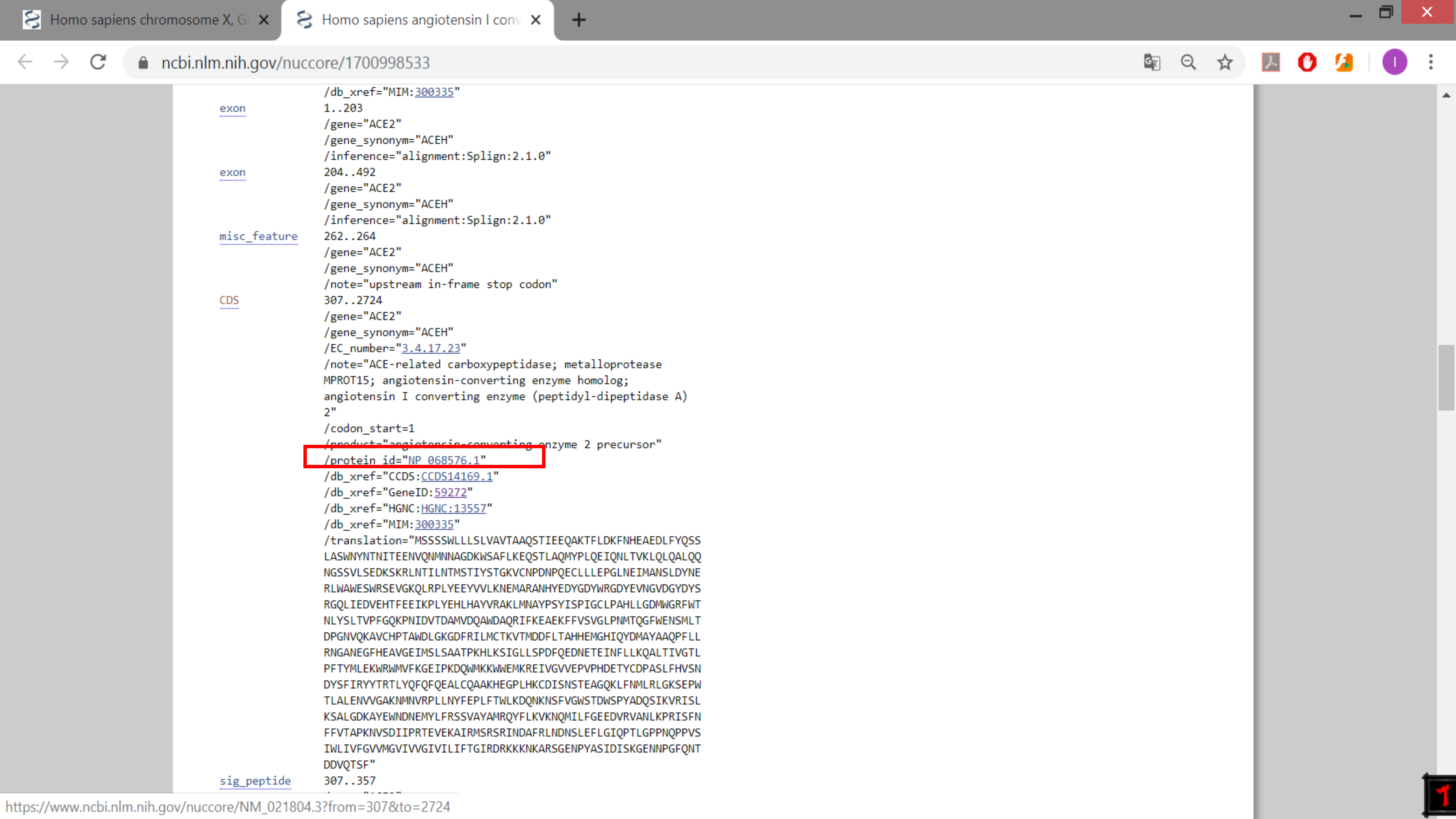

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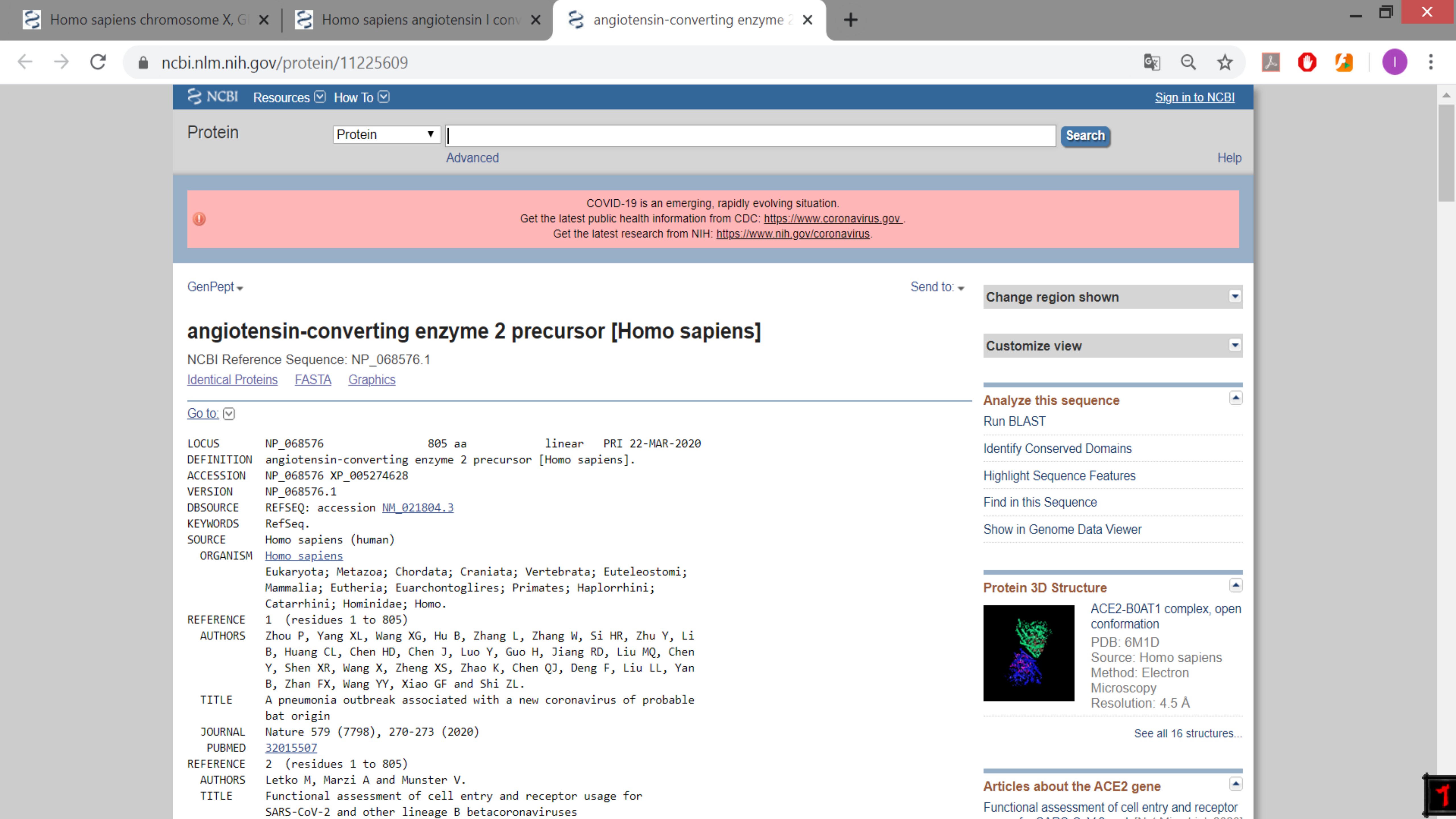

COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: https://www.coronavirus.gov .
Get the latest research from NIH: https://www.nih.gov/coronavirus.

angiotensin-converting enzyme 2 precursor [Homo sapiens]

NCBI Reference Sequence: NP_068576.1

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VERSION     NP_068576.1
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KEYWORDS    RefSeq.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (residues 1 to 805)
  AUTHORS   Zhou P, Yang XL, Wang XG, Hu B, Zhang L, Zhang W, Si HR, Zhu Y, Li
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            Y, Shen XR, Wang X, Zheng XS, Zhao K, Chen QJ, Deng F, Liu LL, Yan
            B, Zhan FX, Wang YY, Xiao GF and Shi ZL.
  TITLE     A pneumonia outbreak associated with a new coronavirus of probable
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  JOURNAL   Nature 579 (7798), 270-273 (2020)
   PUBMED   32015507
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  AUTHORS   Letko M, Marzi A and Munster V.
  TITLE     Functional assessment of cell entry and receptor usage for
            SARS-CoV-2 and other lineage B betacoronaviruses
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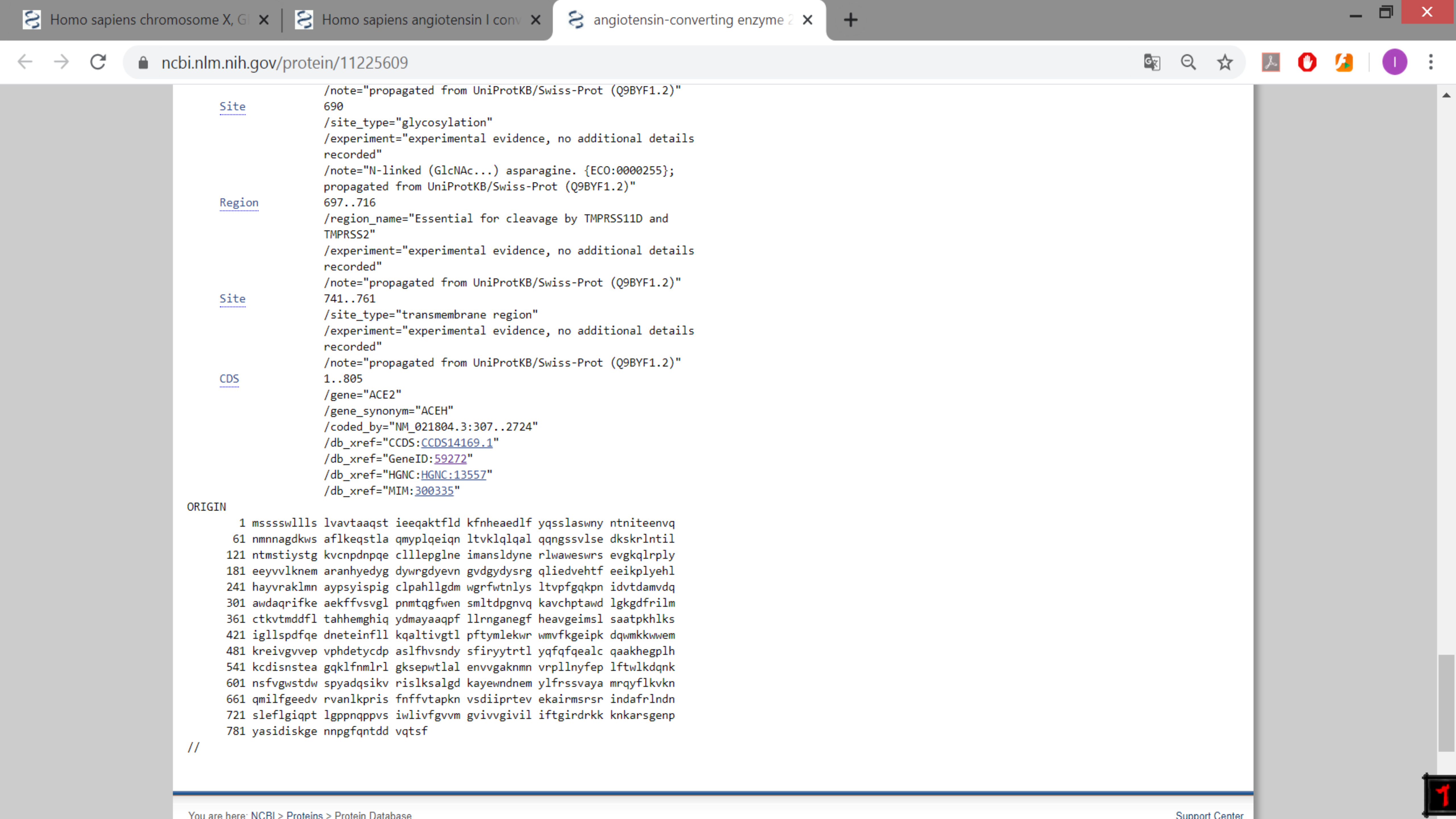
ACE2-B0AT1 complex, open conformation
PDB: 6M1D
Source: Homo sapiens
Method: Electron Microscopy
Resolution: 4.5 Å

Functional assessment of cell entry and receptor



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ORIGIN
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      121 ntmstiystg kvcnpdnpqe clllepglne imansldyne rlwaweswrs evgkqlrply
      181 eeyvvlknem aranhyedyg dywrgdyevn gvdgydysrg qliedvehtf eeikplyehl
      241 hayvraklmn aypsyispig clpahllgdm wgrfwtnlys ltvpfgqkpn idvtdamvdq
      301 awdaqrifke aekffvsvgl pnmtqgfwen smltdpgnvq kavchptawd lgkgdfrilm
      361 ctkvtmddfl tahhemghiq ydmayaaqpf llrnganegf heavgeimsl saatpkhlks
      421 igllspdfqe dneteinfll kqaltivgtl pftymlekwr wmvfkgeipk dqwmkkwwem
      481 kreivgvvep vphdetycdp aslfhvsndy sfiryytrtl yqfqfqealc qaakhegplh
      541 kcdisnstea gqklfnmlrl gksepwtlal envvgaknmn vrpllnyfep lftwlkdqnk
      601 nsfvgwstdw spyadqsikv rislksalgd kayewndnem ylfrssvaya mrqyflkvkn
      661 qmilfgeedv rvanlkpris fnffvtapkn vsdiiprtev ekairmsrsr indafrlndn
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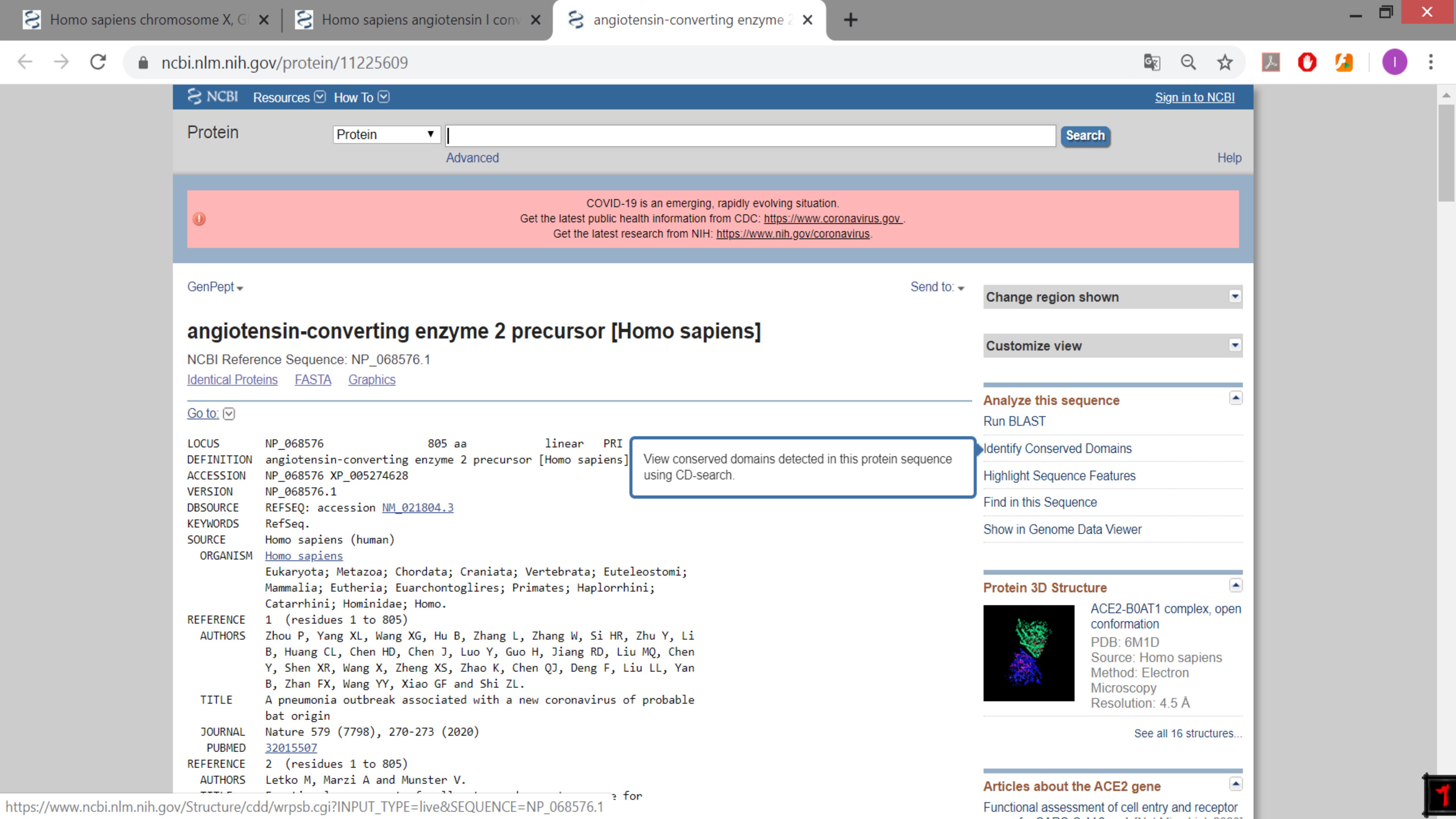

COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: https://www.coronavirus.gov .
Get the latest research from NIH: https://www.nih.gov/coronavirus.

angiotensin-converting enzyme 2 precursor [Homo sapiens]

NCBI Reference Sequence: NP_068576.1

Identical Proteins FASTA Graphics

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LOCUS       NP_068576                805 aa            linear   PRI
DEFINITION  angiotensin-converting enzyme 2 precursor [Homo sapiens]
ACCESSION   NP_068576 XP_005274628
VERSION     NP_068576.1
DBSOURCE    REFSEQ: accession NM_021804.3
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 805)
  AUTHORS   Zhou P, Yang XL, Wang XG, Hu B, Zhang L, Zhang W, Si HR, Zhu Y, Li
            B, Huang CL, Chen HD, Chen J, Luo Y, Guo H, Jiang RD, Liu MQ, Chen
            Y, Shen XR, Wang X, Zheng XS, Zhao K, Chen QJ, Deng F, Liu LL, Yan
            B, Zhan FX, Wang YY, Xiao GF and Shi ZL.
  TITLE     A pneumonia outbreak associated with a new coronavirus of probable
            bat origin
  JOURNAL   Nature 579 (7798), 270-273 (2020)
   PUBMED   32015507
REFERENCE   2  (residues 1 to 805)
  AUTHORS   Letko M, Marzi A and Munster V.
                                                          for
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View conserved domains detected in this protein sequence using CD-search.

Analyze this sequence

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

Protein 3D Structure

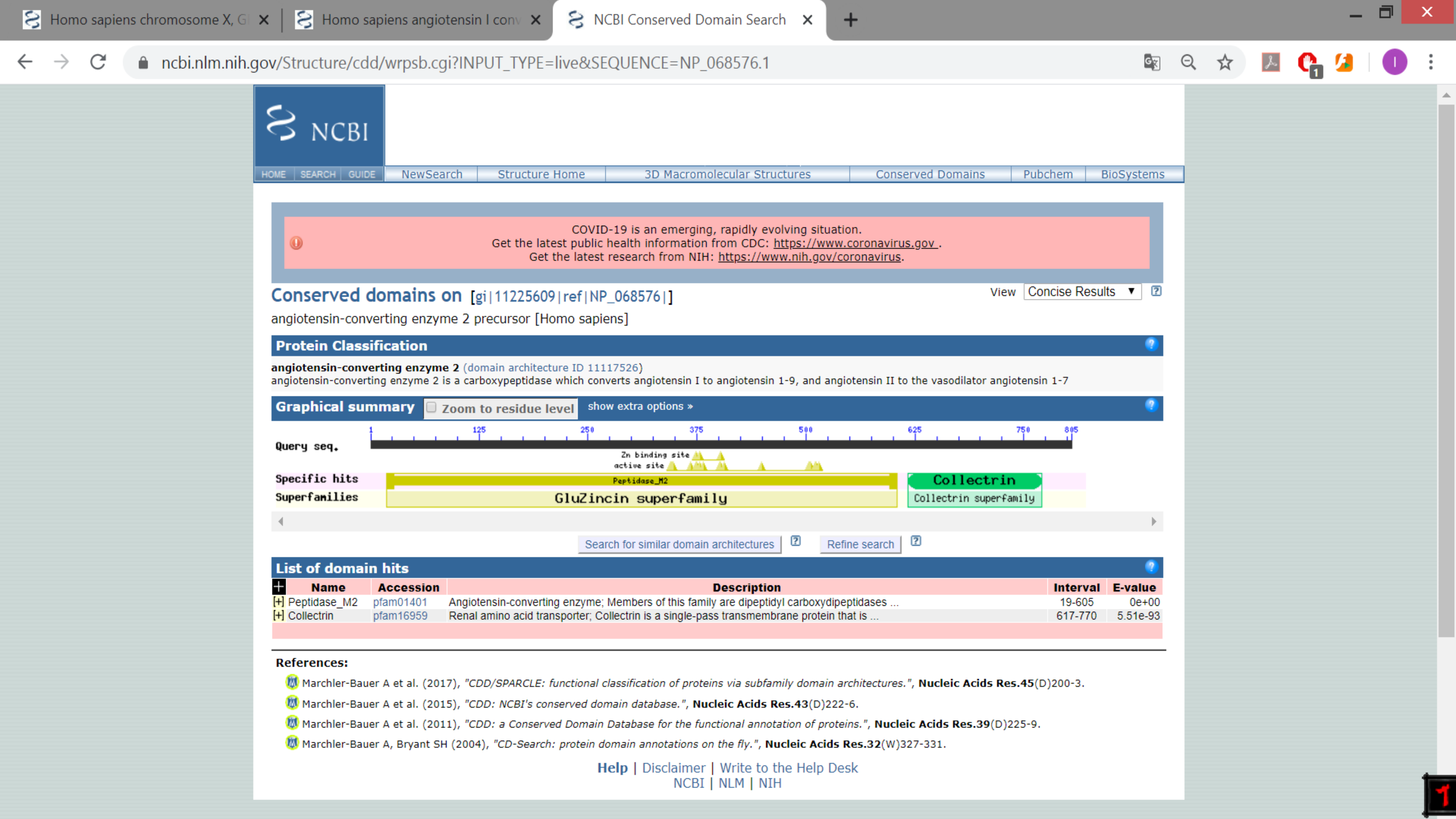
ACE2-B0AT1 complex, open conformation
PDB: 6M1D
Source: Homo sapiens
Method: Electron Microscopy
Resolution: 4.5 Å

See all 16 structures...

Articles about the ACE2 gene

Functional assessment of cell entry and receptor

https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi?INPUT_TYPE=live&SEQUENCE=NP_068576.1



COVID-19 is an emerging, rapidly evolving situation.
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Conserved domains on [gi|11225609|ref|NP_068576|]

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angiotensin-converting enzyme 2 precursor [Homo sapiens]

Protein Classification

angiotensin-converting enzyme 2 (domain architecture ID 11117526)
angiotensin-converting enzyme 2 is a carboxypeptidase which converts angiotensin I to angiotensin 1-9, and angiotensin II to the vasodilator angiotensin 1-7

Graphical summary

☐ Zoom to residue level show extra options »

List of domain hits

Name	Accession	Description	Interval	E-value
[+] Peptidase_M2	pfam01401	Angiotensin-converting enzyme; Members of this family are dipeptidyl carboxydipeptidases ...	19-605	0e+00
[+] Collectrin	pfam16959	Renal amino acid transporter; Collectrin is a single-pass transmembrane protein that is ...	617-770	5.51e-93

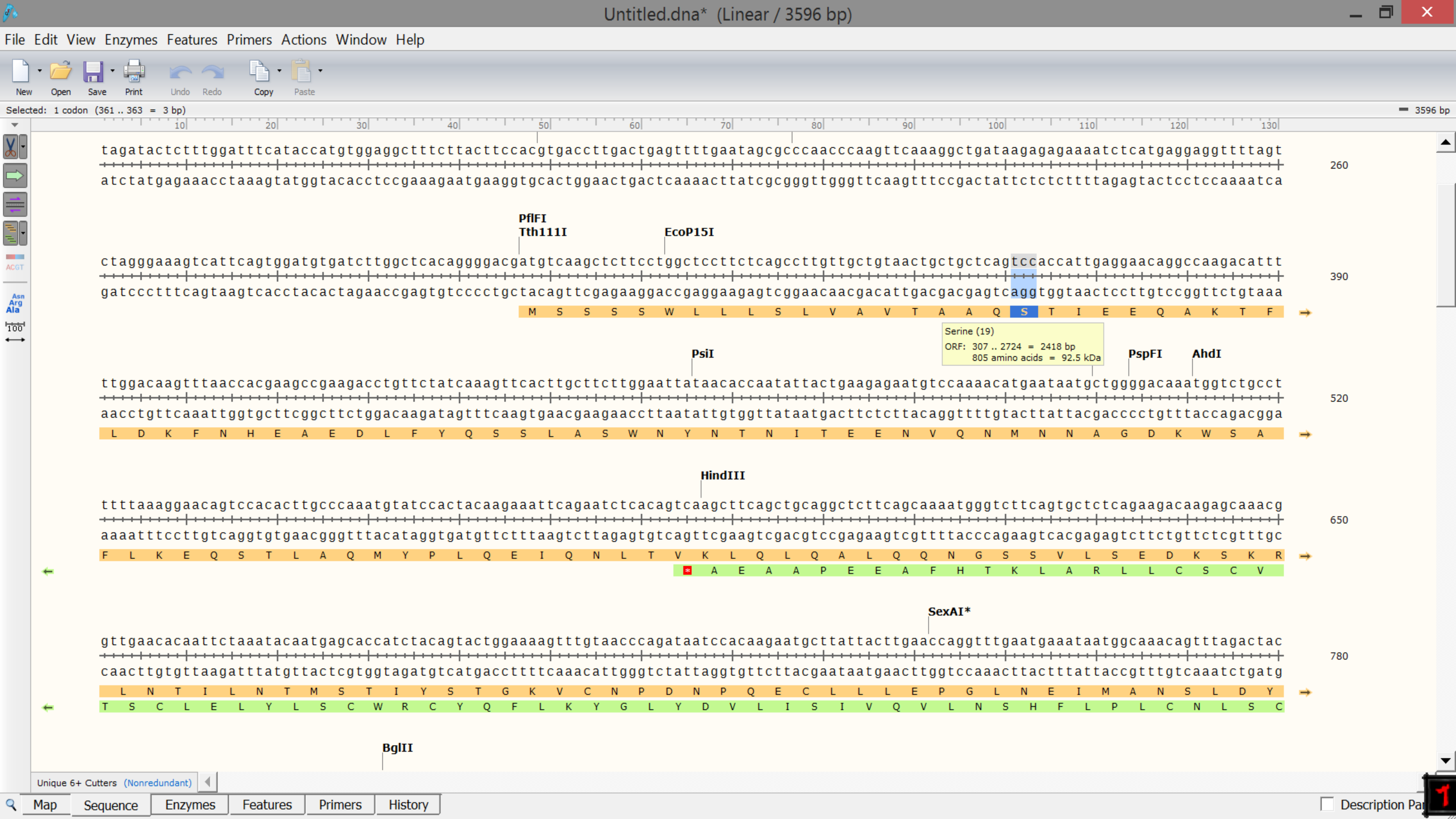
References:

Marchler-Bauer A et al. (2017), *"CDD/SPARCLE: functional classification of proteins via subfamily domain architectures."*, **Nucleic Acids Res.45**(D)200-3.

Marchler-Bauer A et al. (2015), *"CDD: NCBI's conserved domain database."*, **Nucleic Acids Res.43**(D)222-6.

Marchler-Bauer A et al. (2011), *"CDD: a Conserved Domain Database for the functional annotation of proteins."*, **Nucleic Acids Res.39**(D)225-9.

Marchler-Bauer A, Bryant SH (2004), *"CD-Search: protein domain annotations on the fly."*, **Nucleic Acids Res.32**(W)327-331.



Untitled.dna* (Linear / 3596 bp)

Selected: 1 codon (361 .. 363 = 3 bp)   3596 bp

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atctatgagaaacctaaagtatggtacacctccgaaagaatgaaggtgcactggaactgactcaaaacttatcgcgggttgggttcaagtttccgactattctctcttttagagtactcctccaaaatca   260

PflFI
Tth111I   EcoP15I
ctagggaaagtcattcagtggatgtgatcttggctcacaggggacgatgtcaagctcttcctggctccttctcagccttgttgctgtaactgctgctcagtccaccattgaggaacaggccaagacattt
gatccctttcagtaagtcacctacactagaaccgagtgtcccctgctacagttcgagaaggaccgaggaagagtcggaacaacgacattgacgacgagtcaggtggtaactccttgtccggttctgtaaa   390
M S S S S W L L L S L V A V T A A Q S T I E E Q A K T F

Serine (19)
ORF: 307 .. 2724 = 2418 bp
805 amino acids = 92.5 kDa

PsiI   PspFI   AhdI
ttggacaagtttaaccacgaagccgaagacctgttctatcaaagttcacttgcttcttggaattataacaccaatattactgaagagaatgtccaaaacatgaataatgctggggacaaatggtctgcct
aacctgttcaaattggtgcttcggcttctggacaagatagtttcaagtgaacgaagaaccttaatattgtggttataatgacttctcttacaggttttgtacttattacgacccctgtttaccagacgga   520
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HindIII
ttttaaaggaacagtccacacttgcccaaatgtatccactacaagaaattcagaatctcacagtcaagcttcagctgcaggctcttcagcaaaatgggtcttcagtgctctcagaagacaagagcaaacg
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F L K E Q S T L A Q M Y P L Q E I Q N L T V K L Q L Q A L Q Q N G S S V L S E D K S K R
* A E A A P E E A F H T K L A R L L C S C V

SexAI*
gttgaacacaattctaaatacaatgagcaccatctacagtactggaaaagtttgtaacccagataatccacaagaatgcttattacttgaaccaggtttgaatgaaataatggcaaacagtttagactac
caacttgtgttaagatttatgttactcgtggtagatgtcatgaccttttcaaacattgggtctattaggtgttcttacgaataatgaacttggtccaaacttactttattaccgtttgtcaaatctgatg   780
L N T I L N T M S T I Y S T G K V C N P D N P Q E C L L L E P G L N E I M A N S L D Y
T S C L E L Y L S C W R C Y Q F L K Y G L Y D V L I S I V Q V L N S H F L P L C N L S C

BglII
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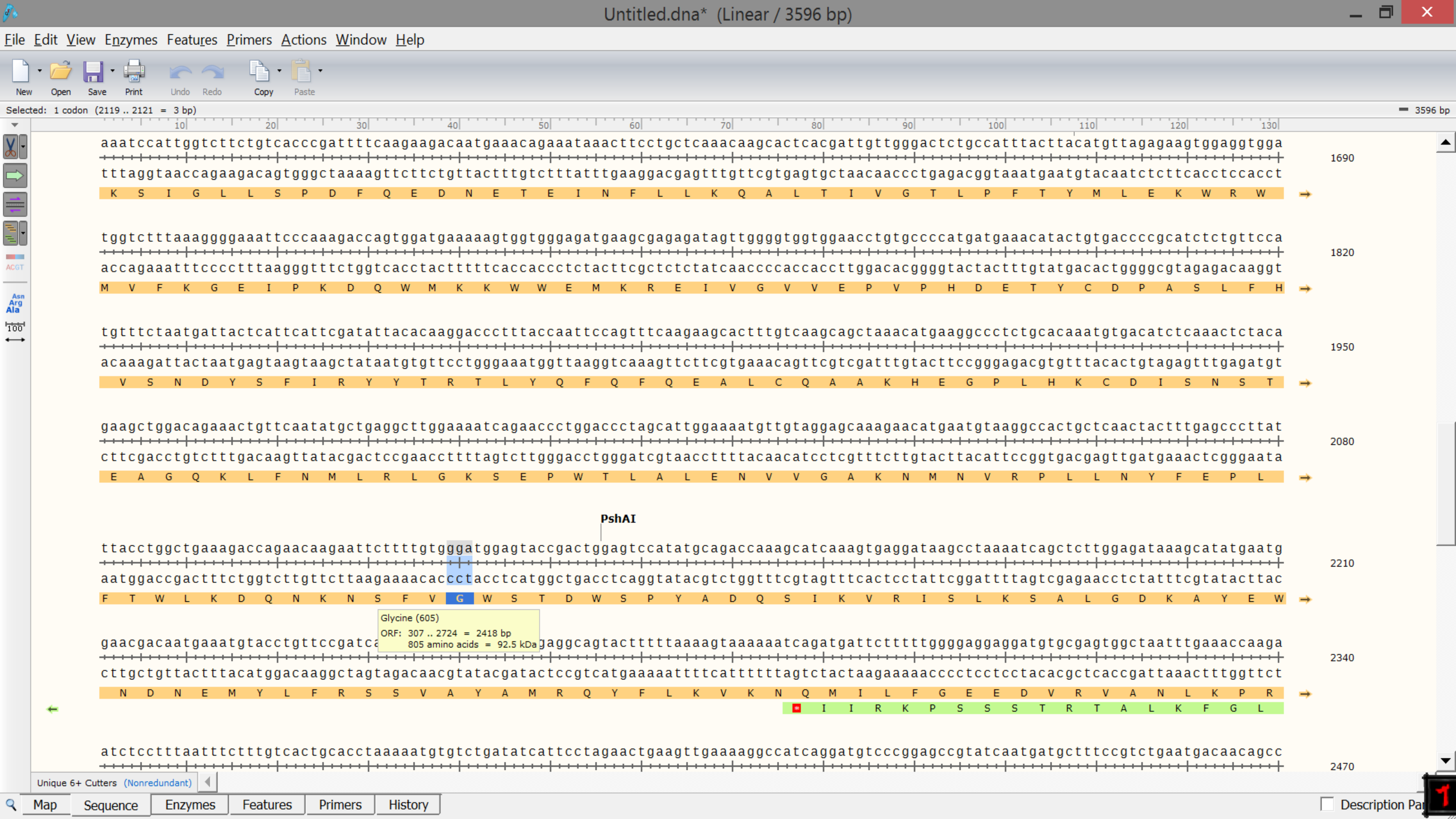

