TP Conception des amorces

par Dr BRAHAMI Nabila

Ensembl genome browser

www.ensembl.org/index.html

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e!Ensembl

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Search all species…

Search: All species for Go

e.g. BRCA2 or rat 5:62797383-63627669 or rs699 or coronary heart disease

Browse a Genome

The Ensembl project produces genome databases for vertebrates and other eukaryotic species, and makes this information freely available online.

Popular genomes

Human
GRCh38.p5

Human
GRCh37

Mouse
GRCm38.p4

Zebrafish
GRCz10

★ Log in to customize this list

All genomes

-- Select a species --

View full list of all Ensembl species

Other species are available in Ensembl *Pre!* and

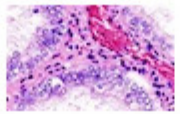
Still using Human GRCh37?

Go to e! GRCh37

Variant Effect Predictor

VeP

Gene expression in different tissues



Find SNPs and other variants for my gene

Retrieve gene sequence

Compare genes across species

Use my own data in Ensembl

ENCODE data in Ensembl

What's New in Ensembl Release 84 (March 20

- 20 haematopoietic primary cell epigenomes from the BLUEPRINT project
- Mouse: update to Ensembl-Havana GENCODE gene se
- Track hub registry interface
- dbSNP 146 for Human, Cow and Dog
- Pairwise LD calculation on LD variant page

Full details | All web updates, by release | More news on our

- 25 Apr 2016: DNA day and Malaria day: a story of scientific endeavour
- 31 Mar 2016: Ensembl 85 and Ensembl Genomes 32
- 29 Mar 2016: Ensembl Genomes 31 has been released!

Go to Ensembl

Tweets by @ensembl

Ensembl @ensembl
The ESR1 gene is expressed in the female human reproductive system: buff.ly/26OwoIh #Geneoftheweek

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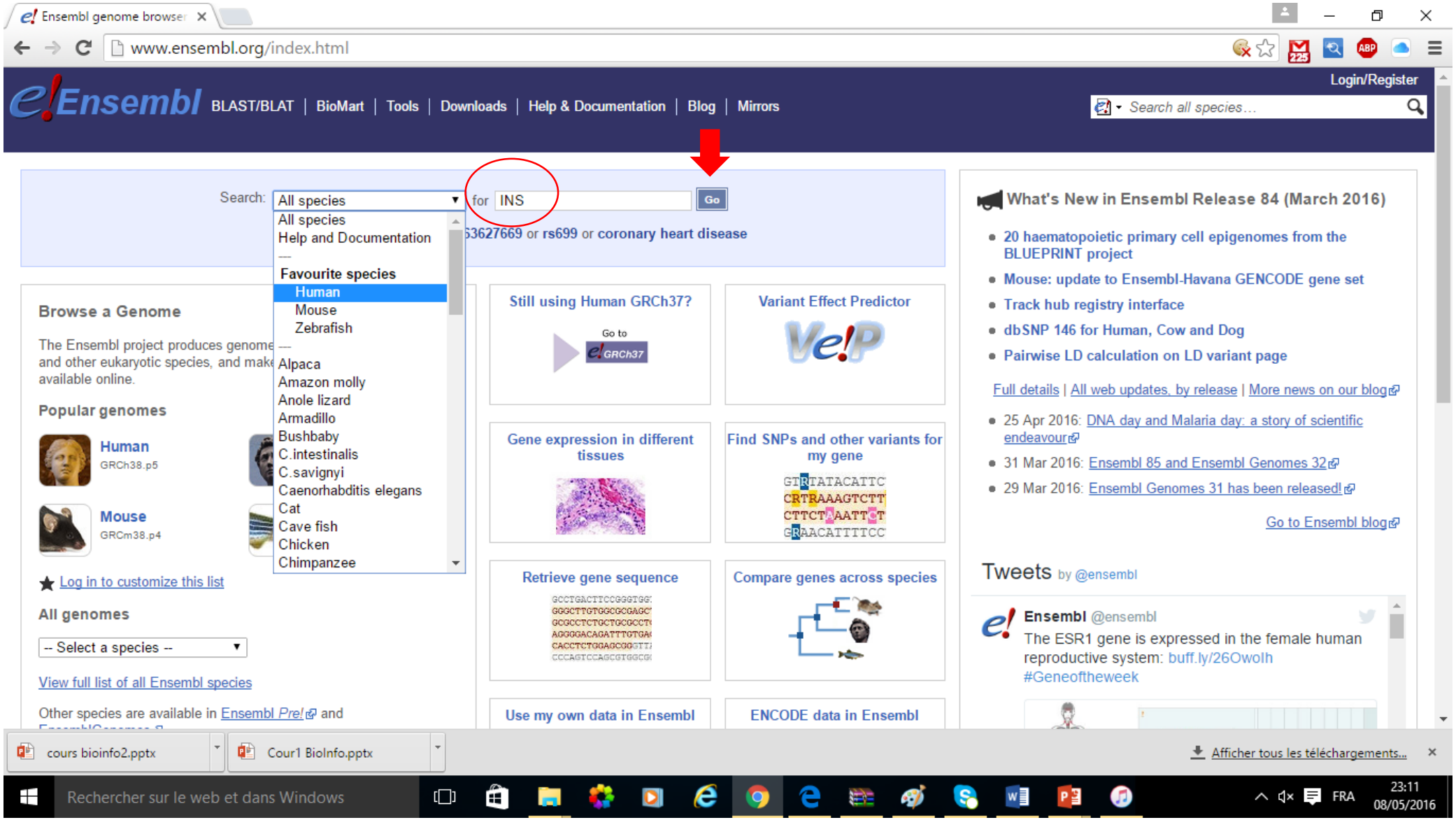
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Alpaca
Amazon molly
Anole lizard
Armadillo
Bushbaby
C.intestinalis
C.savignyi
Caenorhabditis elegans
Cat
Cave fish
Chicken
Chimpanzee
rs699 or coronary heart disease
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and other eukaryotic species, and make
available online.
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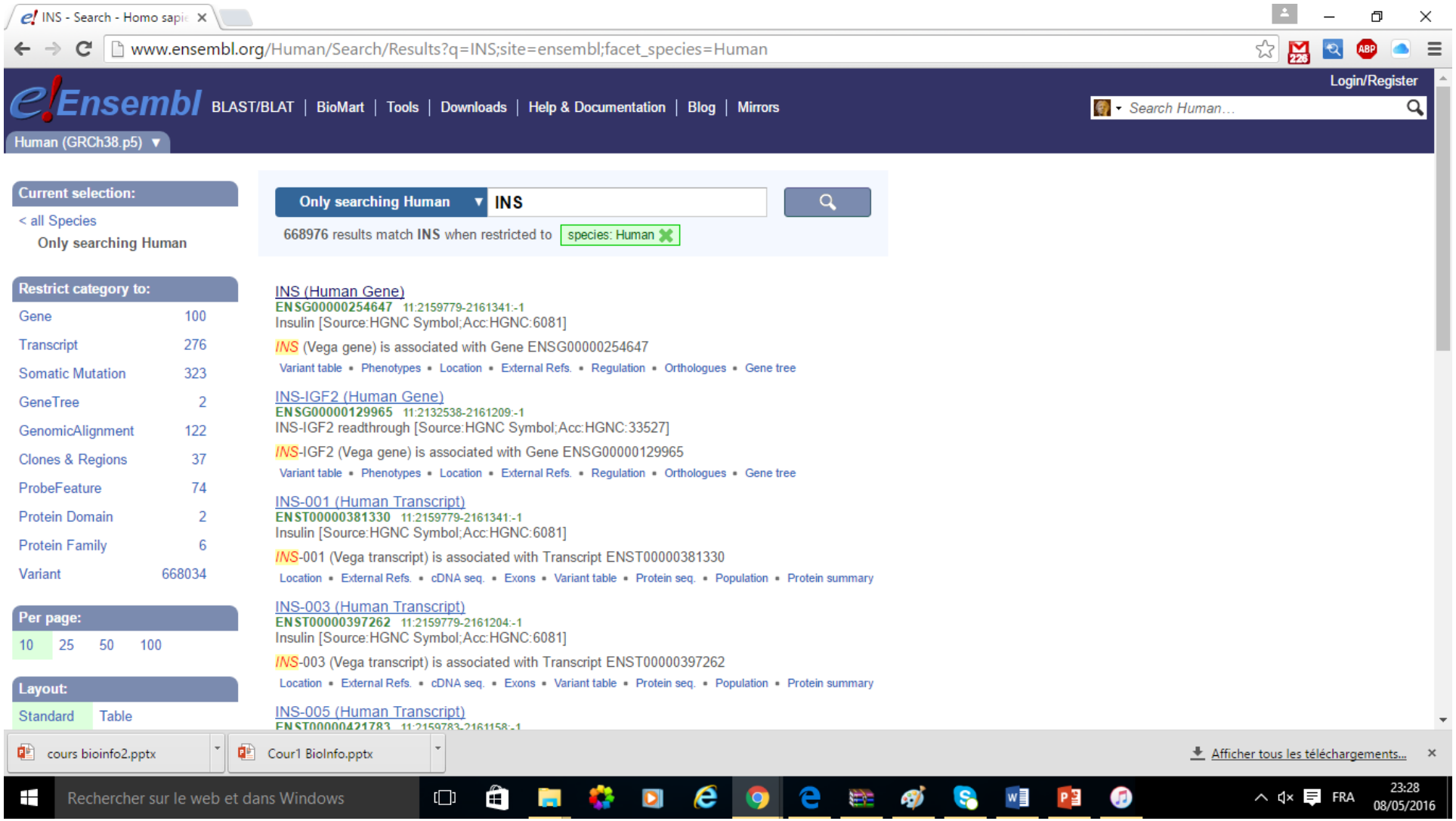
INS - Search - Homo sapi
www.ensembl.org/Human/Search/Results?q=INS;site=ensembl;facet_species=Human
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Human (GRCh38.p5)
Current selection:
< all Species
Only searching Human
Restrict category to:
Gene 100
Transcript 276
Somatic Mutation 323
GeneTree 2
GenomicAlignment 122
Clones & Regions 37
ProbeFeature 74
Protein Domain 2
Protein Family 6
Variant 668034
Per page:
10 25 50 100
Layout:
Standard Table
Only searching Human
INS
668976 results match INS when restricted to species: Human
INS (Human Gene)
ENSG00000254647 11:2159779-2161341:-1
Insulin [Source:HGNC Symbol;Acc:HGNC:6081]
INS (Vega gene) is associated with Gene ENSG00000254647
Variant table • Phenotypes • Location • External Refs. • Regulation • Orthologues • Gene tree
INS-IGF2 (Human Gene)
ENSG00000129965 11:2132538-2161209:-1
INS-IGF2 readthrough [Source:HGNC Symbol;Acc:HGNC:33527]
INS-IGF2 (Vega gene) is associated with Gene ENSG00000129965
Variant table • Phenotypes • Location • External Refs. • Regulation • Orthologues • Gene tree
INS-001 (Human Transcript)
ENST00000381330 11:2159779-2161341:-1
Insulin [Source:HGNC Symbol;Acc:HGNC:6081]
INS-001 (Vega transcript) is associated with Transcript ENST00000381330
Location • External Refs. • cDNA seq. • Exons • Variant table • Protein seq. • Population • Protein summary
INS-003 (Human Transcript)
ENST00000397262 11:2159779-2161204:-1
Insulin [Source:HGNC Symbol;Acc:HGNC:6081]
INS-003 (Vega transcript) is associated with Transcript ENST00000397262
Location • External Refs. • cDNA seq. • Exons • Variant table • Protein seq. • Population • Protein summary
INS-005 (Human Transcript)
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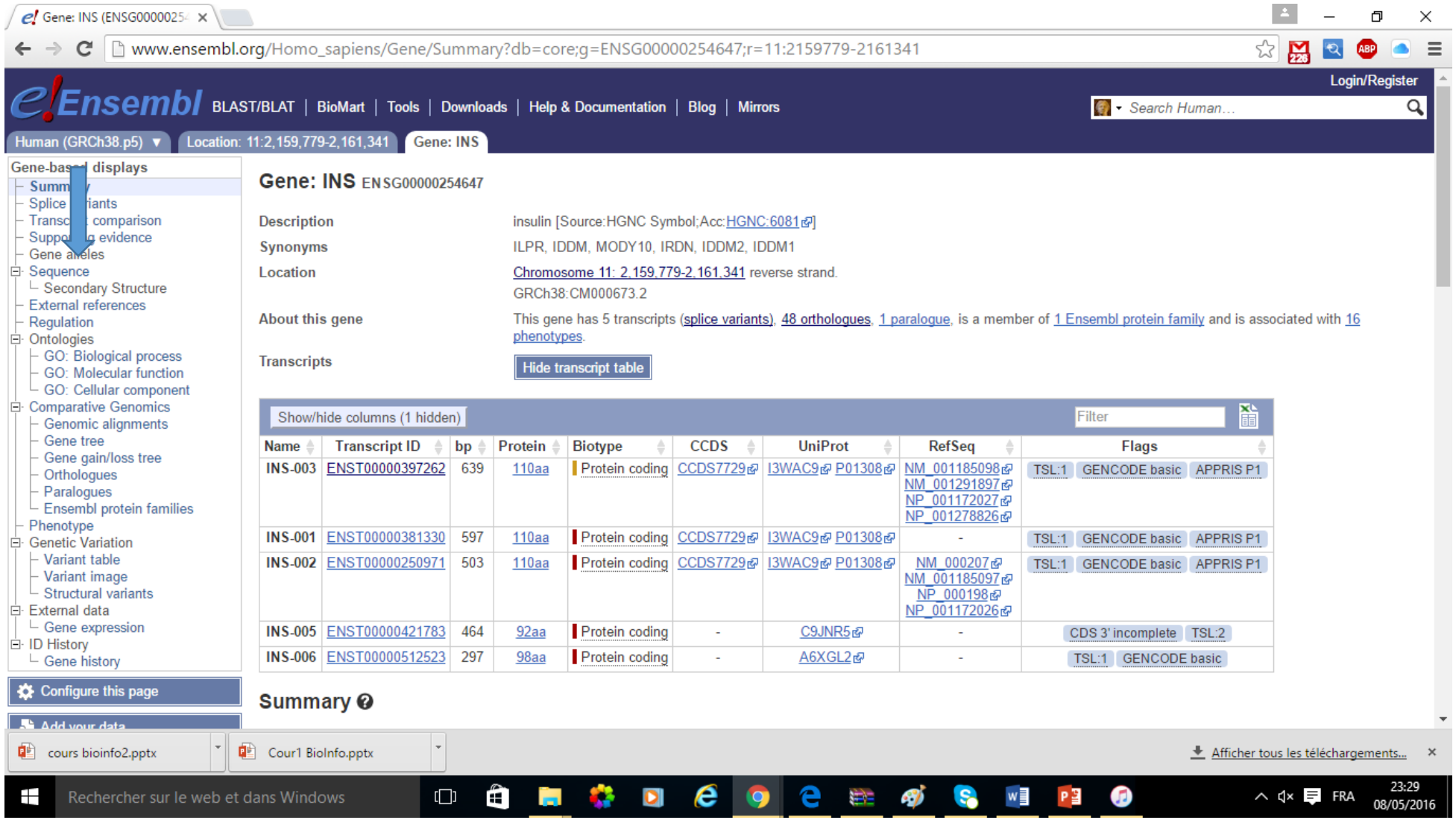
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www.ensembl.org/Homo_sapiens/Gene/Summary?db=core;g=ENSG00000254647;r=11:2159779-2161341
Ensembl
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Login/Register
Search Human...
Human (GRCh38.p5)
Location: 11:2,159,779-2,161,341
Gene: INS
Gene-based displays
Summary
Splice variants
Transcript comparison
Supporting evidence
Gene alleles
Sequence
Secondary Structure
External references
Regulation
Ontologies
GO: Biological process
GO: Molecular function
GO: Cellular component
Comparative Genomics
Genomic alignments
Gene tree
Gene gain/loss tree
Orthologues
Paralogues
Ensembl protein families
Phenotype
Genetic Variation
Variant table
Variant image
Structural variants
External data
Gene expression
ID History
Gene history