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 K  S  I  G  L  L  S  P  D  F  Q  E  D  N  E  T  E  I  N  F  L  L  K  Q  A  L  T  I  V  G  T  L  P  F  T  Y  M  L  E  K  W  R  W  →

tggtctttaaaggggaaattcccaaagaccagtggatgaaaaagtggtgggagatgaagcgagagatagttggggtggtggaacctgtgccccatgatgaaacatactgtgaccccgcatctctgttcca
accagaaatttcccctttaagggtttctggtcacctactttttcaccaccctctacttcgctctctatcaaccccaccaccttggacacggggtactactttgtatgacactggggcgtagagacaaggt   1820
M  V  F  K  G  E  I  P  K  D  Q  W  M  K  K  W  W  E  M  K  R  E  I  V  G  V  V  E  P  V  P  H  D  E  T  Y  C  D  P  A  S  L  F  H  →

tgtttctaatgattactcattcattcgatattacacaaggaccctttaccaattccagtttcaagaagcactttgtcaagcagctaaacatgaaggccctctgcacaaatgtgacatctcaaactctaca
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  V  S  N  D  Y  S  F  I  R  Y  Y  T  R  T  L  Y  Q  F  Q  F  Q  E  A  L  C  Q  A  A  K  H  E  G  P  L  H  K  C  D  I  S  N  S  T  →

gaagctggacagaaactgttcaatatgctgaggcttggaaaatcagaaccctggaccctagcattggaaaatgttgtaggagcaaagaacatgaatgtaaggccactgctcaactactttgagcccttat
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 E  A  G  Q  K  L  F  N  M  L  R  L  G  K  S  E  P  W  T  L  A  L  E  N  V  V  G  A  K  N  M  N  V  R  P  L  L  N  Y  F  E  P  L  →

                                                                         PshAI
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F  T  W  L  K  D  Q  N  K  N  S  F  V  G  W  S  T  D  W  S  P  Y  A  D  Q  S  I  K  V  R  I  S  L  K  S  A  L  G  D  K  A  Y  E  W  →

gaacgacaatgaaatgtacctgttccgatca                      gaggcagtacttttaaaagtaaaaaatcagatgattcttttggggaggaggatgtgcgagtggctaatttgaaaccaaga
cttgctgttactttacatggacaaggctagtagacaacgtatacgatactccgtcatgaaaaatttcatttttagtctactaagaaaaacccctcctcctacacgctcaccgattaaactttggttct   2340
   N  D  N  E  M  Y  L  F  R  S  S  V  A  Y  A  M  R  Q  Y  F  L  K  V  K  N  Q  M  I  L  F  G  E  D  V  R  V  A  N  L  K  P  R  →
←                                                                                 ■  I  I  R  K  P  S  S  S  T  R  T  A  L  K  F  G  L

atctcctttaatttctttgtcactgcacctaaaaatgtgtctgatatcattcctagaactgaagttgaaaaggccatcaggatgtcccggagccgtatcaatgatgctttccgtctgaatgacaacagcc
                                                                                                                                       2470
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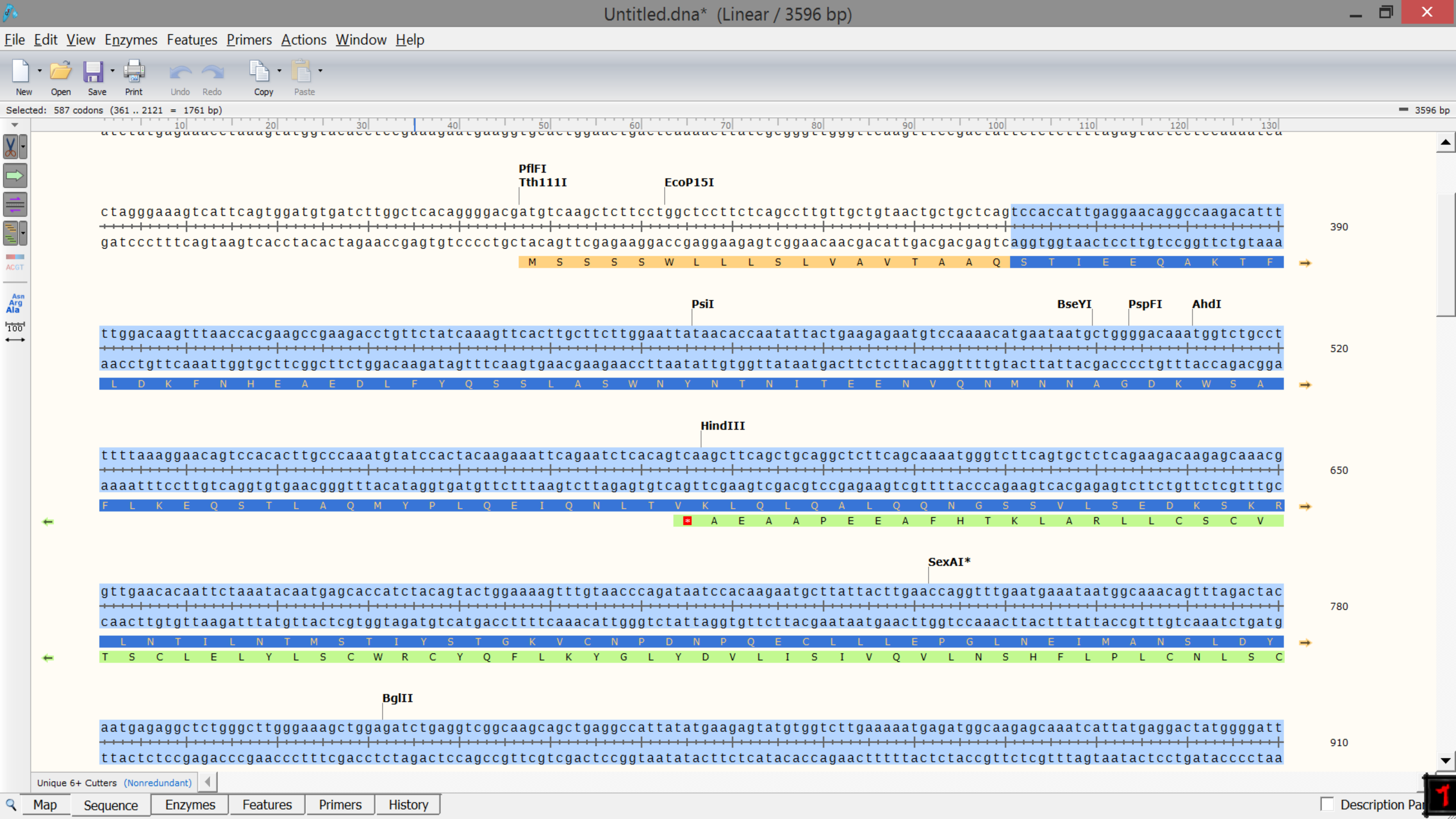
Glycine (605)
ORF: 307 .. 2724 = 2418 bp
805 amino acids = 92.5 kDa



Selected: 587 codons (361 .. 2121 = 1761 bp)

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                                                   Tth111I         EcoP15I
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                                              M  S  S  S  S  W  L  L  L  S  L  V  A  V  T  A  A  Q  S  T  I  E  E  Q  A  K  T  F

                                                                        PsiI                                    BseYI  PspFI  AhdI
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aacctgttcaaattggtgcttcggcttctggacaagatagtttcaagtgaacgaagaaccttaatattgtggttataatgacttctcttacaggttttgtacttattacgacccctgtttaccagacgga   520
 L  D  K  F  N  H  E  A  E  D  L  F  Y  Q  S  S  L  A  S  W  N  Y  N  T  N  I  T  E  E  N  V  Q  N  M  N  N  A  G  D  K  W  S  A

                                                                         HindIII
ttttaaaggaacagtccacacttgcccaaatgtatccactacaagaaattcagaatctcacagtcaagcttcagctgcaggctcttcagcaaaatgggtcttcagtgctctcagaagacaagagcaaacg
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 F  L  K  E  Q  S  T  L  A  Q  M  Y  P  L  Q  E  I  Q  N  L  T  V  K  L  Q  L  Q  A  L  Q  Q  N  G  S  S  V  L  S  E  D  K  S  K  R
                                                                      *  A  E  A  A  P  E  E  A  F  H  T  K  L  A  R  L  L  C  S  C  V

                                                                                             SexAI*
gttgaacacaattctaaatacaatgagcaccatctacagtactggaaaagtttgtaacccagataatccacaagaatgcttattacttgaaccaggtttgaatgaaataatggcaaacagtttagactac
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  L  N  T  I  L  N  T  M  S  T  I  Y  S  T  G  K  V  C  N  P  D  N  P  Q  E  C  L  L  L  E  P  G  L  N  E  I  M  A  N  S  L  D  Y
T  S  C  L  E  L  Y  L  S  C  W  R  C  Y  Q  F  L  K  Y  G  L  Y  D  V  L  I  S  I  V  Q  V  L  N  S  H  F  L  P  L  C  N  L  S  C

                               BglII
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ttactctccgagacccgaaccctttcgacctctagactccagccgttcgtcgactccggtaatatacttctcatacaccagaactttttactctaccgttctcgtttagtaatactcctgataccccctaa   910
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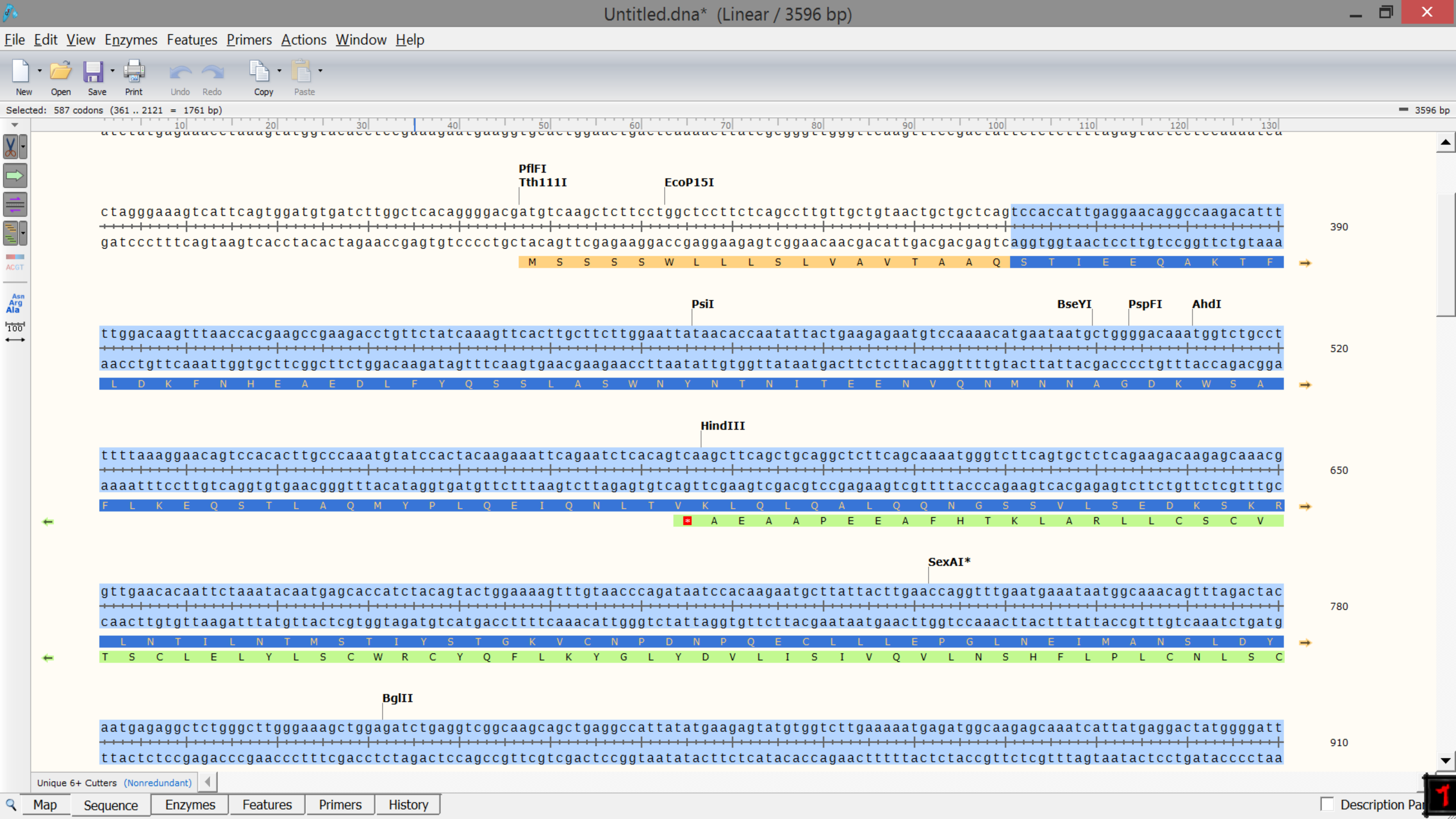

Selected: 587 codons (361 .. 2121 = 1761 bp)

3596 bp

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                                             PflFI
                                             Tth111I      EcoP15I
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gatccctttcagtaagtcacctacactagaaccgagtgtcccctgctacagttcgagaaggaccgaggaagagtcggaacaacgacattgacgacgagtcaggtggtaactccttgtccggttctgtaaa
                                             M  S  S  S  S  W  L  L  L  S  L  V  A  V  T  A  A  Q  S  T  I  E  E  Q  A  K  T  F  →

                                                                PsiI                                                 BseYI   PspFI  AhdI
ttggacaagtttaaccacgaagccgaagacctgttctatcaaagttcacttgcttcttggaattataacaccaatattactgaagagaatgtccaaaacatgaataatgctggggacaaatggtctgcct   520
aacctgttcaaattggtgcttcggcttctggacaagatagtttcaagtgaacgaagaaccttaatattgtggttataatgacttctcttacaggttttgtacttattacgacccctgtttaccagacgga
 L  D  K  F  N  H  E  A  E  D  L  F  Y  Q  S  S  L  A  S  W  N  Y  N  T  N  I  T  E  E  N  V  Q  N  M  N  N  A  G  D  K  W  S  A  →

                                                                 HindIII
ttttaaaggaacagtccacacttgcccaaatgtatccactacaagaaattcagaatctcacagtcaagcttcagctgcaggctcttcagcaaaatgggtcttcagtgctctcagaagacaagagcaaacg   650
aaaatttccttgtcaggtgtgaacgggtttacataggtgatgttctttaagtcttagagtgtcagttcgaagtcgacgtccgagaagtcgttttacccagaagtcacgagagtcttctgttctcgtttgc
F  L  K  E  Q  S  T  L  A  Q  M  Y  P  L  Q  E  I  Q  N  L  T  V  K  L  Q  L  Q  A  L  Q  Q  N  G  S  S  V  L  S  E  D  K  S  K  R  →
←                                                              *  A  E  A  A  P  E  E  A  F  H  T  K  L  A  R  L  L  C  S  C  V