Configure this page
Add your data
Gene: INS ENSG00000254647
Description
insulin [Source:HGNC Symbol;Acc:HGNC:6081]
Synonyms
ILPR, IDDM, MODY10, IRDN, IDDM2, IDDM1
Location
Chromosome 11: 2,159,779-2,161,341 reverse strand.
GRCh38:CM000673.2
About this gene
This gene has 5 transcripts (splice variants), 48 orthologues, 1 paralogue, is a member of 1 Ensembl protein family and is associated with 16 phenotypes.
Transcripts
Hide transcript table
Show/hide columns (1 hidden)
Filter
Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | RefSeq | Flags
INS-003 | ENST00000397262 | 639 | 110aa | Protein coding | CCDS7729 | I3WAC9 P01308 | NM_001185098 NM_001291897 NP_001172027 NP_001278826 | TSL:1 GENCODE basic APPRIS P1
INS-001 | ENST00000381330 | 597 | 110aa | Protein coding | CCDS7729 | I3WAC9 P01308 | - | TSL:1 GENCODE basic APPRIS P1
INS-002 | ENST00000250971 | 503 | 110aa | Protein coding | CCDS7729 | I3WAC9 P01308 | NM_000207 NM_001185097 NP_000198 NP_001172026 | TSL:1 GENCODE basic APPRIS P1
INS-005 | ENST00000421783 | 464 | 92aa | Protein coding | - | C9JNR5 | - | CDS 3' incomplete TSL:2
INS-006 | ENST00000512523 | 297 | 98aa | Protein coding | - | A6XGL2 | - | TSL:1 GENCODE basic
Summary
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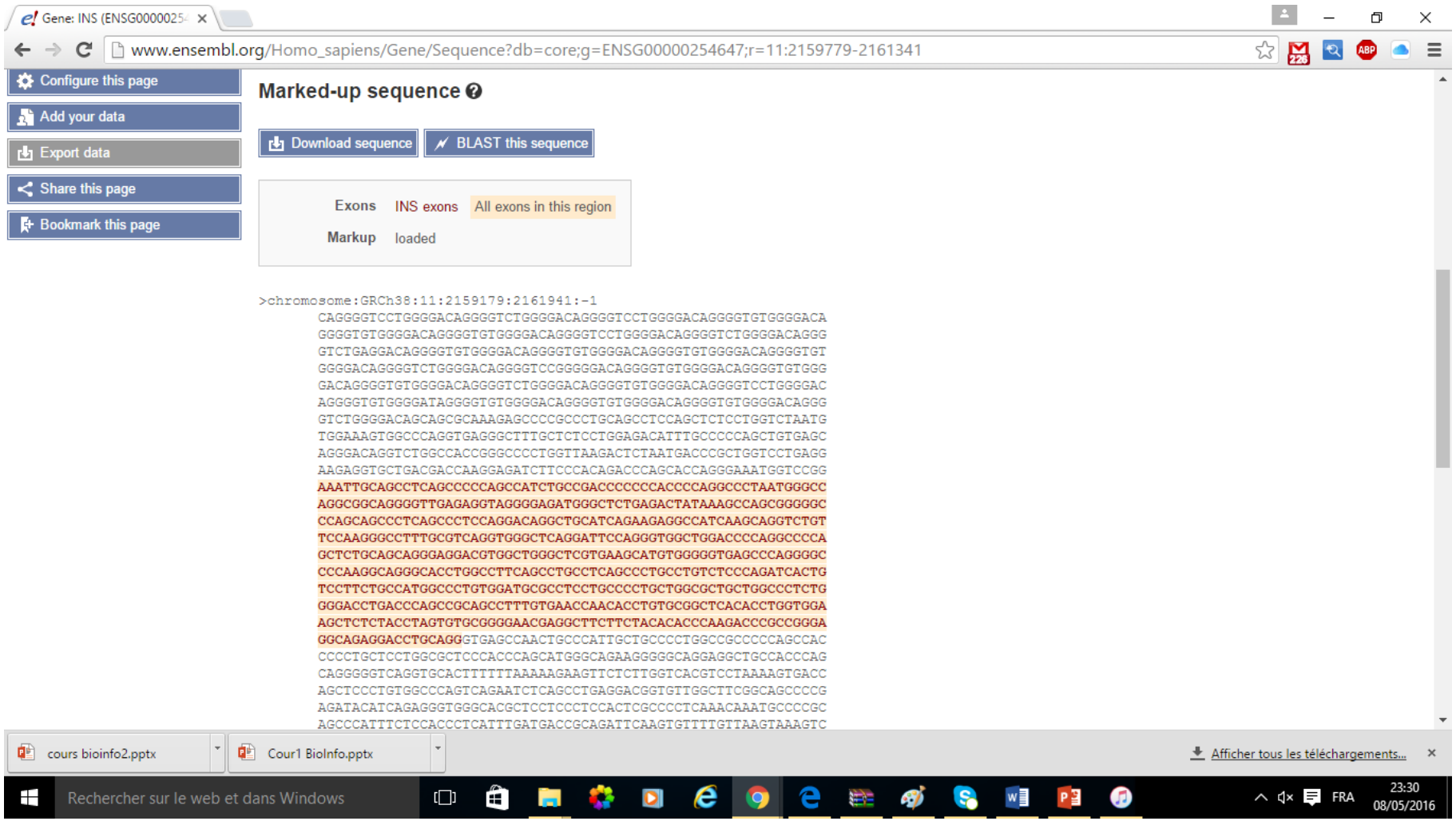
Gene: INS (ENSG0000025
www.ensembl.org/Homo_sapiens/Gene/Sequence?db=core;g=ENSG00000254647;r=11:2159779-2161341
Configure this page
Add your data
Export data
Share this page
Bookmark this page
Marked-up sequence
Download sequence
BLAST this sequence
Exons
INS exons
All exons in this region
Markup
loaded
>chromosome:GRCh38:11:2159179:2161941:-1
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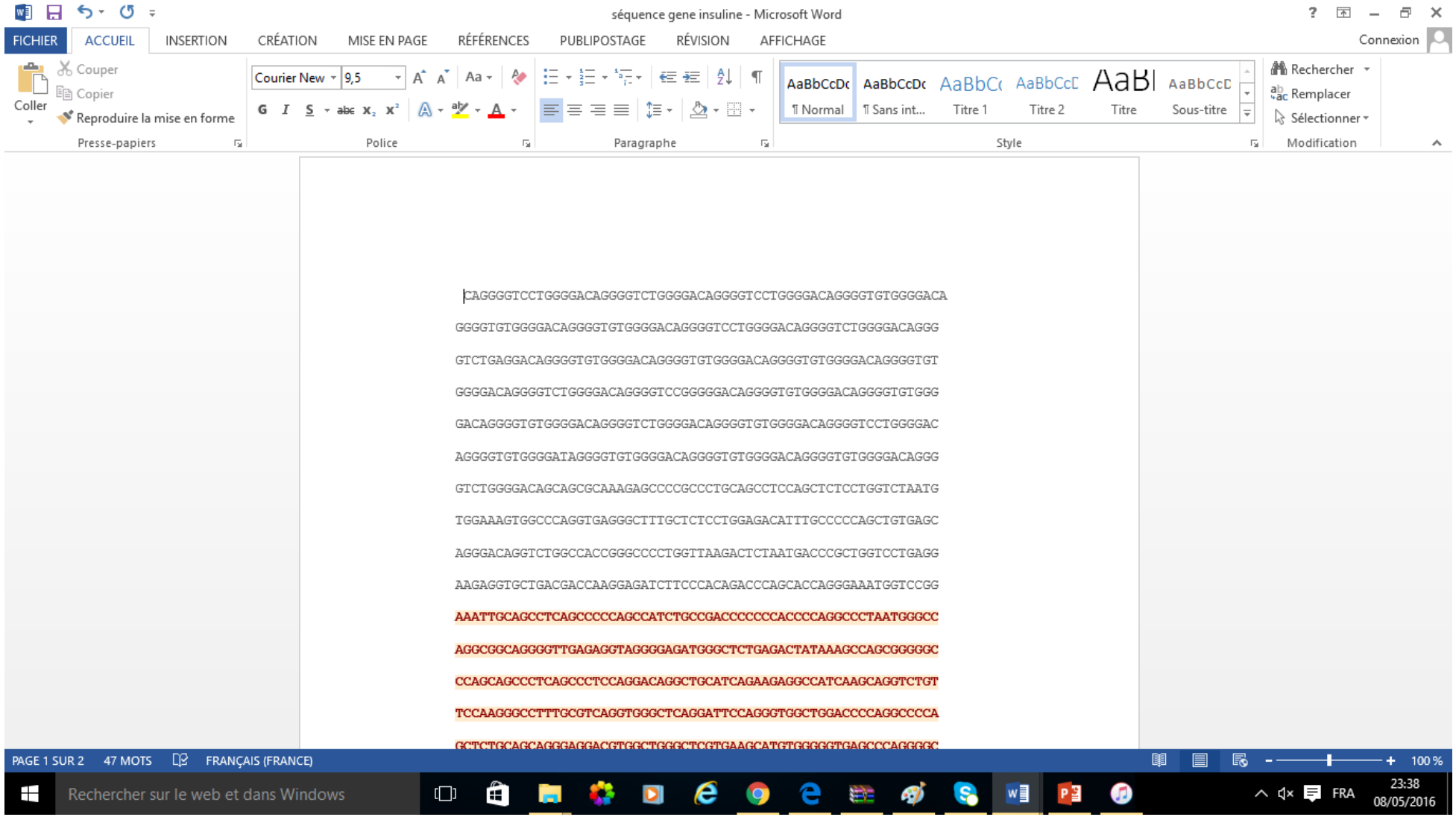
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Titre 2
Titre
Sous-titre
Style
Rechercher
Remplacer
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Modification
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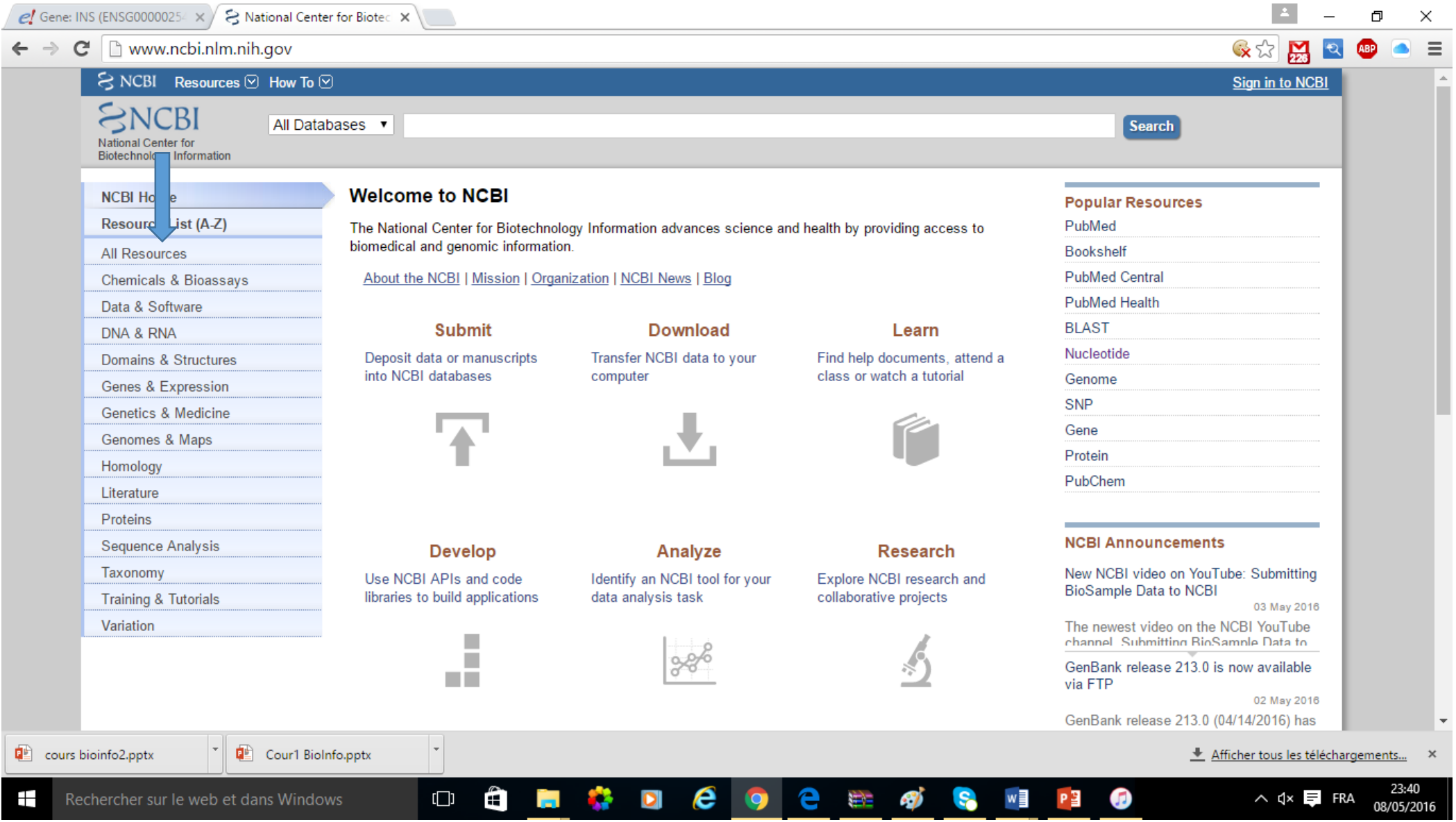
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New NCBI video on YouTube: Submitting BioSample Data to NCBI
03 May 2016
The newest video on the NCBI YouTube channel, Submitting BioSample Data to
GenBank release 213.0 is now available via FTP
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GenBank release 213.0 (04/14/2016) has
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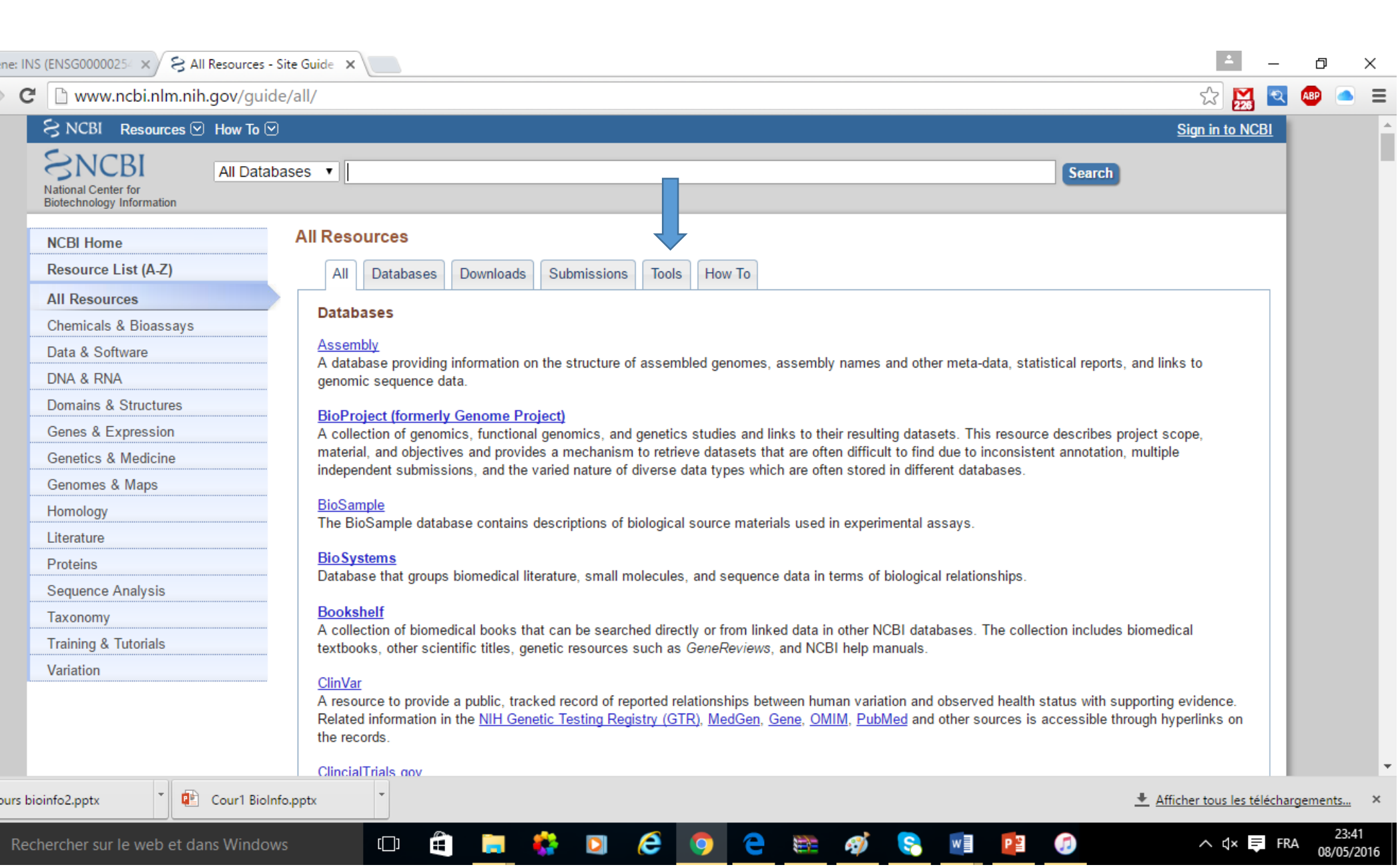
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All Resources - Site Guide
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Genes & Expression
Genetics & Medicine
Genomes & Maps
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Literature
Proteins
Sequence Analysis
Taxonomy
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Variation
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All
Databases
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Submissions
Tools
How To
Databases
Assembly
A database providing information on the structure of assembled genomes, assembly names and other meta-data, statistical reports, and links to genomic sequence data.
BioProject (formerly Genome Project)
A collection of genomics, functional genomics, and genetics studies and links to their resulting datasets. This resource describes project scope, material, and objectives and provides a mechanism to retrieve datasets that are often difficult to find due to inconsistent annotation, multiple independent submissions, and the varied nature of diverse data types which are often stored in different databases.
BioSample
The BioSample database contains descriptions of biological source materials used in experimental assays.
BioSystems
Database that groups biomedical literature, small molecules, and sequence data in terms of biological relationships.
Bookshelf
A collection of biomedical books that can be searched directly or from linked data in other NCBI databases. The collection includes biomedical textbooks, other scientific titles, genetic resources such as GeneReviews, and NCBI help manuals.
ClinVar
A resource to provide a public, tracked record of reported relationships between human variation and observed health status with supporting evidence. Related information in the NIH Genetic Testing Registry (GTR), MedGen, Gene, OMIM, PubMed and other sources is accessible through hyperlinks on the records.
ClinicalTrials.gov
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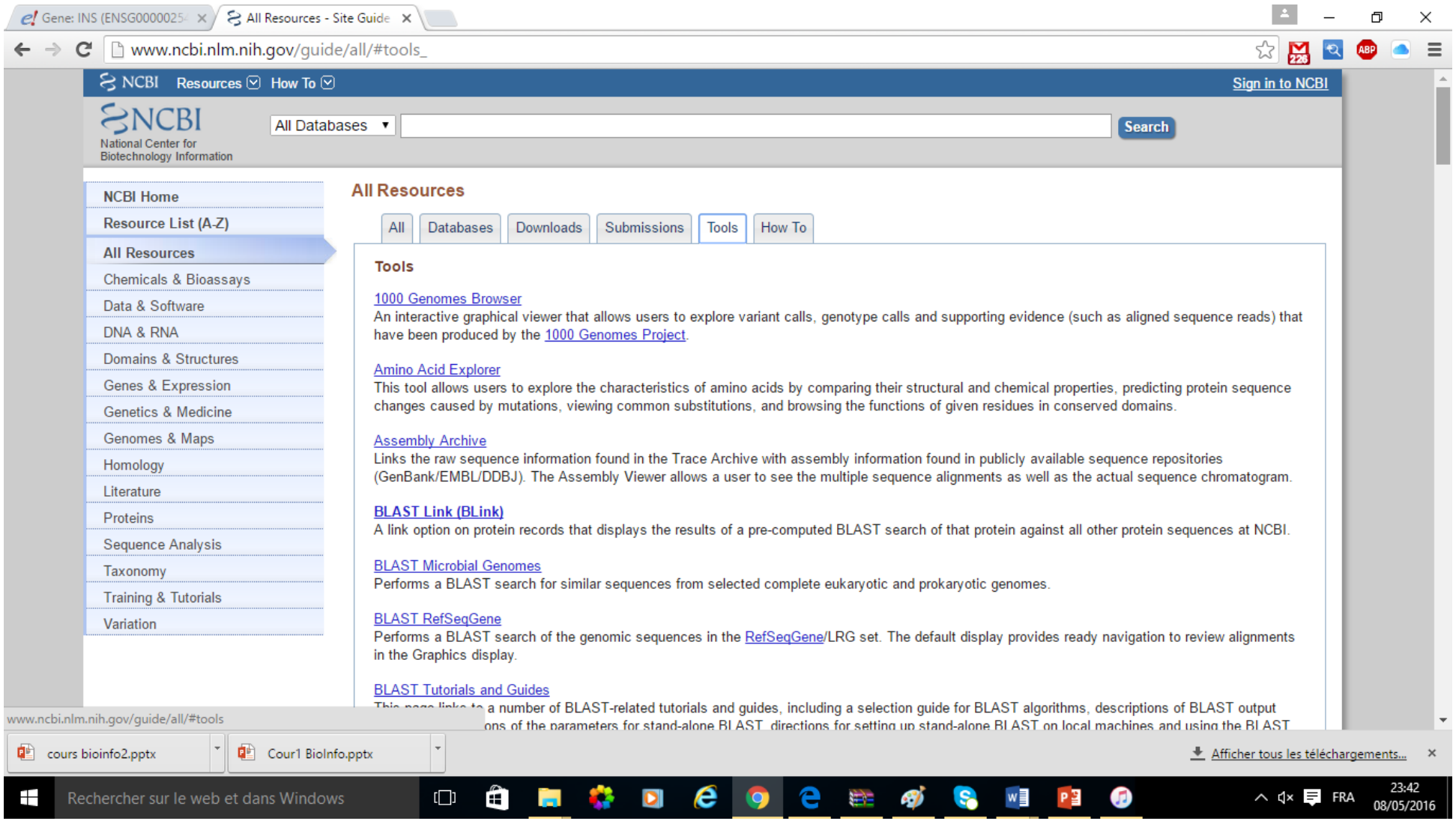
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Literature
Proteins
Sequence Analysis
Taxonomy
Training & Tutorials
Variation
All Resources
All
Databases
Downloads
Submissions
Tools
How To
Tools
1000 Genomes Browser
An interactive graphical viewer that allows users to explore variant calls, genotype calls and supporting evidence (such as aligned sequence reads) that have been produced by the 1000 Genomes Project.
Amino Acid Explorer
This tool allows users to explore the characteristics of amino acids by comparing their structural and chemical properties, predicting protein sequence changes caused by mutations, viewing common substitutions, and browsing the functions of given residues in conserved domains.
Assembly Archive
Links the raw sequence information found in the Trace Archive with assembly information found in publicly available sequence repositories (GenBank/EMBL/DDBJ). The Assembly Viewer allows a user to see the multiple sequence alignments as well as the actual sequence chromatogram.
BLAST Link (BLink)
A link option on protein records that displays the results of a pre-computed BLAST search of that protein against all other protein sequences at NCBI.
BLAST Microbial Genomes
Performs a BLAST search for similar sequences from selected complete eukaryotic and prokaryotic genomes.
BLAST RefSeqGene
Performs a BLAST search of the genomic sequences in the RefSeqGene/LRG set. The default display provides ready navigation to review alignments in the Graphics display.
BLAST Tutorials and Guides
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Gene: INS (ENSG0000025 | All Resources - Site Guide