                                                                                    SexAI*
gttgaacacaattctaaatacaatgagcaccatctacagtactggaaaagtttgtaacccagataatccacaagaatgcttattacttgaaccaggtttgaatgaaataatggcaaacagtttagactac   780
caacttgtgttaagatttatgttactcgtggtagatgtcatgaccttttcaaacattgggtctattaggtgttcttacgaataatgaacttggtccaaacttactttattaccgtttgtcaaatctgatg
  L  N  T  I  L  N  T  M  S  T  I  Y  S  T  G  K  V  C  N  P  D  N  P  Q  E  C  L  L  L  E  P  G  L  N  E  I  M  A  N  S  L  D  Y  →
← T  S  C  L  E  L  Y  L  S  C  W  R  C  Y  Q  F  L  K  Y  G  L  Y  D  V  L  I  S  I  V  Q  V  L  N  S  H  F  L  P  L  C  N  L  S  C

                               BglII
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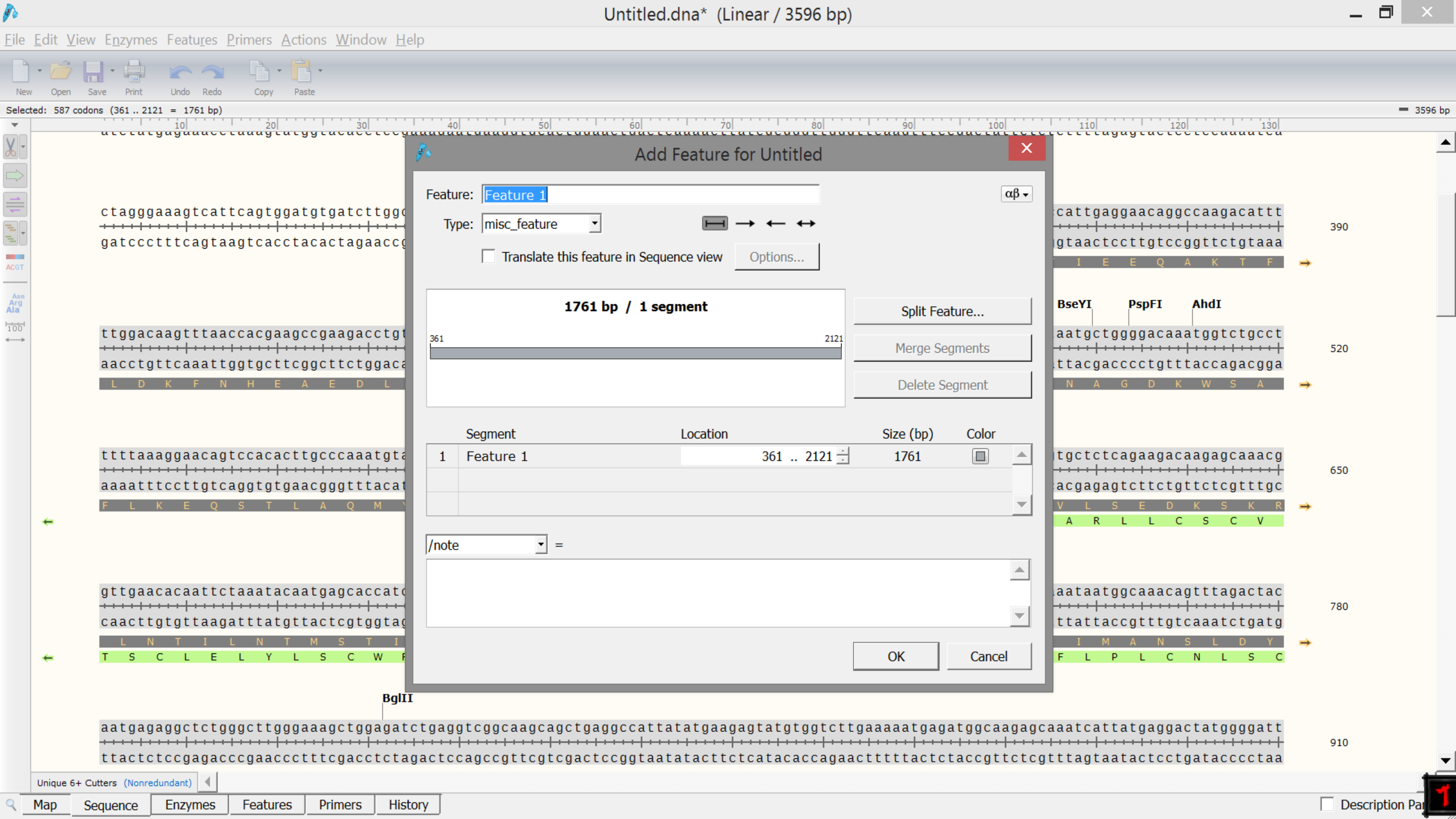


Untitled.dna* (Linear / 3596 bp)

Selected: 587 codons (361 .. 2121 = 1761 bp)

Add Feature for Untitled

Feature: Feature 1

Type: misc_feature

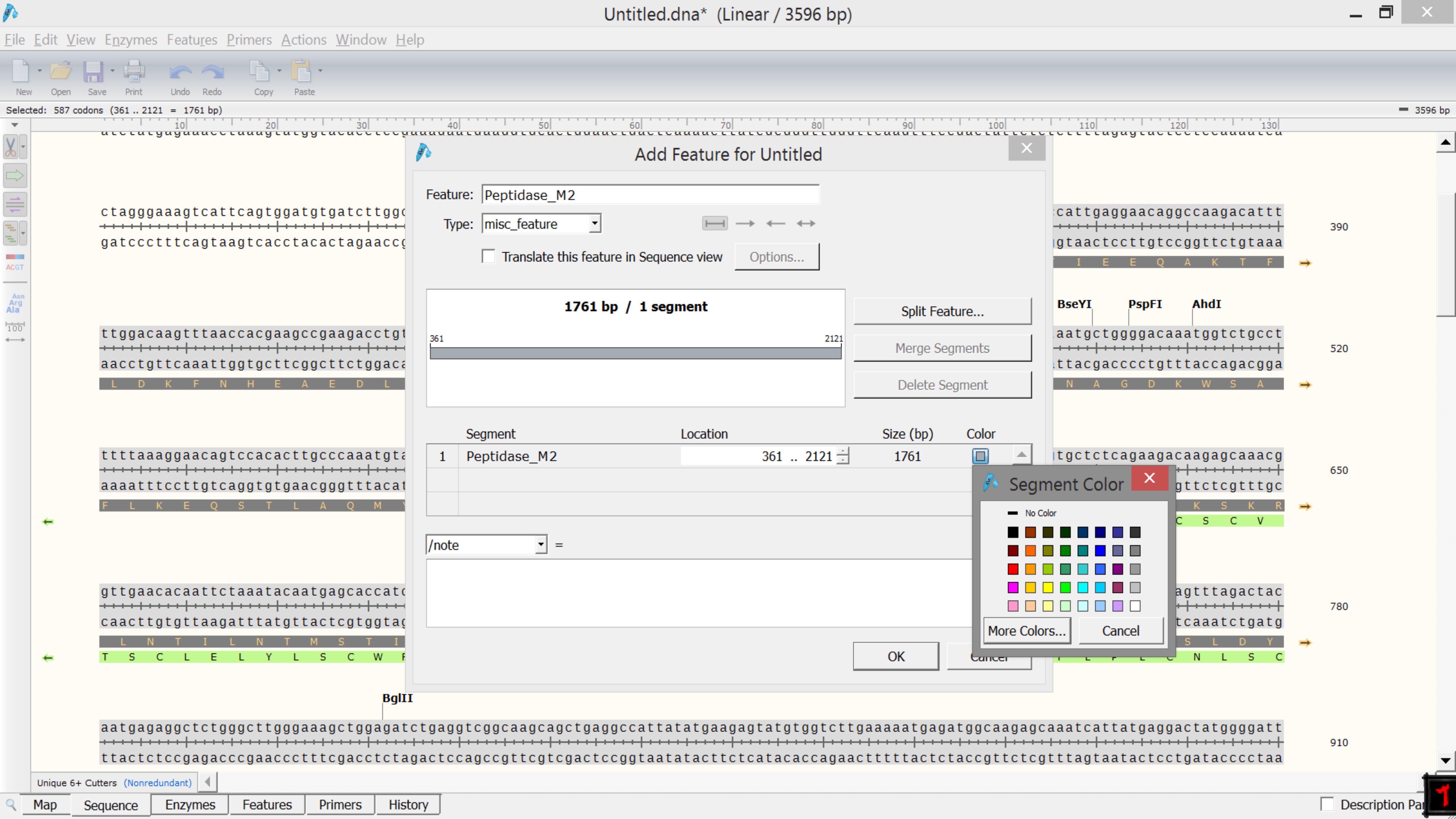
☐ Translate this feature in Sequence view

1761 bp / 1 segment

361 … 2121

	Segment	Location	Size (bp)	Color
1	Feature 1	361 .. 2121	1761	

/note =



Untitled.dna* (Linear / 3596 bp)

Selected: 587 codons (361 .. 2121 = 1761 bp)

Add Feature for Untitled

Feature: Peptidase_M2

Type: misc_feature

☐ Translate this feature in Sequence view

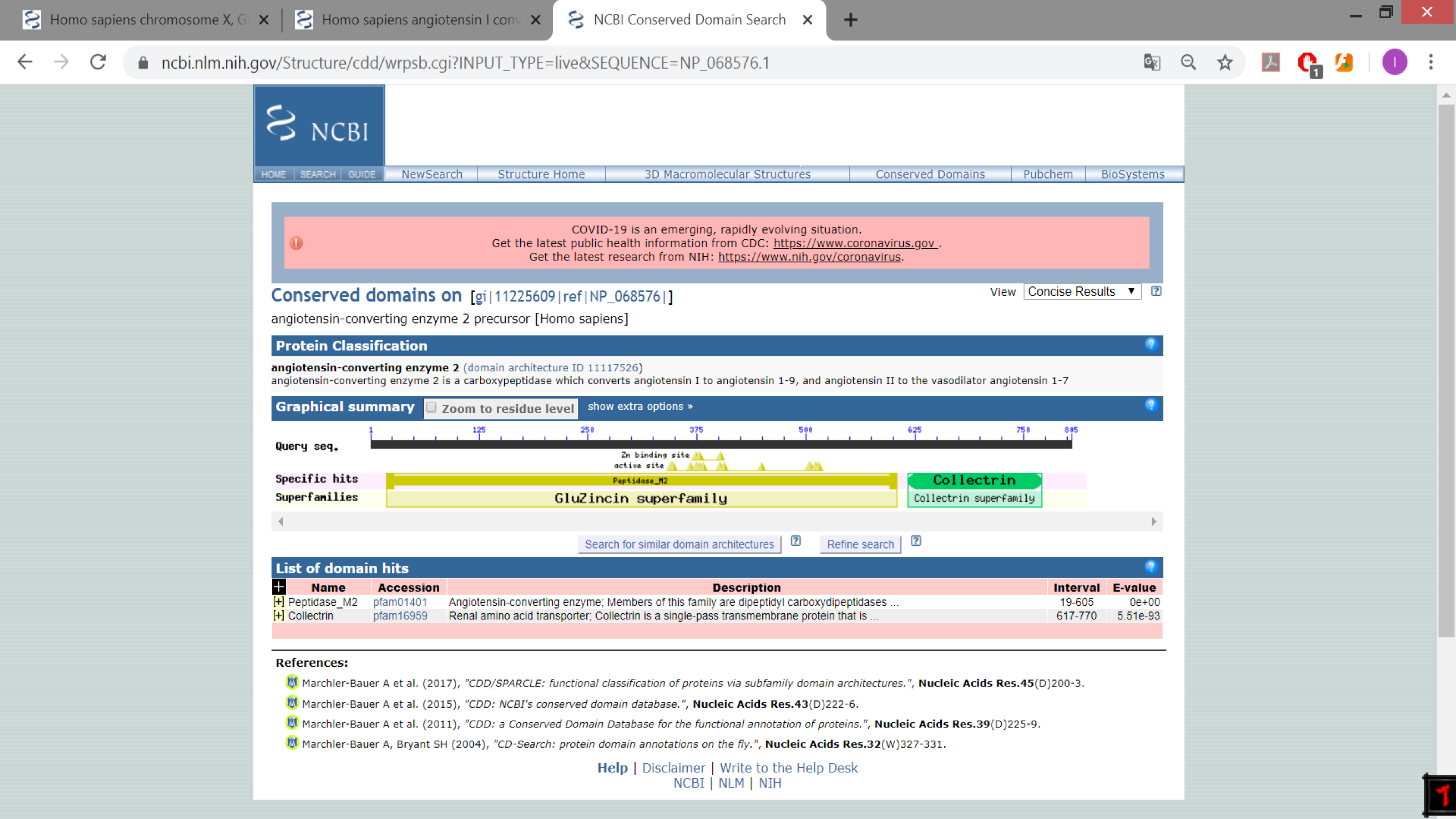
1761 bp / 1 segment

361 2121

	Segment	Location	Size (bp)	Color
1	Peptidase_M2	361 .. 2121	1761	▢

/note =

Segment Color



COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: https://www.coronavirus.gov .
Get the latest research from NIH: https://www.nih.gov/coronavirus.

Conserved domains on [gi|11225609|ref|NP_068576|]

angiotensin-converting enzyme 2 precursor [Homo sapiens]

View: Concise Results ▼

Protein Classification

angiotensin-converting enzyme 2 (domain architecture ID 11117526)
angiotensin-converting enzyme 2 is a carboxypeptidase which converts angiotensin I to angiotensin 1-9, and angiotensin II to the vasodilator angiotensin 1-7

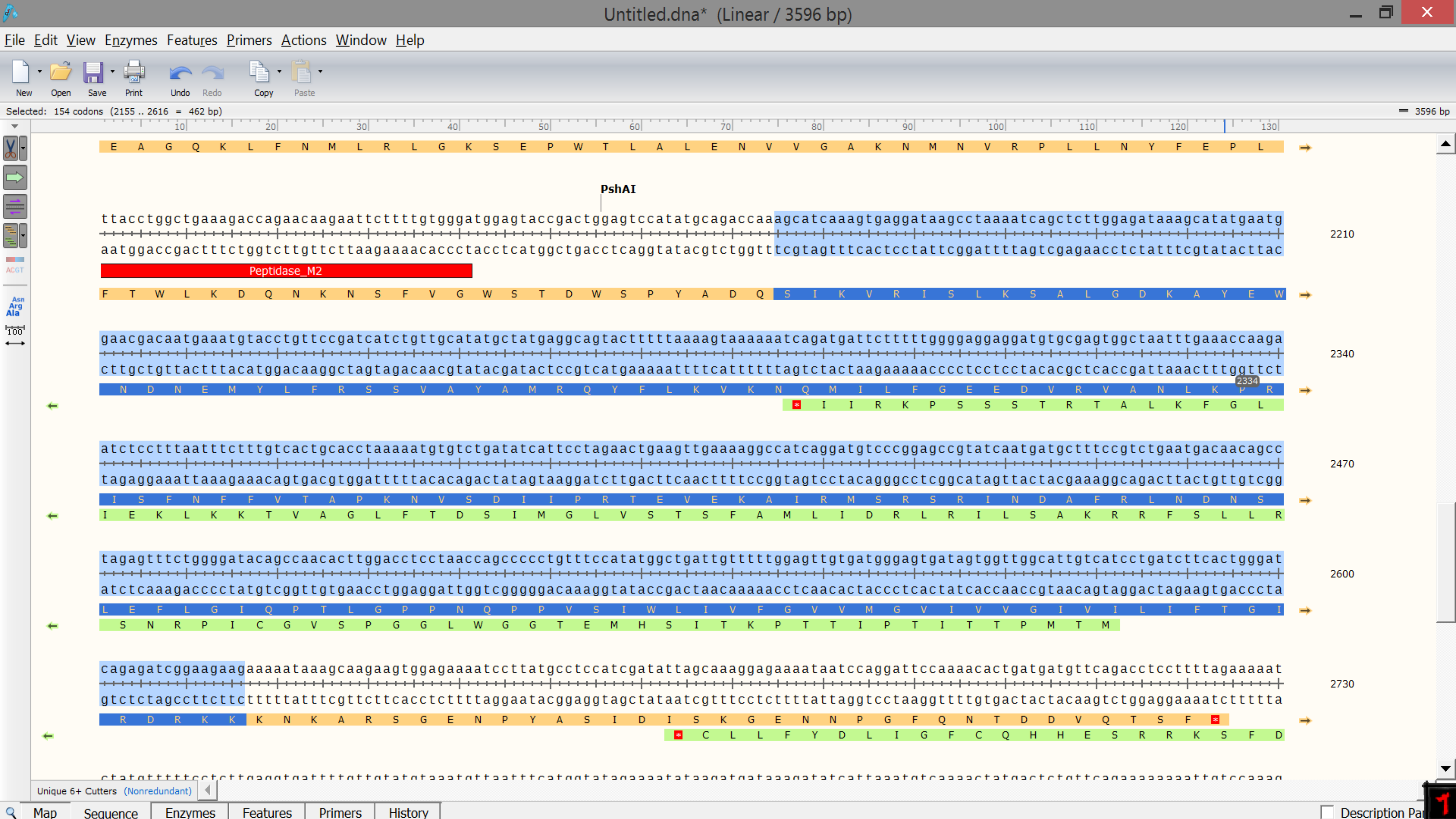
Graphical summary

List of domain hits

	Name	Accession	Description	Interval	E-value
[+]	Peptidase_M2	pfam01401	Angiotensin-converting enzyme; Members of this family are dipeptidyl carboxydipeptidases ...	19-605	0e+00
[+]	Collectrin	pfam16959	Renal amino acid transporter; Collectrin is a single-pass transmembrane protein that is ...	617-770	5.51e-93

References:

- Marchler-Bauer A et al. (2017), *"CDD/SPARCLE: functional classification of proteins via subfamily domain architectures."*, **Nucleic Acids Res.45**(D)200-3.
- Marchler-Bauer A et al. (2015), *"CDD: NCBI's conserved domain database."*, **Nucleic Acids Res.43**(D)222-6.
- Marchler-Bauer A et al. (2011), *"CDD: a Conserved Domain Database for the functional annotation of proteins."*, **Nucleic Acids Res.39**(D)225-9.
- Marchler-Bauer A, Bryant SH (2004), *"CD-Search: protein domain annotations on the fly."*, **Nucleic Acids Res.32**(W)327-331.



Selected: 154 codons (2155 .. 2616 = 462 bp)

3596 bp

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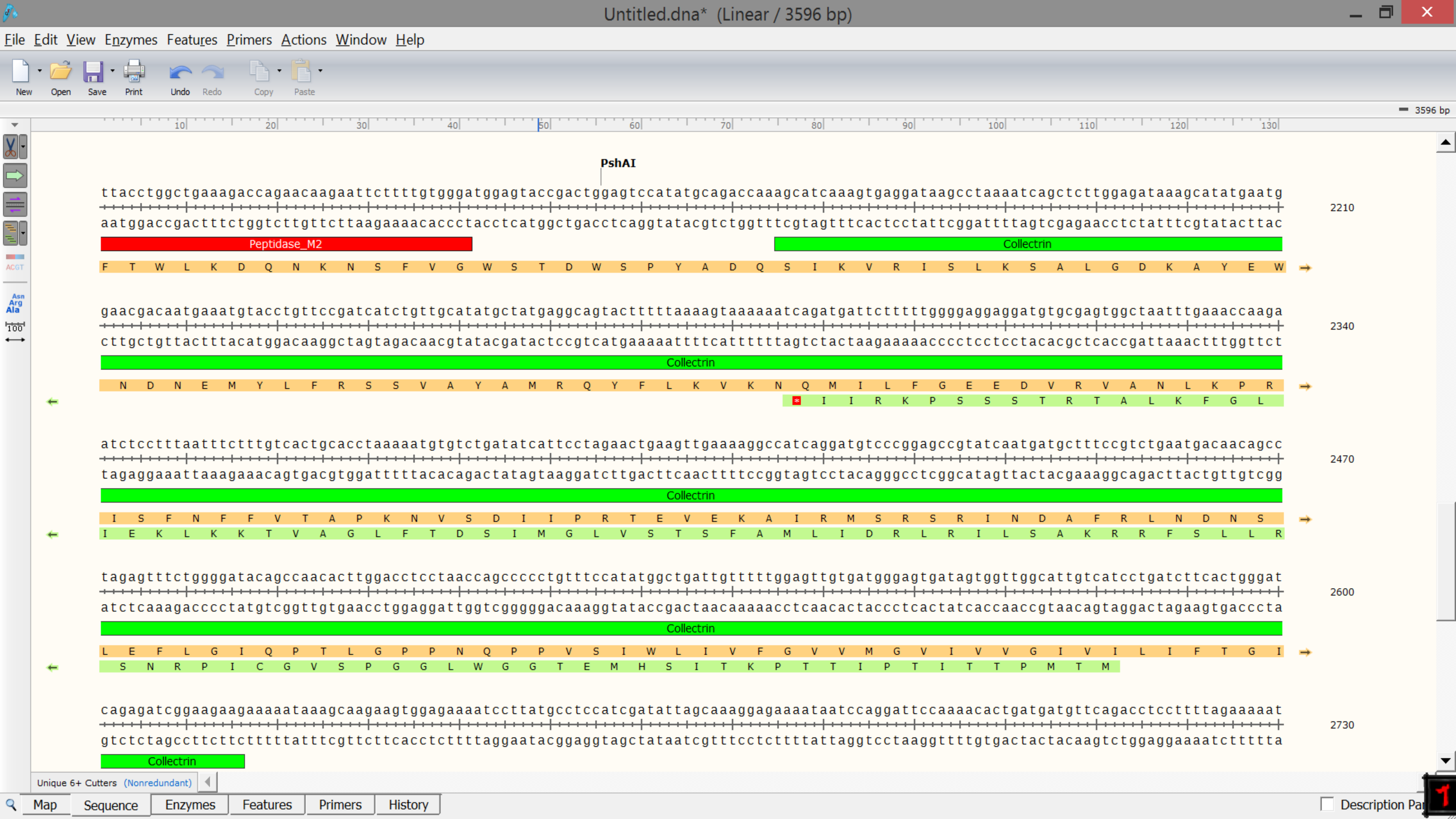

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Peptidase_M2                                                                                Collectrin
F  T  W  L  K  D  Q  N  K  N  S  F  V  G  W  S  T  D  W  S  P  Y  A  D  Q  S  I  K  V  R  I  S  L  K  S  A  L  G  D  K  A  Y  E  W  →

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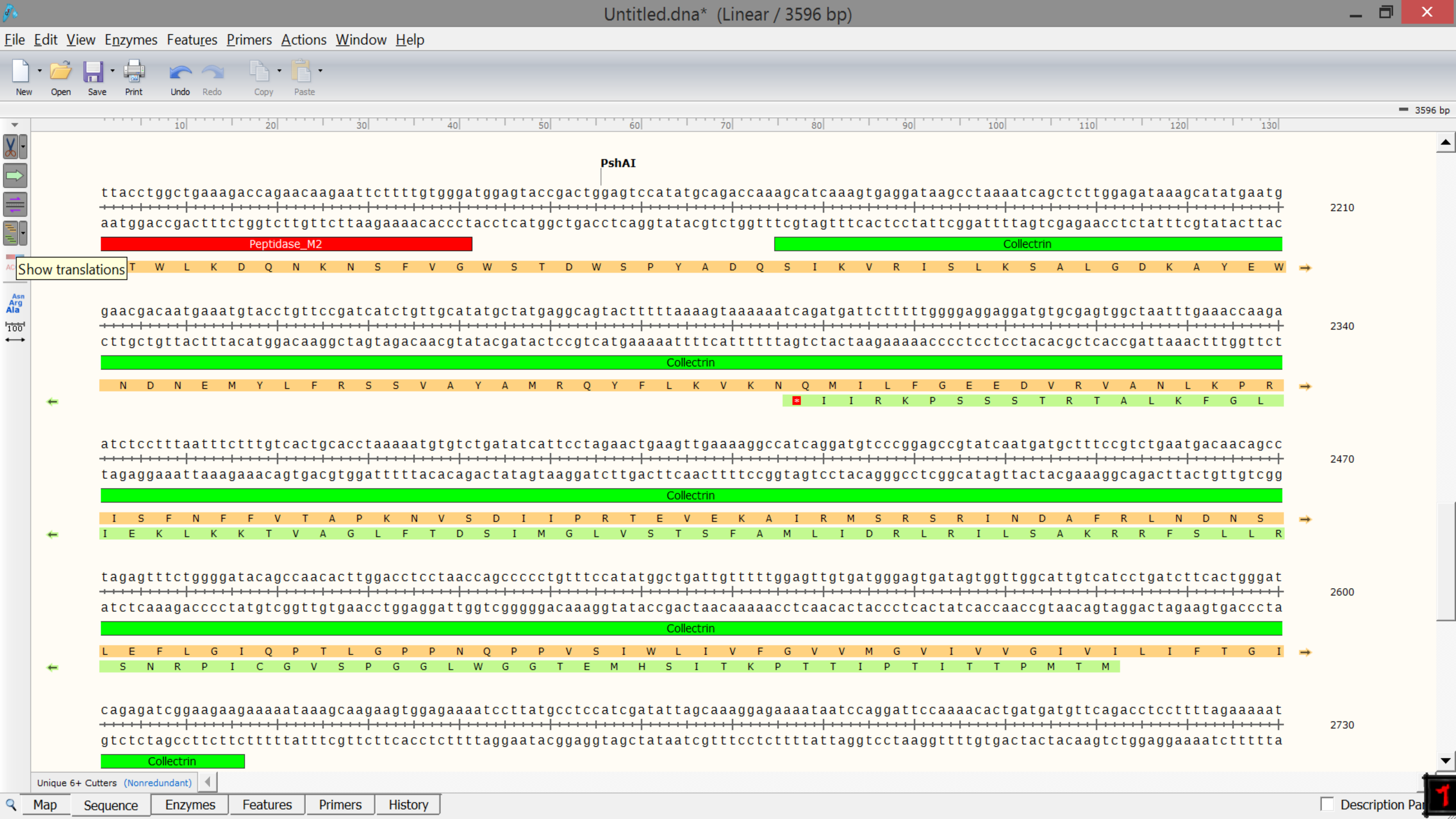

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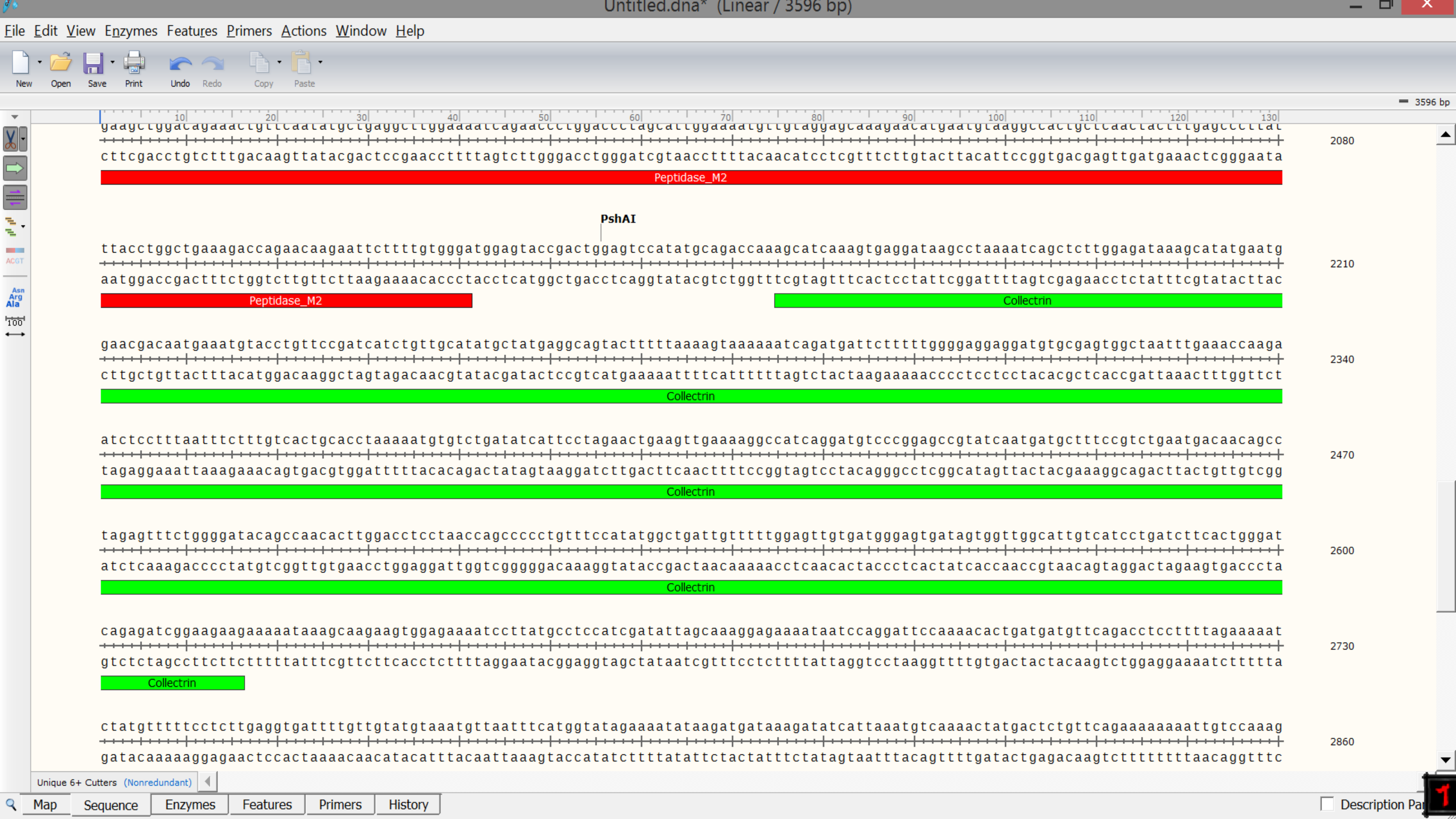