www.ncbi.nlm.nih.gov/guide/all/#tools_

Toolbox is primarily designed to read records in Abstract Syntax Notation 1 (ASN.1) format, an International Standards Organization (ISO) data representation format.

OSIRIS
A public domain quality assurance software package that facilitates the assessment of multiplex short tandem repeat (STR) DNA profiles based on laboratory-specific protocols. OSIRIS evaluates the raw electrophoresis data using an independently derived mathematically-based sizing algorithm. It offers two new peak quality measures - fit level and sizing residual. It can be customized to accommodate laboratory-specific signatures such as background noise settings, customized naming conventions and additional internal laboratory controls.

Open Reading Frame Finder (ORF Finder)
A graphical analysis tool that finds all open reading frames in a user's sequence or in a sequence already in the database. Sixteen different genetic codes can be used. The deduced amino acid sequence can be saved in various formats and searched against protein databases using BLAST.

PSSM Viewer
Allows users to display, sort, subset and download position-specific score matrices (PSSMs) either from CDD records or from Position Specific Iterated (PSI)-BLAST protein searches. The tool also can align a query protein to the PSSM and highlight positions of high conservation.

Phenotype-Genotype Integrator (PheGenI)
Supports finding human phenotype/genotype relationships with queries by phenotype, chromosome location, gene, and SNP identifiers. Currently includes information from dbGaP, the NHGRI GWAS Catalog, and GTeX. Displays results on the genome, on sequence, or in tables for download.

Primer-BLAST
The Primer-BLAST tool uses Primer3 to design PCR primers to a sequence template. The potential products are then automatically analyzed with a BLAST search against user specified databases, to check the specificity to the target intended.

ProSplign
A utility for computing alignment of proteins to genomic nucleotide sequence. It is based on a variation of the Needleman Wunsch global alignment algorithm and specifically accounts for introns and splice signals. Due to this algorithm, ProSplign is accurate in determining splice sites and tolerant to sequencing errors.

PubChem Power User Gateway (PUG)
PUG provides access to PubChem services via a programmatic interface. PUG allows users to download data, initiate chemical structure searches, standardize chemical structures and interact with the E-utilities. PUG can be accessed using either standard URLs or via SOAP.