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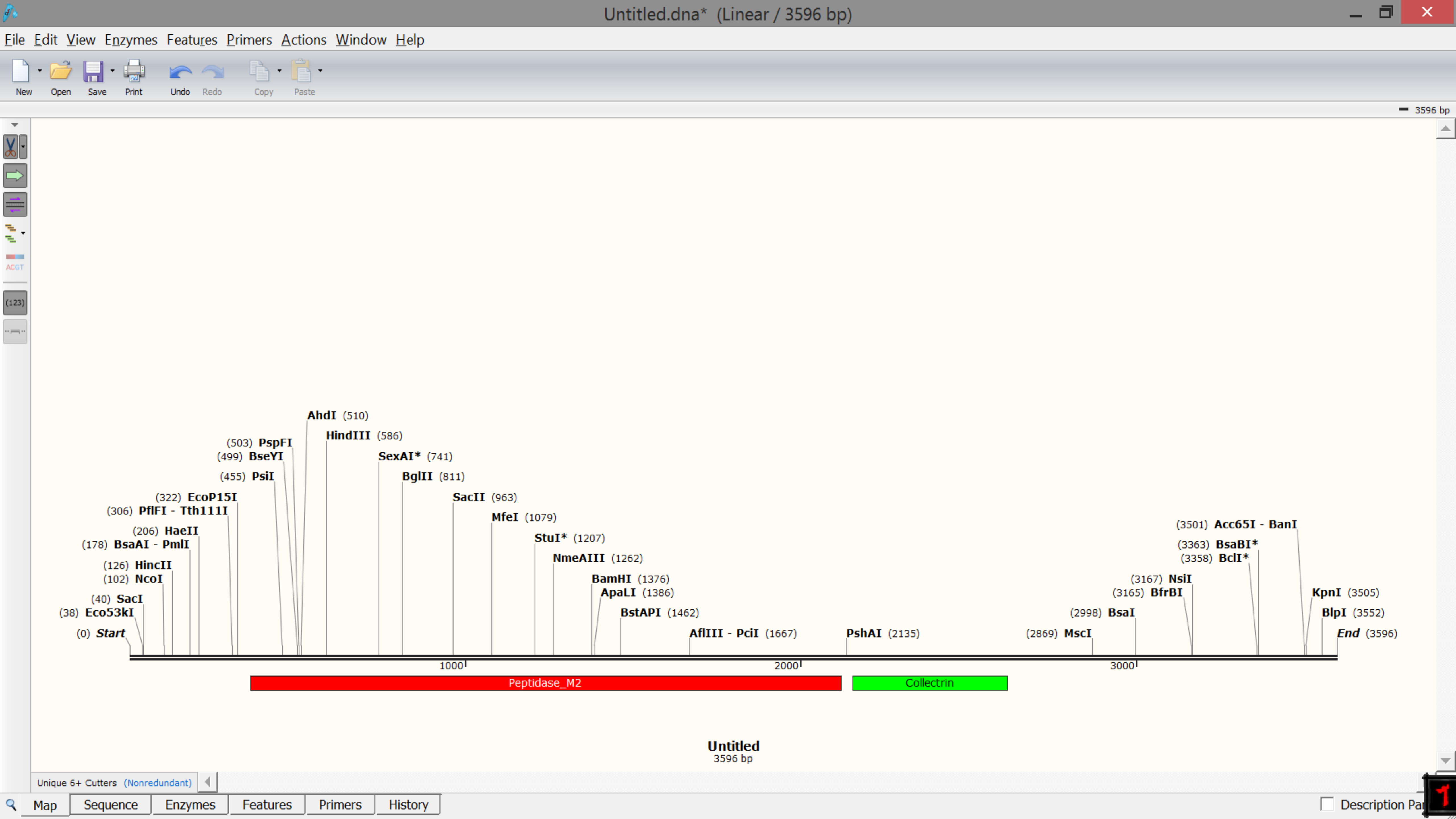Untitled.dna* (Linear / 3596 bp)
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HindIII (586)
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History
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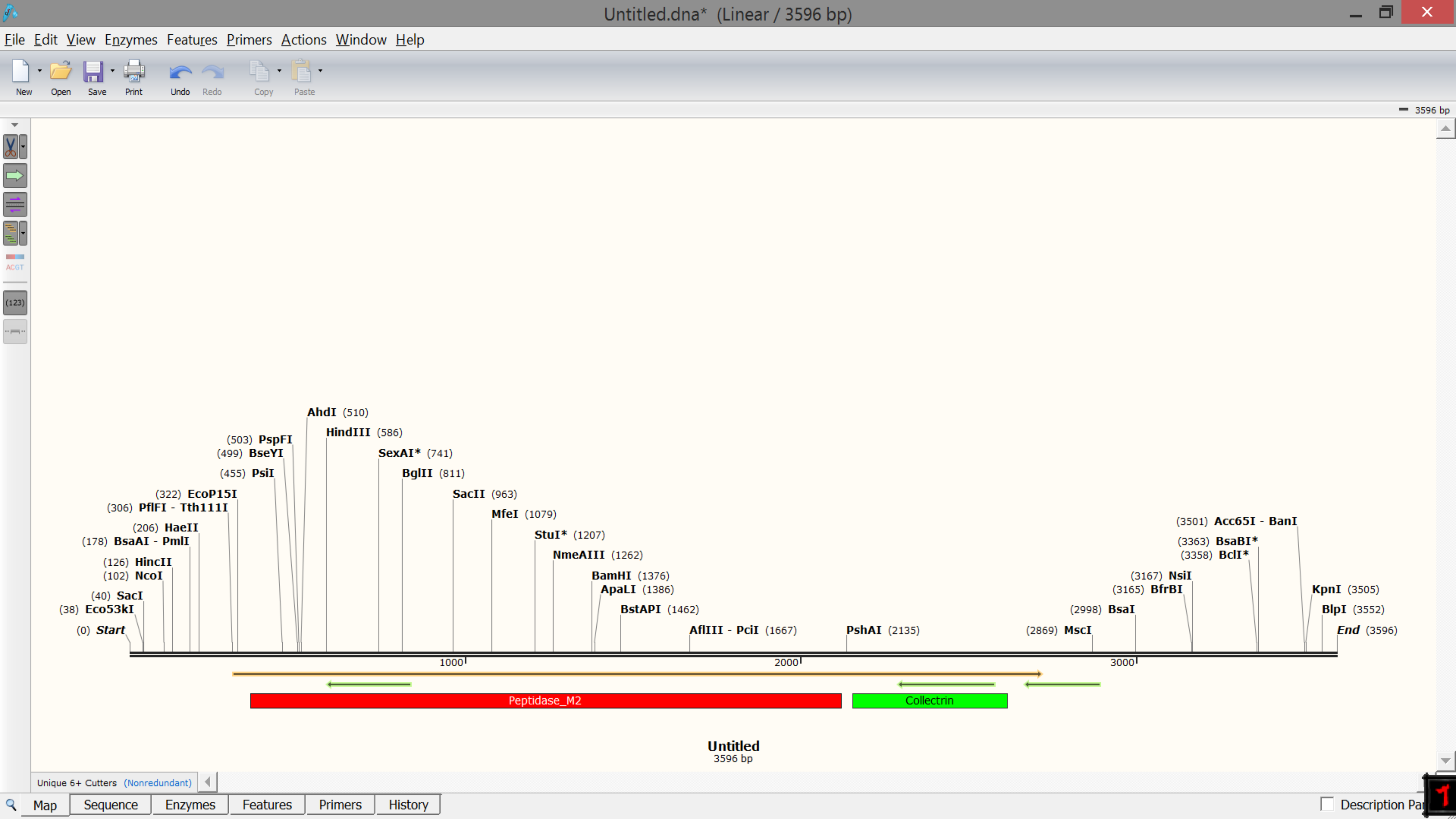
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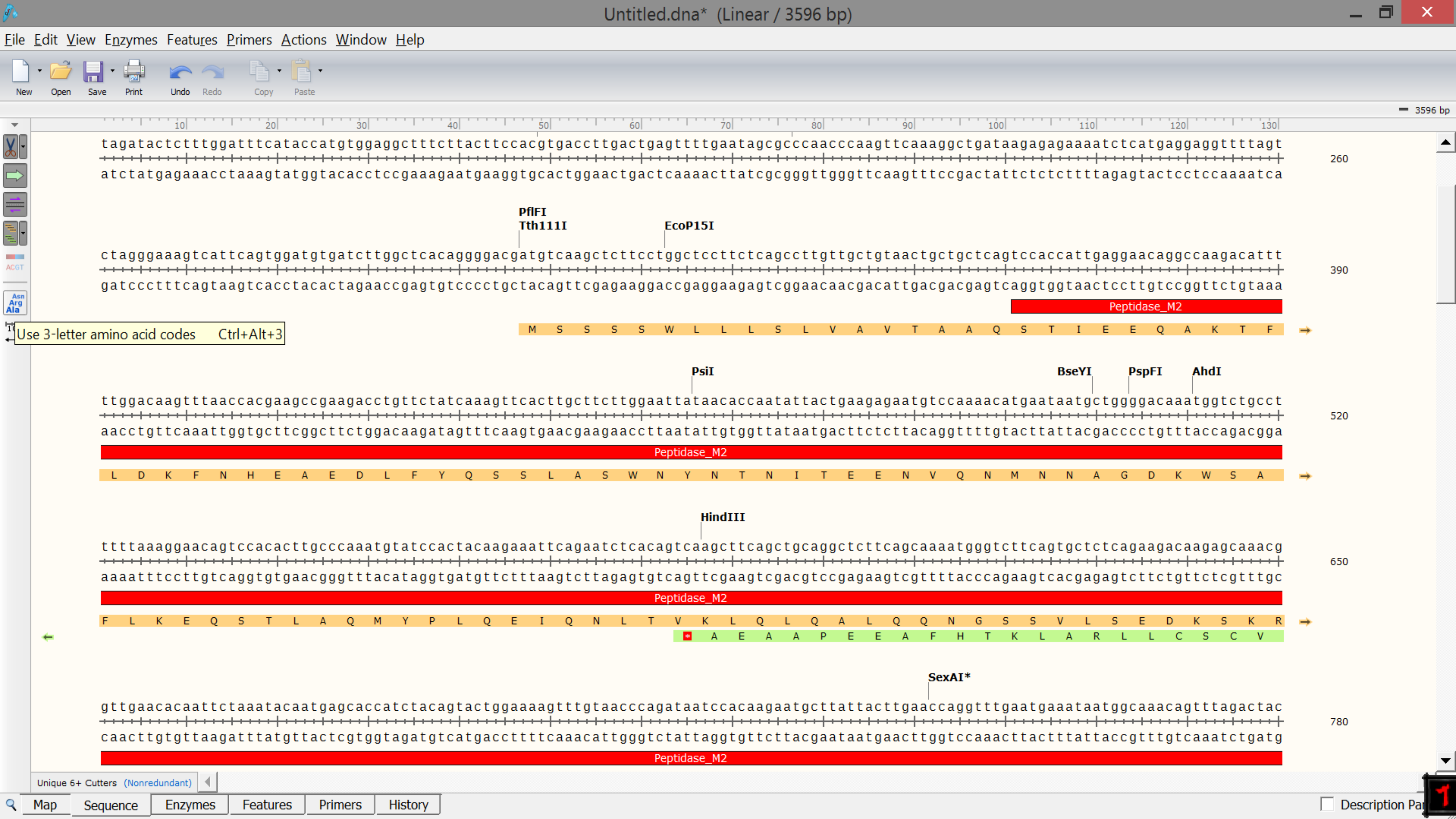

Use 3-letter amino acid codes Ctrl+Alt+3

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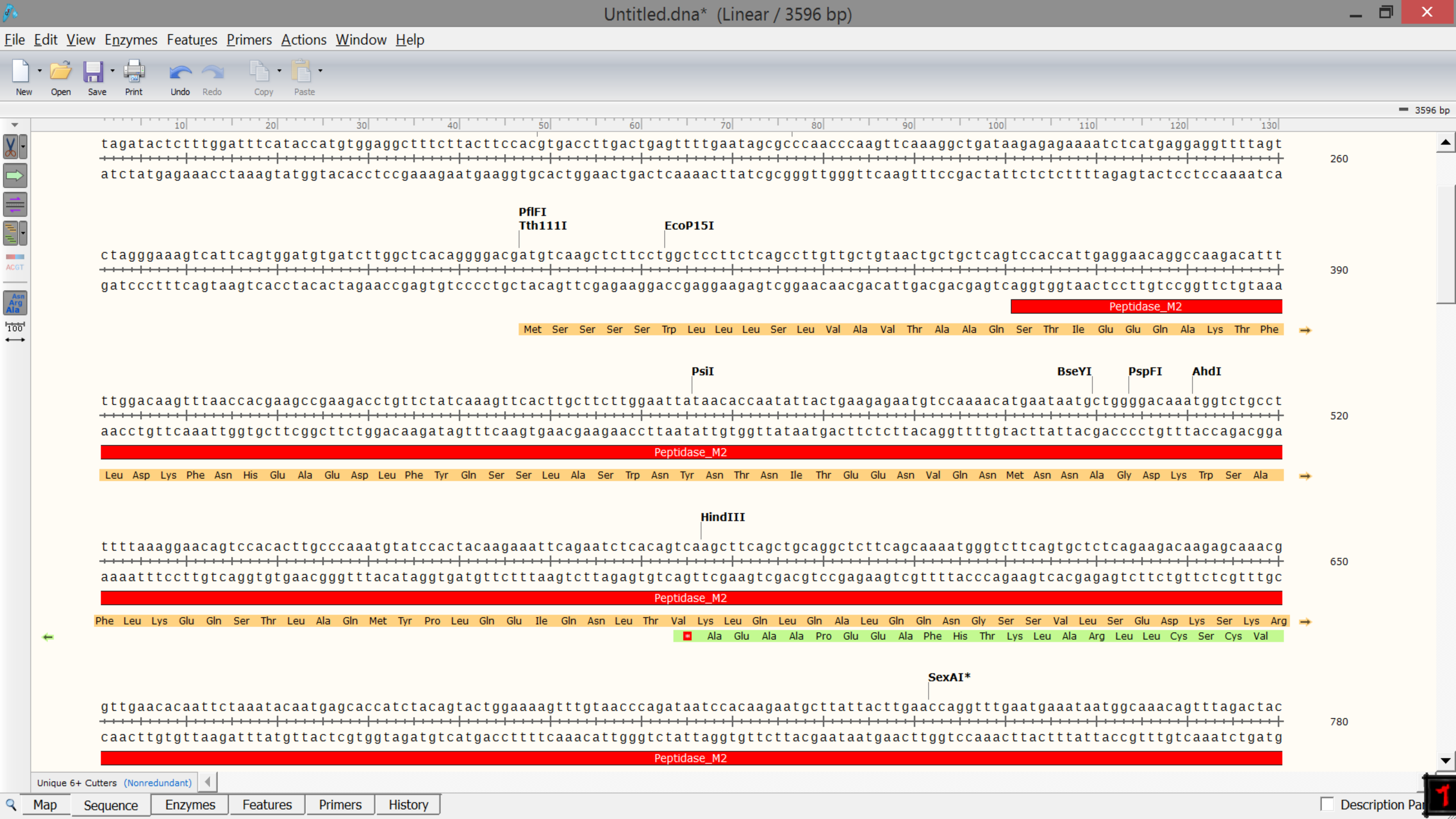

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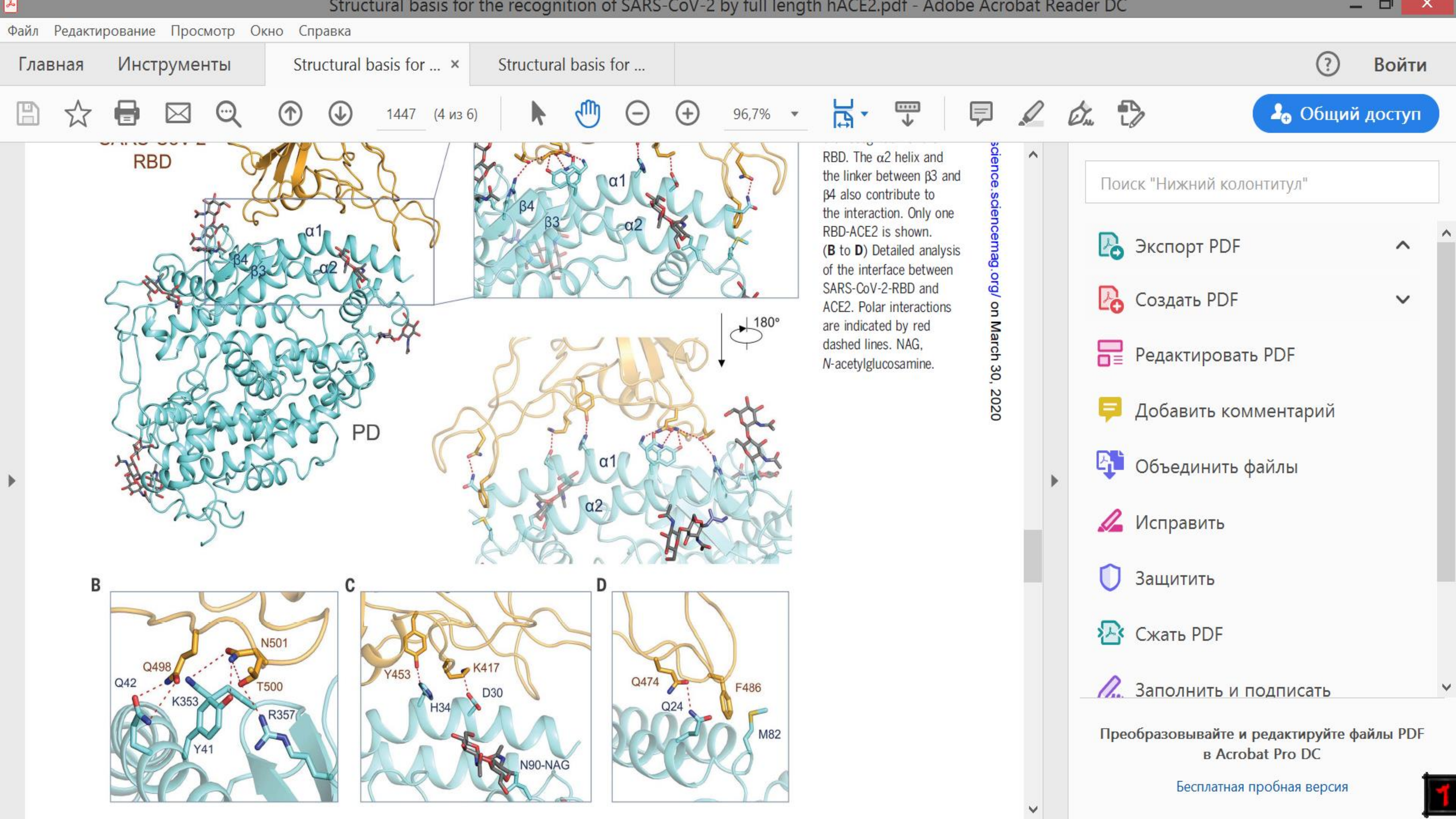
atctatgagaaacctaaagtatggtacacctccgaaagaatgaaggtgcactggaactgactcaaaacttatcgcgggttgggttcaagtttccgactattctctcttttagagtactcctccaaaatca

                                             PflFI
                                             Tth111I          EcoP15I
ctagggaaagtcattcagtggatgtgatcttggctcacaggggacgatgtcaagctcttcctggctccttctcagccttgttgctgtaactgctgctcagtccaccattgaggaacaggccaagacattt   390
gatccctttcagtaagtcacctacactagaaccgagtgtcccctgctacagttcgagaaggaccgaggaagagtcggaacaacgacattgacgacgagtcaggtggtaactccttgtccggttctgtaaa
                                                                                                              Peptidase_M2
                                             Met Ser Ser Ser Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Ala Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys Thr Phe →

                                                           PsiI                                       BseYI    PspFI   AhdI
ttggacaagtttaaccacgaagccgaagacctgttctatcaaagttcacttgcttcttggaattataacaccaatattactgaagagaatgtccaaaacatgaataatgctggggacaaatggtctgcct   520
aacctgttcaaattggtgcttcggcttctggacaagatagtttcaagtgaacgaagaaccttaatattgtggttataatgacttctcttacaggttttgtacttattacgacccctgtttaccagacgga
                                                        Peptidase_M2
Leu Asp Lys Phe Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn Ala Gly Asp Lys Trp Ser Ala →

                                                            HindIII
ttttaaaggaacagtccacacttgcccaaatgtatccactacaagaaattcagaatctcacagtcaagcttcagctgcaggctcttcagcaaaatgggtcttcagtgctctcagaagacaagagcaaacg   650
aaaatttccttgtcaggtgtgaacgggtttacataggtgatgttctttaagtcttagagtgtcagttcgaagtcgacgtccgagaagtcgttttacccagaagtcacgagagtcttctgttctcgtttgc
                                                        Peptidase_M2
Phe Leu Lys Glu Gln Ser Thr Leu Ala Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys Ser Lys Arg →
←                                                          ■ Ala Glu Ala Ala Pro Glu Glu Ala Phe His Thr Lys Leu Ala Arg Leu Leu Cys Ser Cys Val

                                                                                    SexAI*
gttgaacacaattctaaatacaatgagcaccatctacagtactggaaaagtttgtaacccagataatccacaagaatgcttattacttgaaccaggtttgaatgaaataatggcaaacagtttagactac   780
caacttgtgttaagatttatgttactcgtggtagatgtcatgaccttttcaaacattgggtctattaggtgttcttacgaataatgaacttggtccaaacttactttattaccgtttgtcaaatctgatg
                                                        Peptidase_M2
```



RBD. The α2 helix and the linker between β3 and β4 also contribute to the interaction. Only one RBD-ACE2 is shown. (**B** to **D**) Detailed analysis of the interface between SARS-CoV-2-RBD and ACE2. Polar interactions are indicated by red dashed lines. NAG, *N*-acetylglucosamine.

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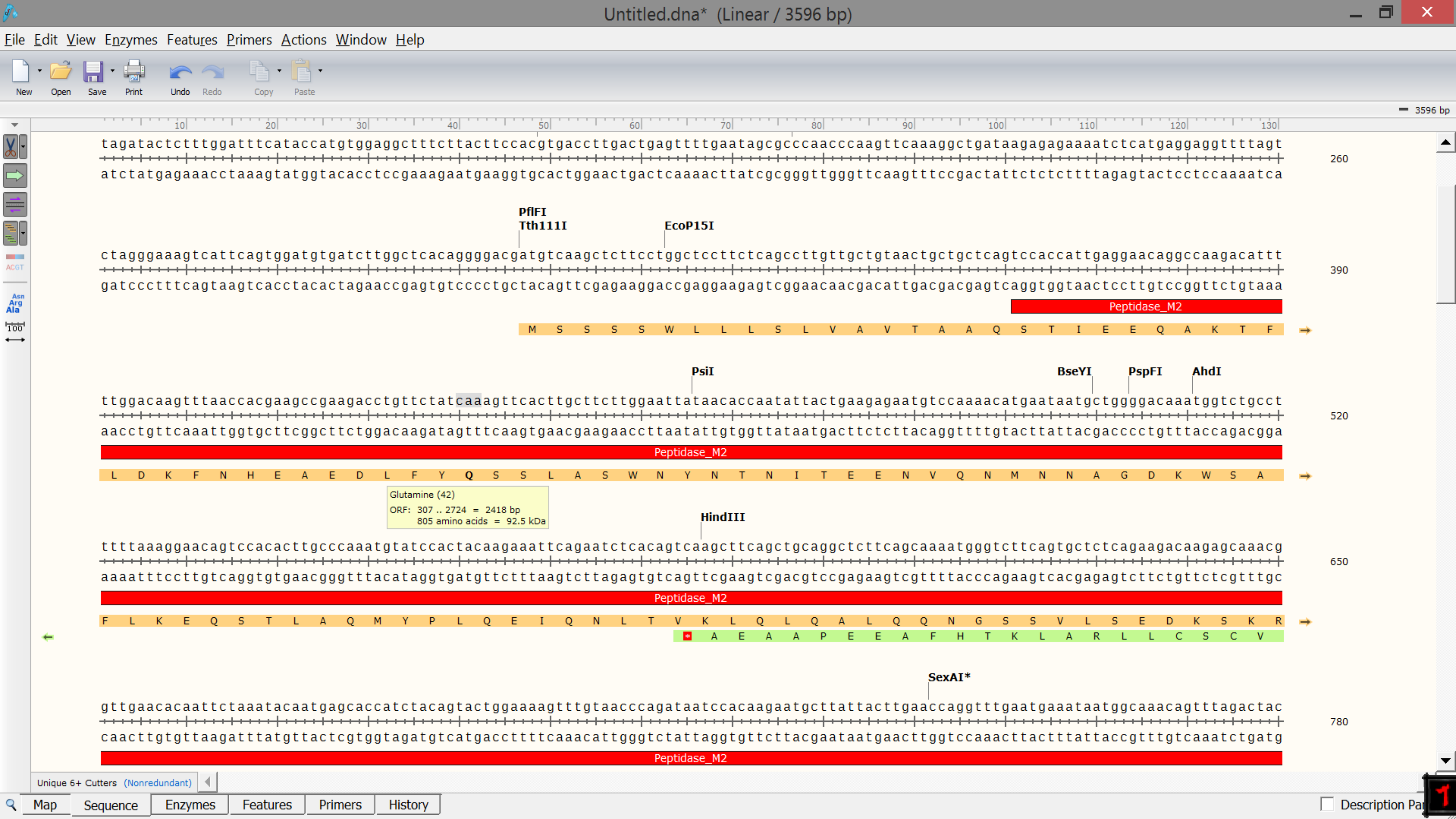

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PflFI
Tth111I  EcoP15I
ctagggaaagtcattcagtggatgtgatcttggctcacaggggacgatgtcaagctcttcctggctccttctcagccttgttgctgtaactgctgctcagtccaccattgaggaacaggccaagacattt
gatccctttcagtaagtcacctacactagaaccgagtgtcccctgctacagttcgagaaggaccgaggaagagtcggaacaacgacattgacgacgagtcaggtggtaactccttgtccggttctgtaaa   390
Peptidase_M2
M S S S S W L L L S L V A V T A A Q S T I E E Q A K T F

PsiI  BseYI  PspFI  AhdI
ttggacaagtttaaccacgaagccgaagacctgttctatcaaagttcacttgcttcttggaattataacaccaatattactgaagagaatgtccaaaacatgaataatgctggggacaaatggtctgcct
aacctgttcaaattggtgcttcggcttctggacaagatagtttcaagtgaacgaagaaccttaatattgtggttataatgacttctcttacaggttttgtacttattacgacccctgtttaccagacgga   520
Peptidase_M2
L D K F N H E A E D L F Y Q S S L A S W N Y N T N I T E E N V Q N M N N A G D K W S A
```

Glutamine (42)
ORF: 307 .. 2724 = 2418 bp
805 amino acids = 92.5 kDa

```
HindIII
ttttaaaggaacagtccacacttgcccaaatgtatccactacaagaaattcagaatctcacagtcaagcttcagctgcaggctcttcagcaaaatgggtcttcagtgctctcagaagacaagagcaaacg
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Peptidase_M2
F L K E Q S T L A Q M Y P L Q E I Q N L T V K L Q L Q A L Q Q N G S S V L S E D K S K R
* A E A A P E E A F H T K L A R L L C S C V

SexAI*
gttgaacacaattctaaatacaatgagcaccatctacagtactggaaaagtttgtaacccagataatccacaagaatgcttattacttgaaccaggtttgaatgaaataatggcaaacagtttagactac
caacttgtgttaagatttatgttactcgtggtagatgtcatgaccttttcaaacattgggtctattaggtgttcttacgaataatgaacttggtccaaacttactttattaccgtttgtcaaatctgatg   780
Peptidase_M2
```

```
Y   W   R   G   D   Y   E   V   N   G   V   D   G   Y   D   Y   S   R   G   Q   L   I   E   D   V   E   H   T   F   E   E   I   K   P   L   Y   E   H   L   H   A   Y   V   R

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ccgtttcaactacttacggataggaaggatatagtcaggttaacctacggagggacgagtaaacgaaccactatacaccccatctaaaacctgtttagacatgagaaactgtcaagggaaacctgtcttt
  A   K   L   M   N   A   Y   P   S   Y   I   S   P   I   G   C   L   P   A   H   L   L   G   D   M   W   G   R   F   W   T   N   L   Y   S   L   T   V   P   F   G   Q   K

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 P   N   I   D   V   T   D   A   M   V   D   Q   A   W   D   A   Q   R   I   F   K   E   A   E   K   F   F   V   S   V   G   L   P   N   M   T   Q   G   F   W   E   N   S

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M   L   T   D   P   G   N   V   Q   K   A   V   C   H   P   T   A   W   D   L   G   K   G   D   F   R   I   L   M   C   T   K   V   T   M   D   D   F   L   T   A   H   H   E

gatggggcatatccagtatgatatggcatatgctgcacaacctttttctgctaagaaatggagctaatgaaggattccatgaagctgttggggaaatcatgtcactttctgcagccacacctaagcattta    1560
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  M   G   H   I   Q   Y   D   M   A   Y   A   A   Q   P   F   L   L   R   N   G   A   N   E   G   F   H   E   A   V   G   E   I   M   S   L   S   A   A   T   P   K   H   L
```

Lysine (353)
ORF: 307 .. 2724 = 2418 bp
805 amino acids = 92.5 kDa

Selected: active (1363 .. 1365 = 3 bp)   3596 bp

```
        10        20        30        40        50        60        70        80        90        100       110       120       130
 Y   W   R   G   D   Y   E   V   N   G   V   D   G   Y   D   Y   S   R   G   Q   L   I   E   D   V   E   H   T   F   E   E   I   K   P   L   Y   E   H   L   H   A   Y   V   R  →

                                        MfeI
ggcaaagttgatgaatgcctatccttcctatatcagtccaattggatgcctccctgctcatttgcttggtgatatgtggggtagattttggacaaatctgtactctttgacagttccctttggacagaaa   1170
ccgtttcaactacttacggataggaaggatatagtcaggttaacctacggagggacgagtaaacgaaccactatacaccccatctaaaacctgtttagacatgagaaactgtcaagggaaacctgtcttt
                                                          Peptidase_M2
  A   K   L   M   N   A   Y   P   S   Y   I   S   P   I   G   C   L   P   A   H   L   L   G   D   M   W   G   R   F   W   T   N   L   Y   S   L   T   V   P   F   G   Q   K  →

                                      StuI*                                                   NmeAIII
ccaaacatagatgttactgatgcaatggtggaccaggcctgggatgcacagagaatattcaaggaggccgagaagttctttgtatctgttggtcttcctaatatgactcaaggattctgggaaaattcca   1300
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                                                          Peptidase_M2
  P   N   I   D   V   T   D   A   M   V   D   Q   A   W   D   A   Q   R   I   F   K   E   A   E   K   F   F   V   S   V   G   L   P   N   M   T   Q   G   F   W   E   N   S  →

                                                                                     BamHI     ApaLI
tgctaacggacccaggaaatgttcagaaagcagtctgccatcccacagcttgggacctggggaaggcgacttcaggatccttatgtgcacaaaggtgacaatggacgacttcctgacagctcatcatga   1430
acgattgcctgggtcctttacaagtctttcgtcagacggtagggtgtcgaaccctggaccccttcccgctgaagtcctaggaatacacgtgtttccactgttacctgctgaaggactgtcgagtagtact
                                                          Peptidase_M2
                                                             active
M   L   T   D   P   G   N   V   Q   K   A   V   C   H   P   T   A   W   D   L   G   K   G   D   F   R   I   L   M   C   T   K   V   T   M   D   D   F   L   T   A   H   H   E  →

                                  BstAPI
gatggggcatatccagtatgatatggcatatgctgcacaacctttttctgctaagaaatggagctaatgaaggattccatgaagctgttggggaaatcatgtcactttctgcagccacacctaagcattta   1560
ctaccccgtataggtcatactataccgtatacgacgtgttggaaaagacgattctttacctcgattacttcctaaggtacttcgacaacccctttagtacagtgaaagacgtcggtgtggattcgtaaat
                                                          Peptidase_M2
  M   G   H   I   Q   Y   D   M   A   Y   A   A   Q   P   F   L   L   R   N   G   A   N   E   G   F   H   E   A   V   G   E   I   M   S   L   S   A   A   T   P   K   H   L  →
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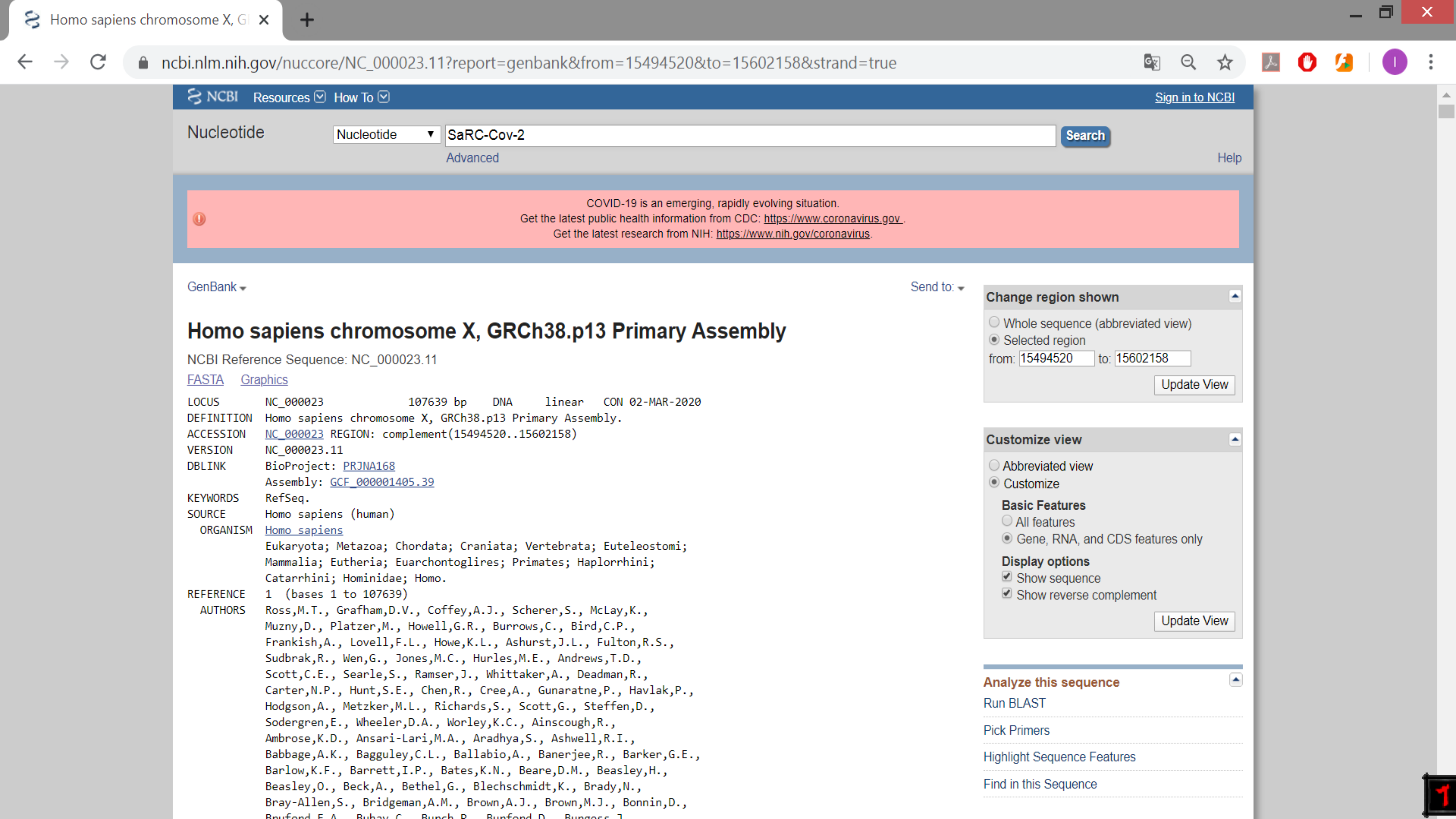

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Homo sapiens chromosome X, GRCh38.p13 Primary Assembly

NCBI Reference Sequence: NC_000023.11

FASTA Graphics