PubChem Standardization Service
Standardization, in PubChem terminology, is the processing of chemical structures in the same way used to create PubChem Compound records from al structures. This service lets users see how PubChem would handle any structure they would like to submit.

www.ncbi.nlm.nih.gov/guide/all/#tools

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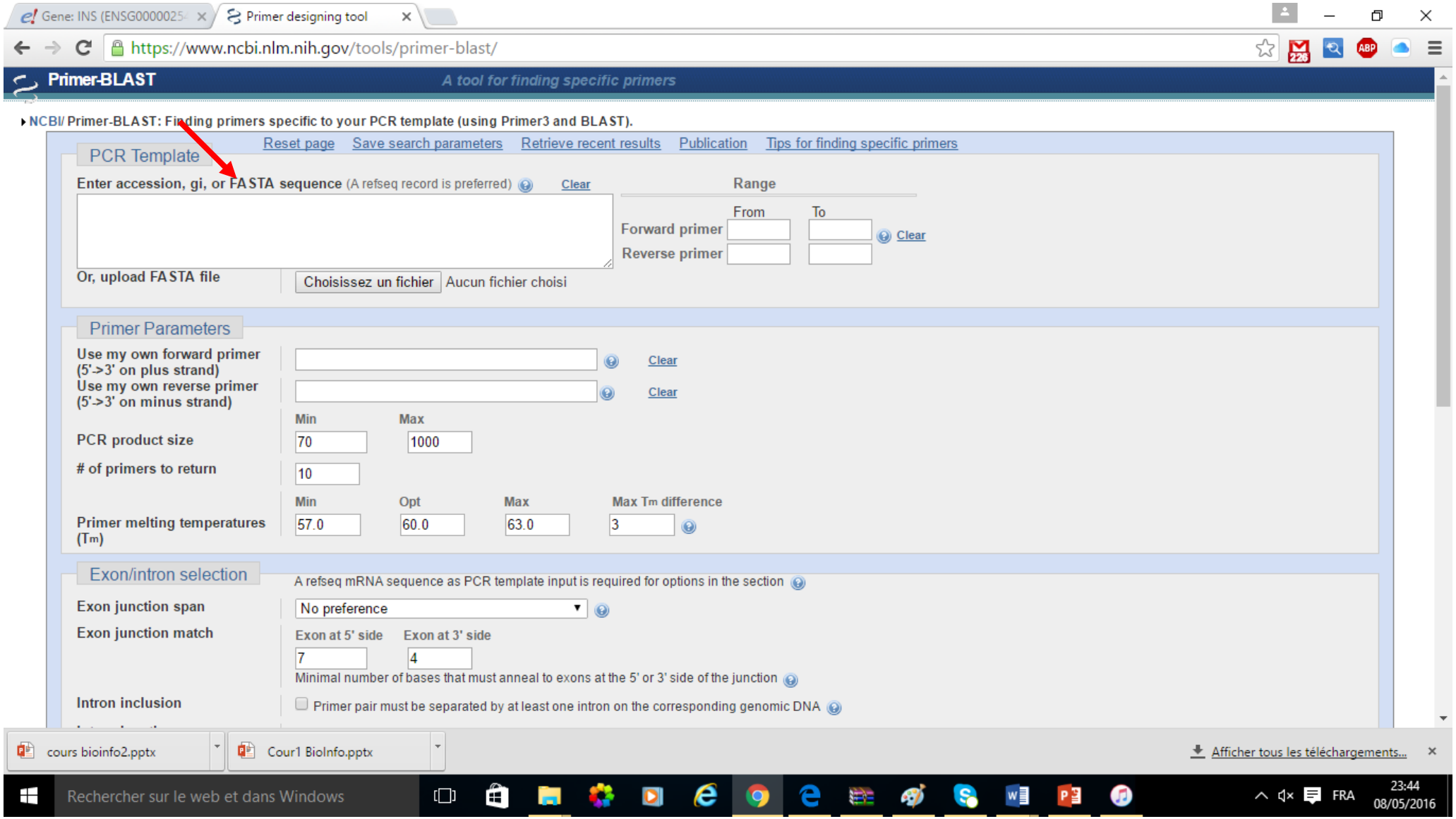
Gene: INS (ENSG0000025
Primer designing tool
https://www.ncbi.nlm.nih.gov/tools/primer-blast/
Primer-BLAST
A tool for finding specific primers
NCBI/ Primer-BLAST: Finding primers specific to your PCR template (using Primer3 and BLAST).
Reset page
Save search parameters
Retrieve recent results
Publication
Tips for finding specific primers
PCR Template
Enter accession, gi, or FASTA sequence (A refseq record is preferred)
Clear
Range
From
To
Forward primer
Reverse primer
Clear
Or, upload FASTA file
Choisissez un fichier
Aucun fichier choisi
Primer Parameters
Use my own forward primer (5'->3' on plus strand)
Use my own reverse primer (5'->3' on minus strand)
Clear
Clear
Min
Max
PCR product size
70
1000
# of primers to return
10
Min
Opt
Max
Max Tm difference
Primer melting temperatures (Tm)
57.0
60.0
63.0
3
Exon/intron selection
A refseq mRNA sequence as PCR template input is required for options in the section
Exon junction span
No preference
Exon junction match
Exon at 5' side
Exon at 3' side
7
4
Minimal number of bases that must anneal to exons at the 5' or 3' side of the junction
Intron inclusion
Primer pair must be separated by at least one intron on the corresponding genomic DNA
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Courier New 9,5 — Police

Paragraphe

¶ Normal ¶ Sans int... Titre 1 Titre 2 Titre Sous-titre — Style

Rechercher Remplacer Sélectionner — Modification

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PAGE 1 SUR 2 17 SUR 47 MOTS FRANÇAIS (FRANCE) 100 %

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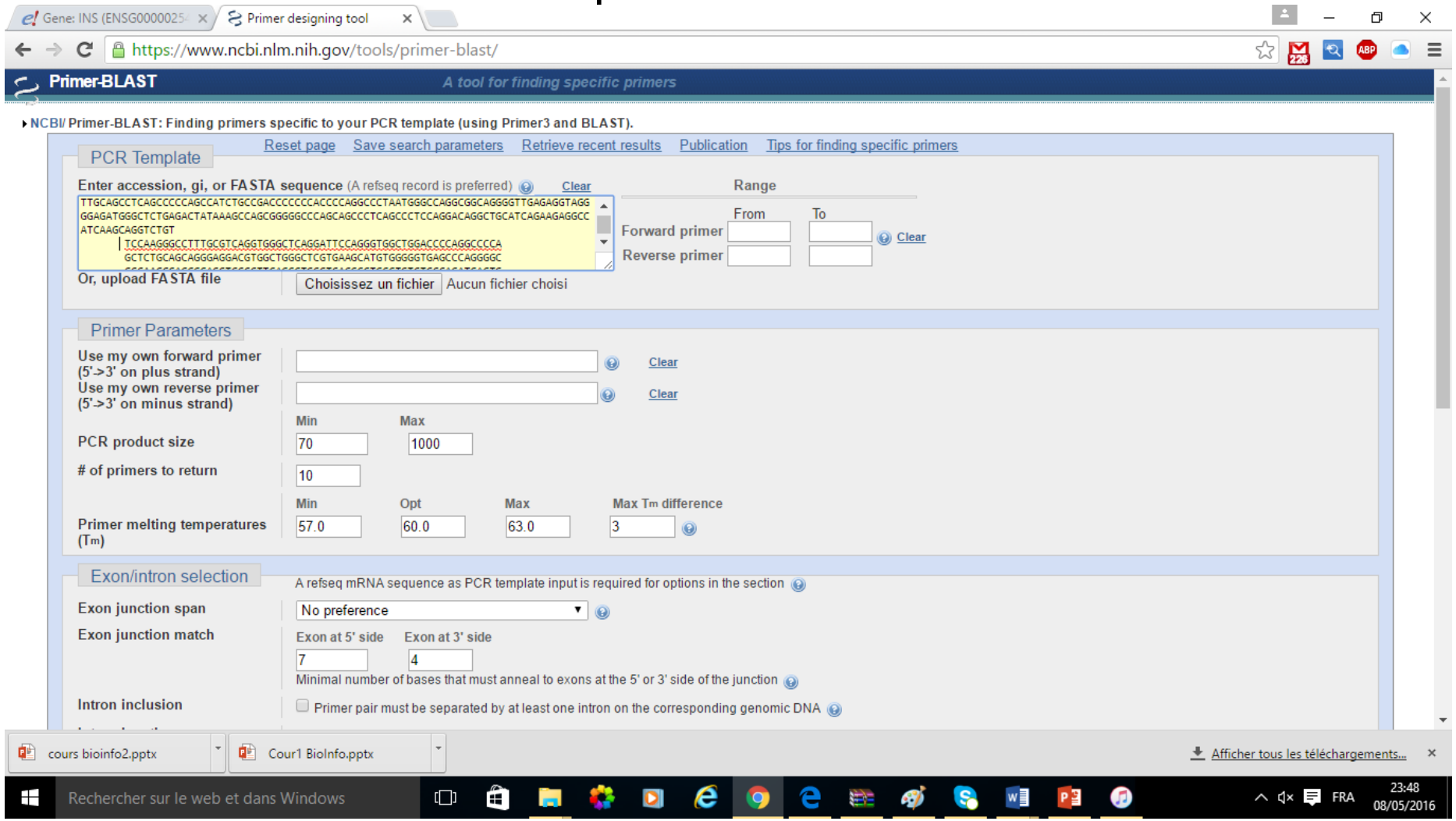

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Copier
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Paragraphe

¶ Normal | ¶ Sans int... | Titre 1 | Titre 2 | Titre | Sous-titre
Style

Rechercher
Remplacer
Sélectionner
Modification

- Bordure inférieure
- Bordure supérieure
- Bordure gauche
- Bordure droite
- Aucune bordure
- Toutes les bordures
- Bordures extérieures
- Bordures intérieures
- Bordure intérieure horizontale
- Bordure intérieure verticale
- Bordure diagonale bas
- Bordure diagonale haut
- Ligne horizontale
- Dessiner un tableau
- Afficher le quadrillage
- Bordure et trame...

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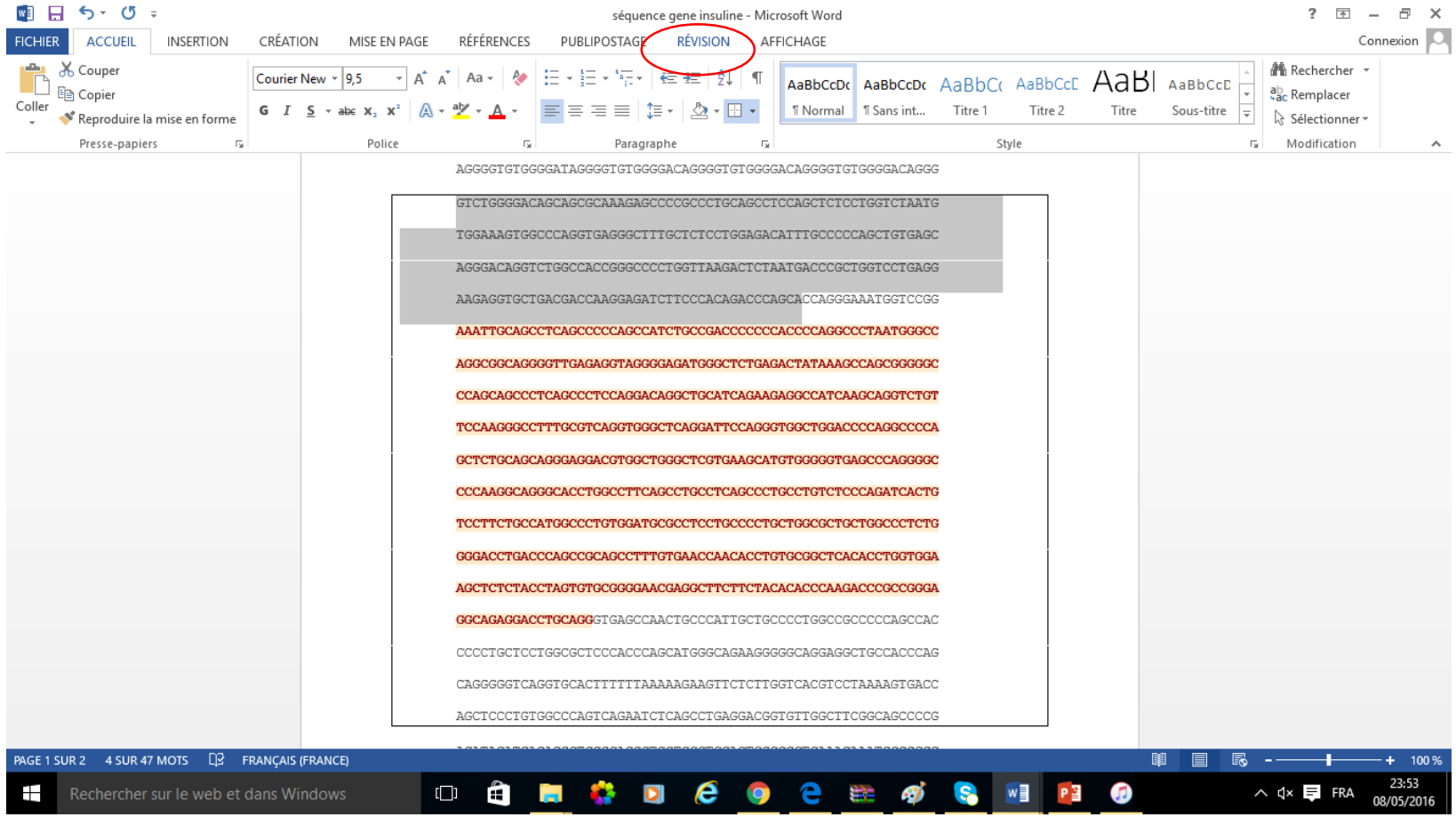
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Titre 1
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PAGE 1 SUR 2
4 SUR 47 MOTS
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ABC Grammaire et orthographe
Définir
Dictionnaire des synonymes
Statistiques
Vérification

Traduire Langue
Langue

Nouveau commentaire
Supprimer
Précédent
Suivant
Afficher les commentaires
Commentaires

Suivi des modifications
Marques simples
Afficher les marques
Volet Vérifications
Suivi

Accepter Refuser
Précédent
Suivant
Modifications

Comparer
Comparer

Bloquer les auteurs
Restreindre la modification
Protéger

Statistiques

Les mots, les caractères, les lignes...
Nous les comptons, pour que vous n'ayez pas à le faire.

Pour connaître immédiatement le nombre total de mots, consultez la barre d'état.

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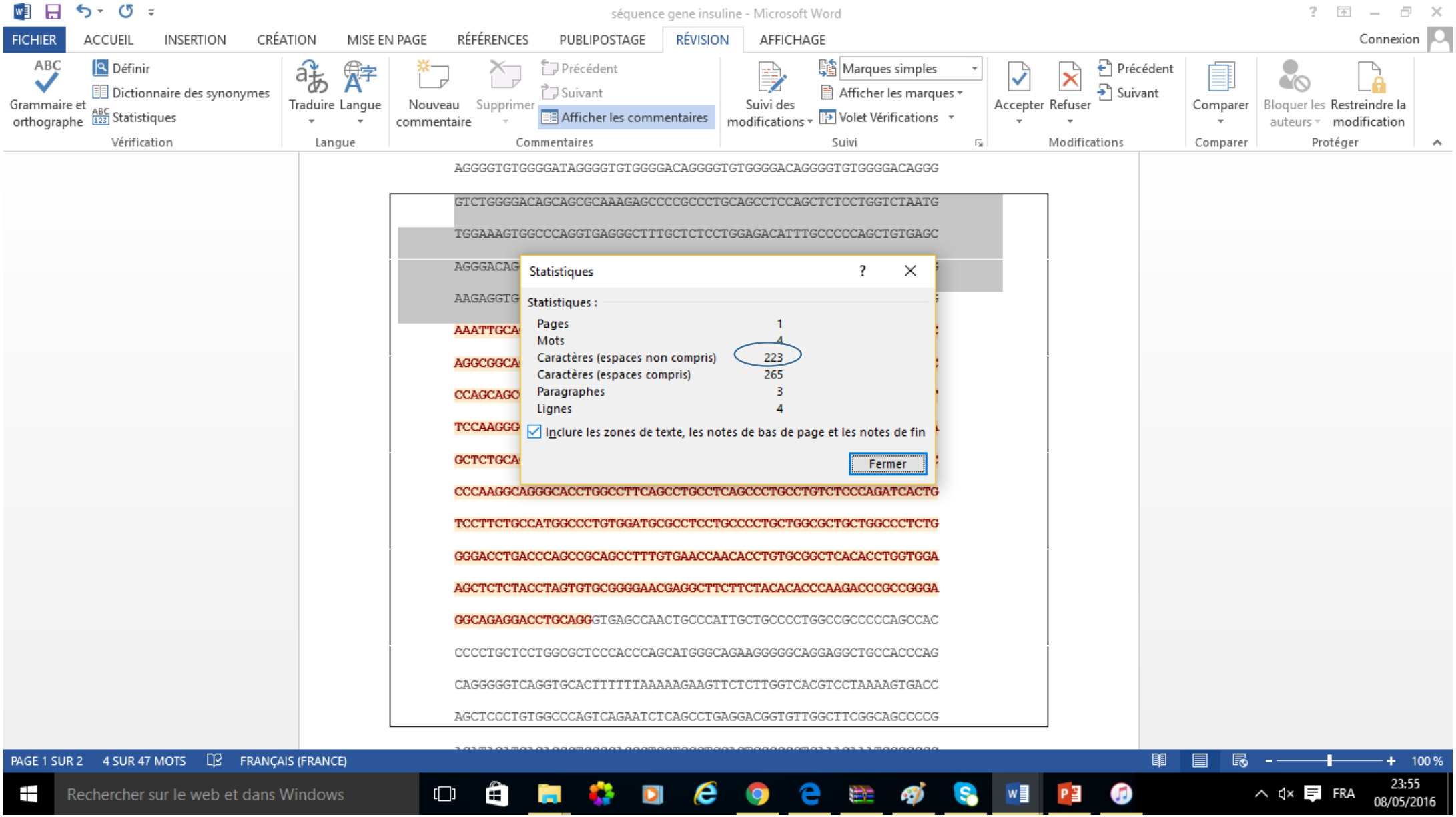
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Nouveau commentaire
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Commentaires
Suivi des modifications
Marques simples
Afficher les marques
Volet Vérifications
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Accepter
Refuser
Précédent
Suivant
Modifications
Comparer
Comparer
Bloquer les auteurs
Restreindre la modification
Protéger
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Statistiques
Statistiques :
Pages 1
Mots 4
Caractères (espaces non compris) 223
Caractères (espaces compris) 265
Paragraphes 3
Lignes 4
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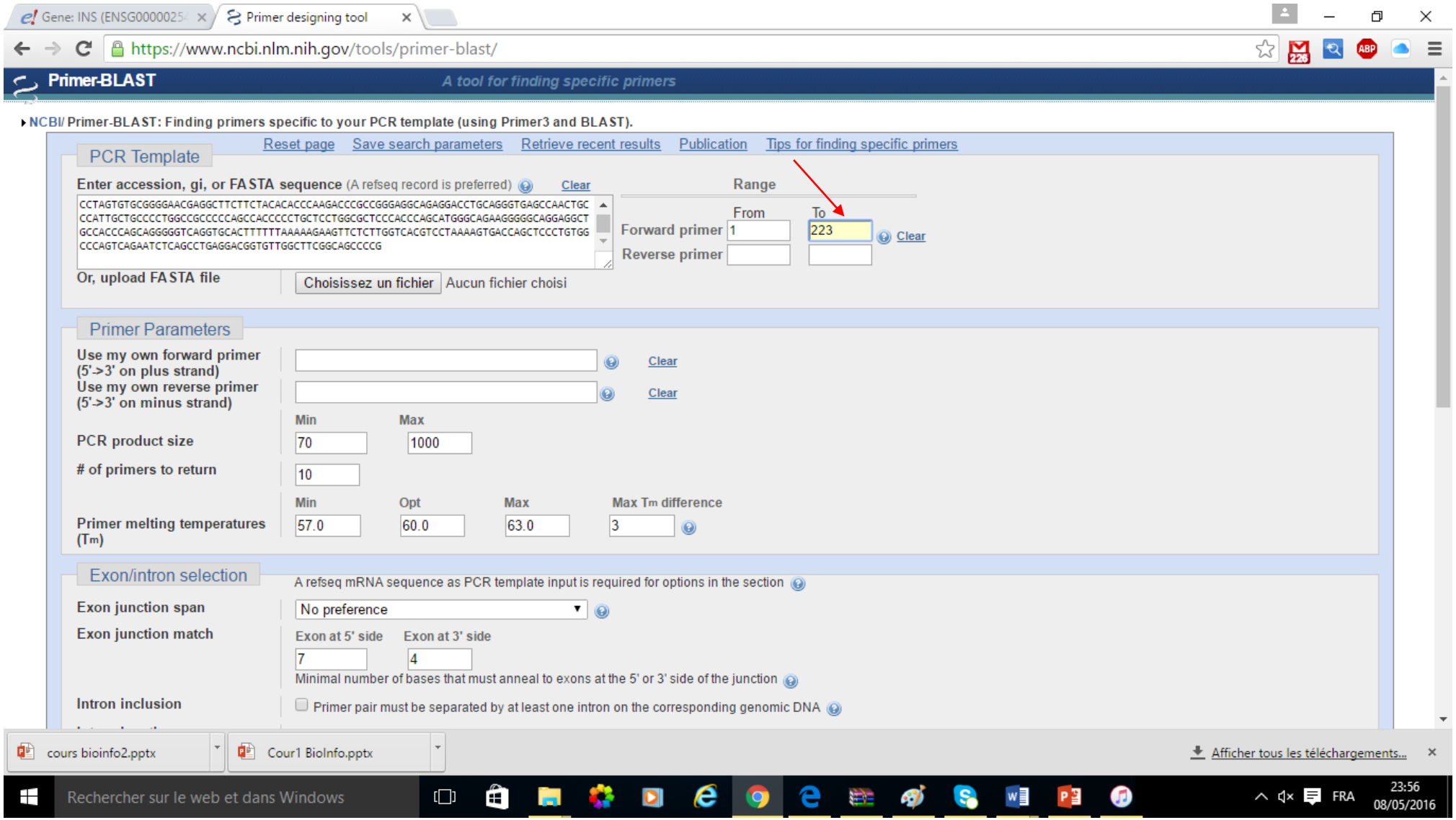
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Primer designing tool
https://www.ncbi.nlm.nih.gov/tools/primer-blast/
Primer-BLAST
A tool for finding specific primers
NCBI/ Primer-BLAST: Finding primers specific to your PCR template (using Primer3 and BLAST).
Reset page
Save search parameters
Retrieve recent results
Publication
Tips for finding specific primers
PCR Template
Enter accession, gi, or FASTA sequence (A refseq record is preferred)
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CCCAGTCAGAATCTCAGCCTGAGGACGGTGTTGGCTTCGGCAGCCCCG
Range
From
To
Forward primer
1
223
Clear
Reverse primer
Or, upload FASTA file
Choisissez un fichier
Aucun fichier choisi
Primer Parameters
Use my own forward primer (5'->3' on plus strand)
Clear
Use my own reverse primer (5'->3' on minus strand)
Clear
Min
Max
PCR product size
70
1000
# of primers to return
10
Min
Opt
Max
Max Tm difference
Primer melting temperatures (Tm)
57.0
60.0
63.0
3
Exon/intron selection
A refseq mRNA sequence as PCR template input is required for options in the section
Exon junction span
No preference
Exon junction match
Exon at 5' side
Exon at 3' side
7
4
Minimal number of bases that must anneal to exons at the 5' or 3' side of the junction
Intron inclusion
Primer pair must be separated by at least one intron on the corresponding genomic DNA
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Cour1 BioInfo.pptx
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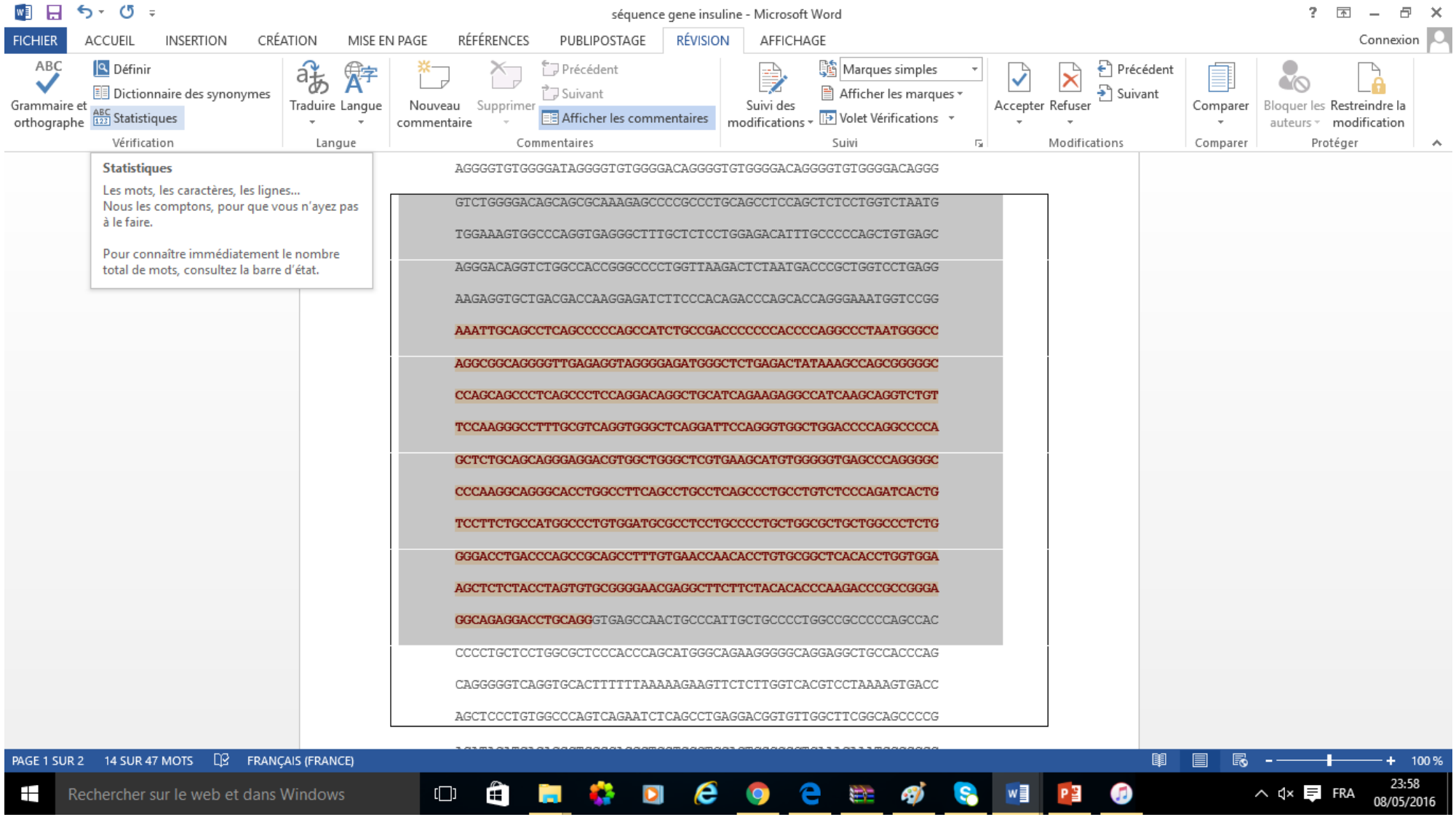
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Restreindre la modification
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Les mots, les caractères, les lignes...
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Pour connaître immédiatement le nombre total de mots, consultez la barre d'état.
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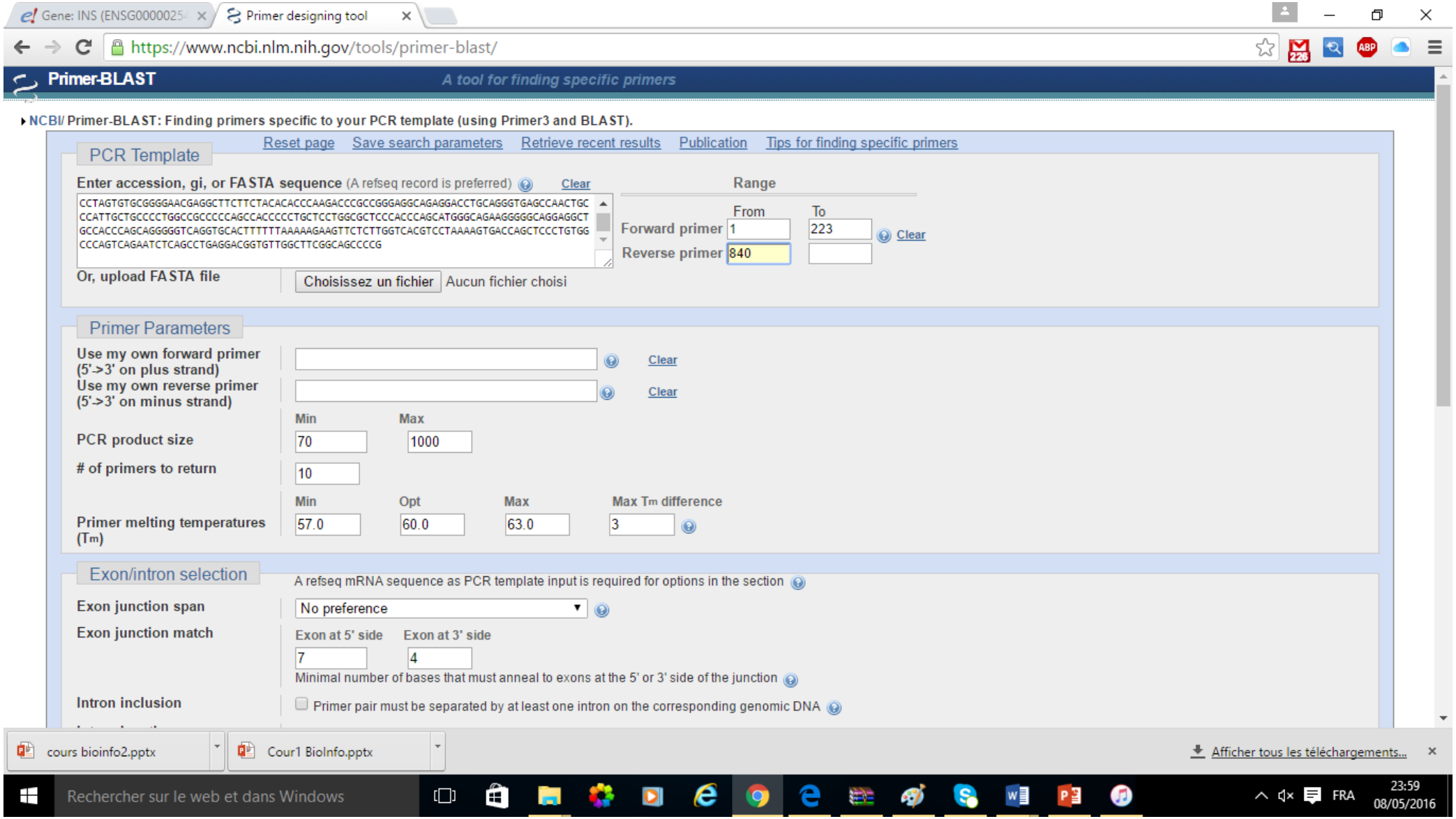
Gene: INS (ENSG0000025
Primer designing tool
https://www.ncbi.nlm.nih.gov/tools/primer-blast/
Primer-BLAST
A tool for finding specific primers
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Reset page
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Tips for finding specific primers
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Enter accession, gi, or FASTA sequence (A refseq record is preferred)
Clear
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CCCAGTCAGAATCTCAGCCTGAGGACGGTGTTGGCTTCGGCAGCCCCG
Range
From
To
Forward primer
1
223
Clear
Reverse primer
840
Or, upload FASTA file
Choisissez un fichier
Aucun fichier choisi
Primer Parameters
Use my own forward primer (5'->3' on plus strand)
Clear
Use my own reverse primer (5'->3' on minus strand)
Clear
Min
Max
PCR product size
70
1000
# of primers to return
10
Min
Opt
Max
Max Tm difference
Primer melting temperatures (Tm)
57.0
60.0
63.0
3
Exon/intron selection
A refseq mRNA sequence as PCR template input is required for options in the section
Exon junction span
No preference
Exon junction match
Exon at 5' side
Exon at 3' side
7
4
Minimal number of bases that must anneal to exons at the 5' or 3' side of the junction
Intron inclusion
Primer pair must be separated by at least one intron on the corresponding genomic DNA
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Cour1 BioInfo.pptx
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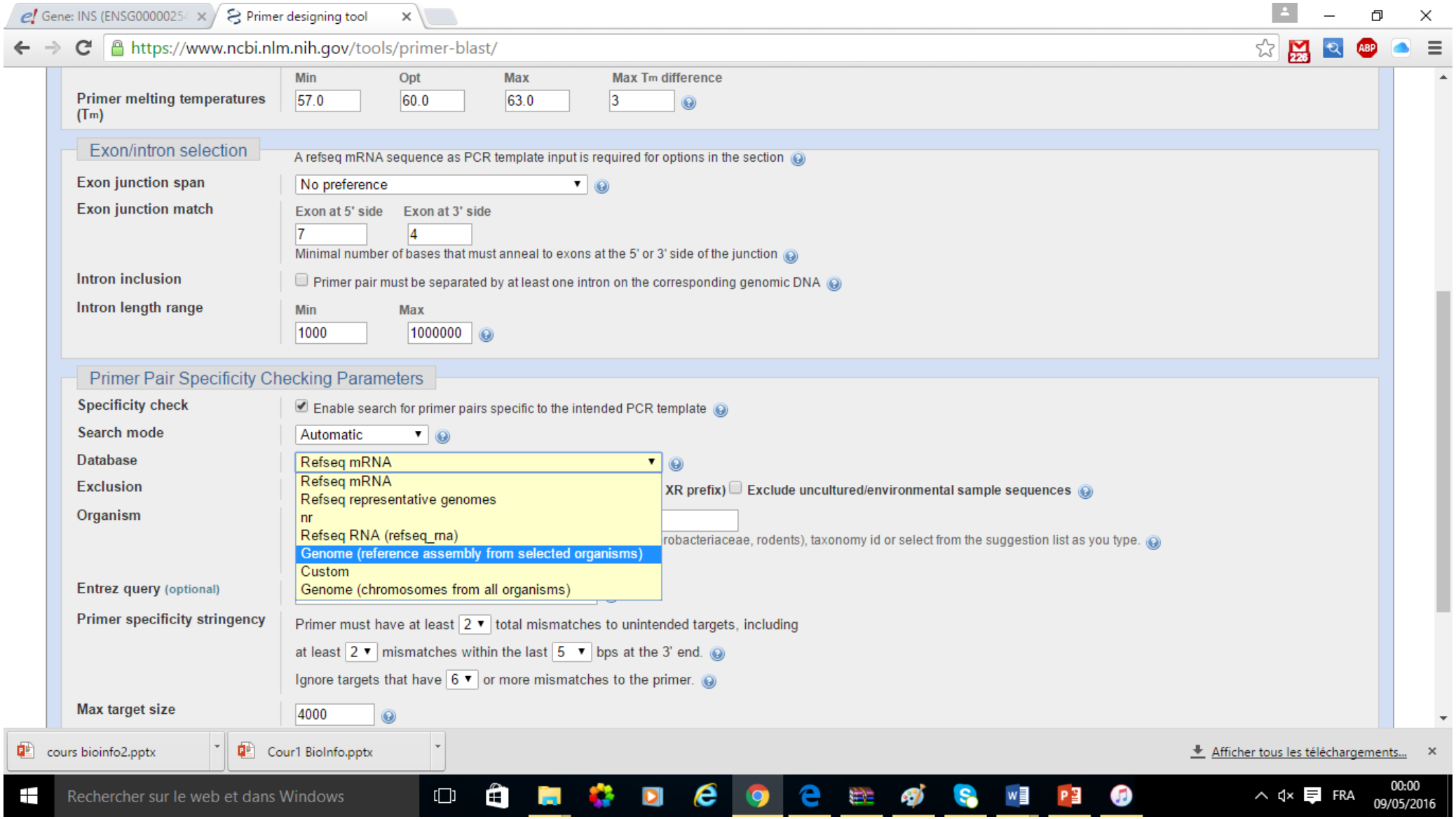
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Primer designing tool
https://www.ncbi.nlm.nih.gov/tools/primer-blast/
Primer melting temperatures (Tm)
Min
Opt
Max
Max Tm difference
57.0
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Exon junction match
Exon at 5' side
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7
4
Minimal number of bases that must anneal to exons at the 5' or 3' side of the junction
Intron inclusion
Primer pair must be separated by at least one intron on the corresponding genomic DNA
Intron length range
Min
Max
1000
1000000
Primer Pair Specificity Checking Parameters
Specificity check
Enable search for primer pairs specific to the intended PCR template
Search mode
Automatic
Database
Refseq mRNA
Refseq mRNA
Refseq representative genomes
nr
Refseq RNA (refseq_rna)
Genome (reference assembly from selected organisms)
Custom
Genome (chromosomes from all organisms)
Exclusion
XR prefix)
Exclude uncultured/environmental sample sequences
Organism
robacteriaceae, rodents), taxonomy id or select from the suggestion list as you type.
Entrez query (optional)
Primer specificity stringency
Primer must have at least 2 total mismatches to unintended targets, including
at least 2 mismatches within the last 5 bps at the 3' end.
Ignore targets that have 6 or more mismatches to the primer.
Max target size
4000
cours bioinfo2.pptx
Cour1 BioInfo.pptx
Afficher tous les téléchargements...
Rechercher sur le web et dans Windows
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Gene: INS (ENSG0000025 | Primer designing tool