```
LOCUS       NC_000023             107639 bp    DNA     linear   CON 02-MAR-2020
DEFINITION  Homo sapiens chromosome X, GRCh38.p13 Primary Assembly.
ACCESSION   NC_000023 REGION: complement(15494520..15602158)
VERSION     NC_000023.11
DBLINK      BioProject: PRJNA168
            Assembly: GCF_000001405.39
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  (bases 1 to 107639)
  AUTHORS   Ross,M.T., Grafham,D.V., Coffey,A.J., Scherer,S., McLay,K.,
            Muzny,D., Platzer,M., Howell,G.R., Burrows,C., Bird,C.P.,
            Frankish,A., Lovell,F.L., Howe,K.L., Ashurst,J.L., Fulton,R.S.,
            Sudbrak,R., Wen,G., Jones,M.C., Hurles,M.E., Andrews,T.D.,
            Scott,C.E., Searle,S., Ramser,J., Whittaker,A., Deadman,R.,
            Carter,N.P., Hunt,S.E., Chen,R., Cree,A., Gunaratne,P., Havlak,P.,
            Hodgson,A., Metzker,M.L., Richards,S., Scott,G., Steffen,D.,
            Sodergren,E., Wheeler,D.A., Worley,K.C., Ainscough,R.,
            Ambrose,K.D., Ansari-Lari,M.A., Aradhya,S., Ashwell,R.I.,
            Babbage,A.K., Bagguley,C.L., Ballabio,A., Banerjee,R., Barker,G.E.,
            Barlow,K.F., Barrett,I.P., Bates,K.N., Beare,D.M., Beasley,H.,
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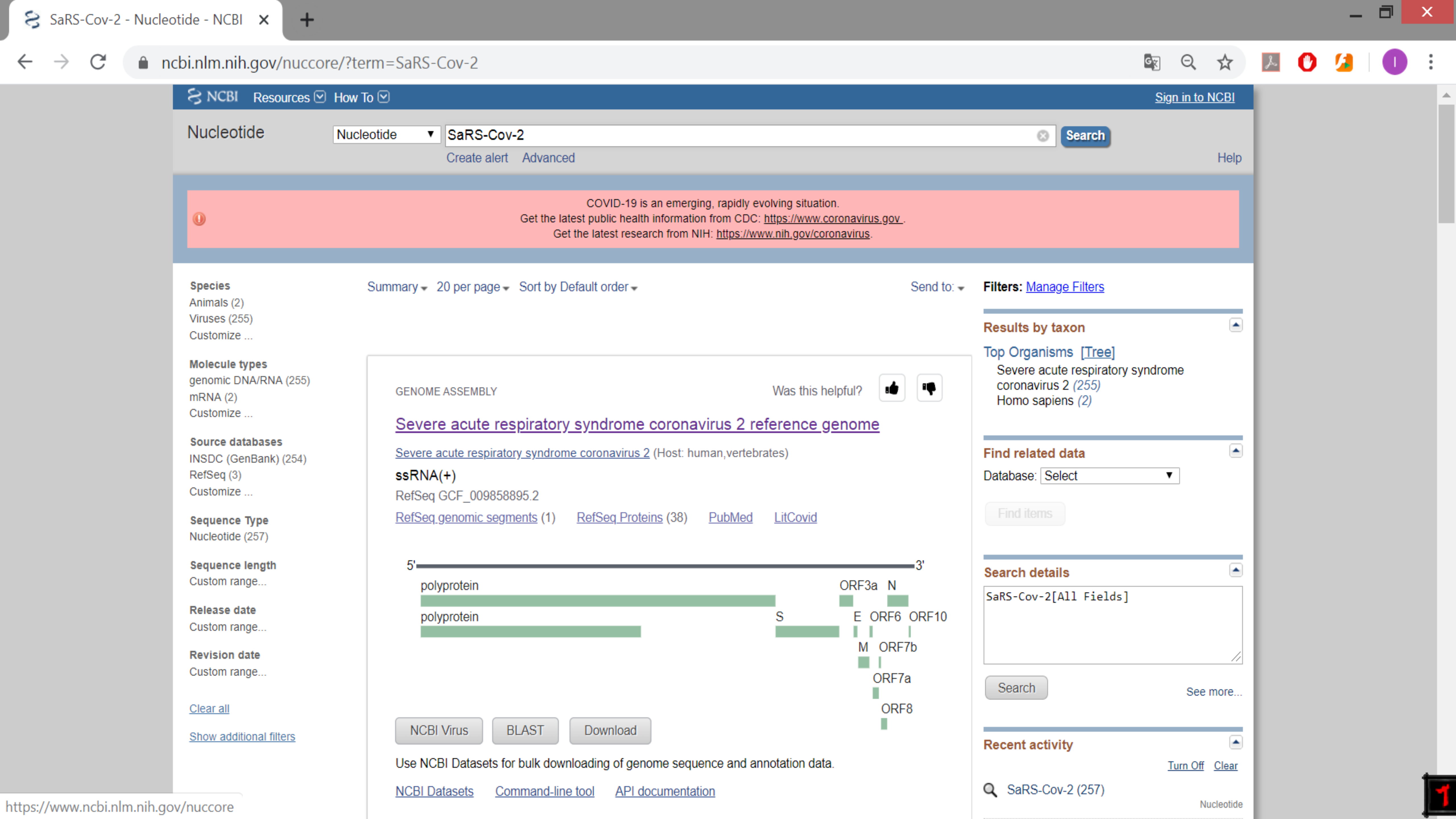

SaRS-Cov-2

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Animals (2)
Viruses (255)
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Molecule types
genomic DNA/RNA (255)
mRNA (2)
Customize ...

Source databases
INSDC (GenBank) (254)
RefSeq (3)
Customize ...

Sequence Type
Nucleotide (257)

Sequence length
Custom range...

Release date
Custom range...

Revision date
Custom range...

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GENOME ASSEMBLY

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Severe acute respiratory syndrome coronavirus 2 reference genome

Severe acute respiratory syndrome coronavirus 2 (Host: human,vertebrates)

ssRNA(+)

RefSeq GCF_009858895.2

RefSeq genomic segments (1) RefSeq Proteins (38) PubMed LitCovid

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NCBI Datasets Command-line tool API documentation

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Search details

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Nucleotide

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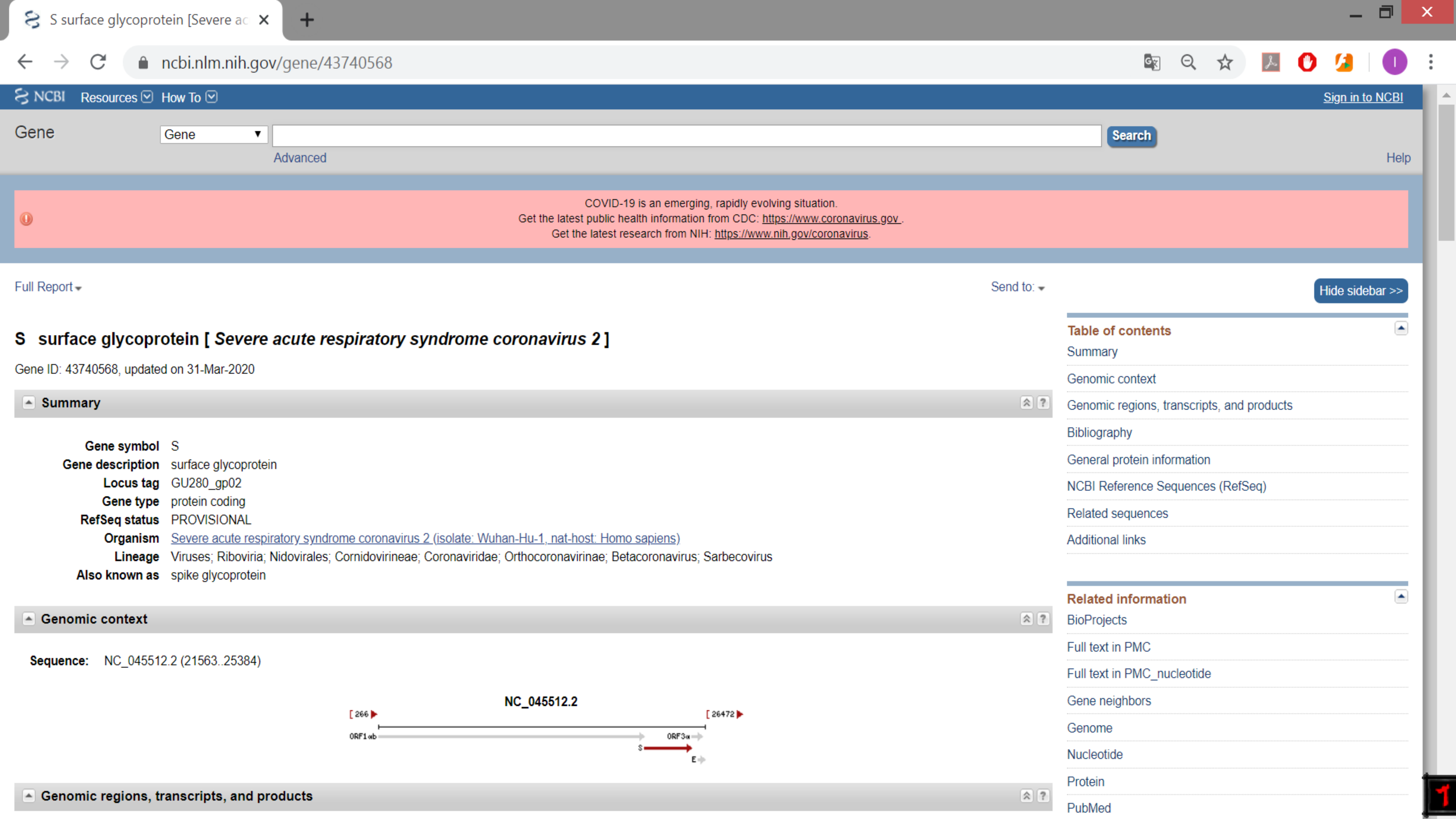

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S surface glycoprotein [*Severe acute respiratory syndrome coronavirus 2*]

Gene ID: 43740568, updated on 31-Mar-2020

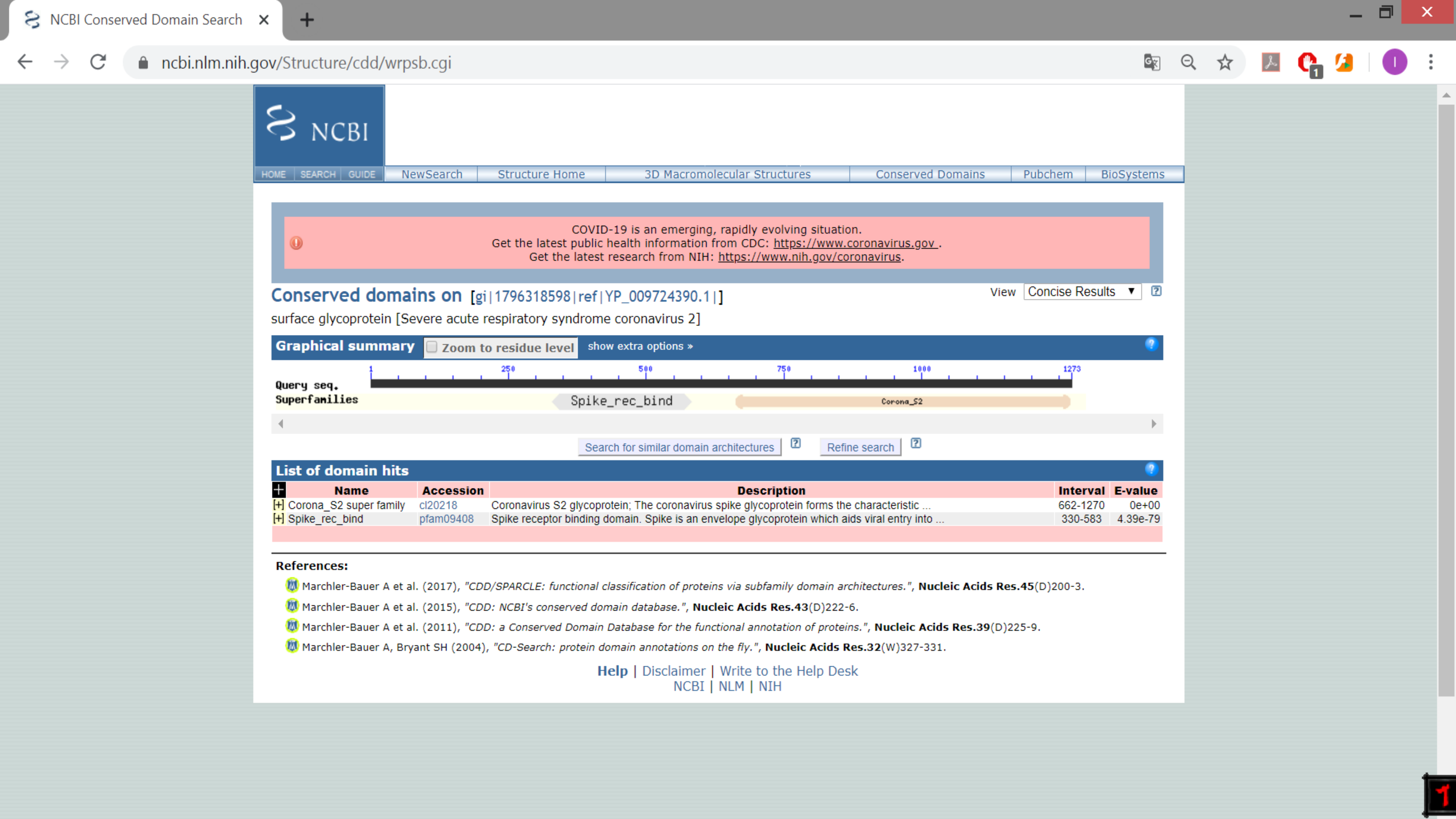
Summary

Gene symbol	S
Gene description	surface glycoprotein
Locus tag	GU280_gp02
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Severe acute respiratory syndrome coronavirus 2 (isolate: Wuhan-Hu-1, nat-host: Homo sapiens)
Lineage	Viruses; Riboviria; Nidovirales; Cornidovirineae; Coronaviridae; Orthocoronavirinae; Betacoronavirus; Sarbecovirus
Also known as	spike glycoprotein

Genomic context

Sequence: NC_045512.2 (21563..25384)

Genomic regions, transcripts, and products



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Conserved domains on [gi|1796318598|ref|YP_009724390.1|]

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surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]

Graphical summary ☐ Zoom to residue level show extra options »

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	Name	Accession	Description	Interval	E-value
[+]	Corona_S2 super family	cl20218	Coronavirus S2 glycoprotein; The coronavirus spike glycoprotein forms the characteristic ...	662-1270	0e+00
[+]	Spike_rec_bind	pfam09408	Spike receptor binding domain. Spike is an envelope glycoprotein which aids viral entry into ...	330-583	4.39e-79

References:

Marchler-Bauer A et al. (2017), *"CDD/SPARCLE: functional classification of proteins via subfamily domain architectures."*, **Nucleic Acids Res.45**(D)200-3.

Marchler-Bauer A et al. (2015), *"CDD: NCBI's conserved domain database."*, **Nucleic Acids Res.43**(D)222-6.

Marchler-Bauer A et al. (2011), *"CDD: a Conserved Domain Database for the functional annotation of proteins."*, **Nucleic Acids Res.39**(D)225-9.

Marchler-Bauer A, Bryant SH (2004), *"CD-Search: protein domain annotations on the fly."*, **Nucleic Acids Res.32**(W)327-331.

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