https://www.ncbi.nlm.nih.gov/tools/primer-blast/

Primer melting temperatures (Tm)	Min	Opt	Max	Max Tm difference
	57.0	60.0	63.0	3

Exon/intron selection

A refseq mRNA sequence as PCR template input is required for options in the section

Exon junction span: No preference

Exon junction match: Exon at 5' side: 7 | Exon at 3' side: 4

Minimal number of bases that must anneal to exons at the 5' or 3' side of the junction

Intron inclusion: Primer pair must be separated by at least one intron on the corresponding genomic DNA

Intron length range: Min: 1000 | Max: 1000000

Note: Parameter values that differ from the default are highlighted in yellow

Primer Pair Specificity Checking Parameters

Specificity check: Enable search for primer pairs specific to the intended PCR template

Search mode: Automatic

Database: Genome (reference assembly from selected organisms)

Exclusion: Exclude predicted Refseq transcripts (accession with XM, XR prefix) Exclude uncultured/environmental sample sequences

Organism: Homo sapiens

Enter an organism name (or organism group name such as enterobacteriaceae, rodents), taxonomy id or select from the suggestion list as you type.

Add more organisms

Entrez query (optional)

Primer specificity stringency

Primer must have at least 2 total mismatches to unintended targets, including

at least 2 mismatches within the last 5 bps at the 3' end.

Ignore targets that have 6 or more mismatches to the primer.

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Rechercher sur le web et dans Windows

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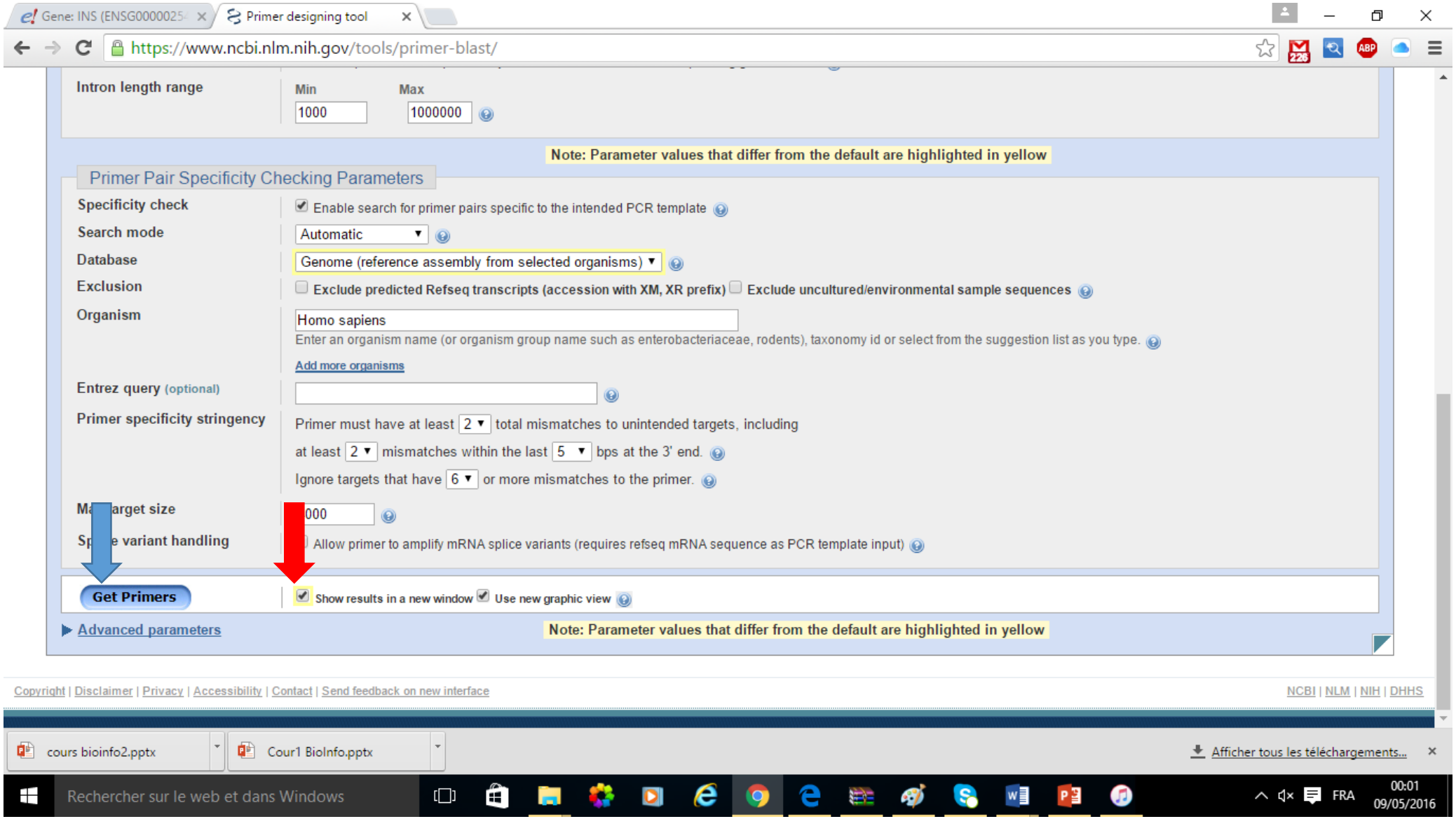
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Primer designing tool
https://www.ncbi.nlm.nih.gov/tools/primer-blast/
Intron length range
Min
1000
Max
1000000
Note: Parameter values that differ from the default are highlighted in yellow
Primer Pair Specificity Checking Parameters
Specificity check
Enable search for primer pairs specific to the intended PCR template
Search mode
Automatic
Database
Genome (reference assembly from selected organisms)
Exclusion
Exclude predicted Refseq transcripts (accession with XM, XR prefix)
Exclude uncultured/environmental sample sequences
Organism
Homo sapiens
Enter an organism name (or organism group name such as enterobacteriaceae, rodents), taxonomy id or select from the suggestion list as you type.
Add more organisms
Entrez query (optional)
Primer specificity stringency
Primer must have at least 2 total mismatches to unintended targets, including
at least 2 mismatches within the last 5 bps at the 3' end.
Ignore targets that have 6 or more mismatches to the primer.
arget size
000
variant handling
Allow primer to amplify mRNA splice variants (requires refseq mRNA sequence as PCR template input)
Get Primers
Show results in a new window
Use new graphic view
Advanced parameters
Note: Parameter values that differ from the default are highlighted in yellow
Copyright | Disclaimer | Privacy | Accessibility | Contact | Send feedback on new interface
NCBI | NLM | NIH | DHHS
cours bioinfo2.pptx
Cour1 BioInfo.pptx
Afficher tous les téléchargements...
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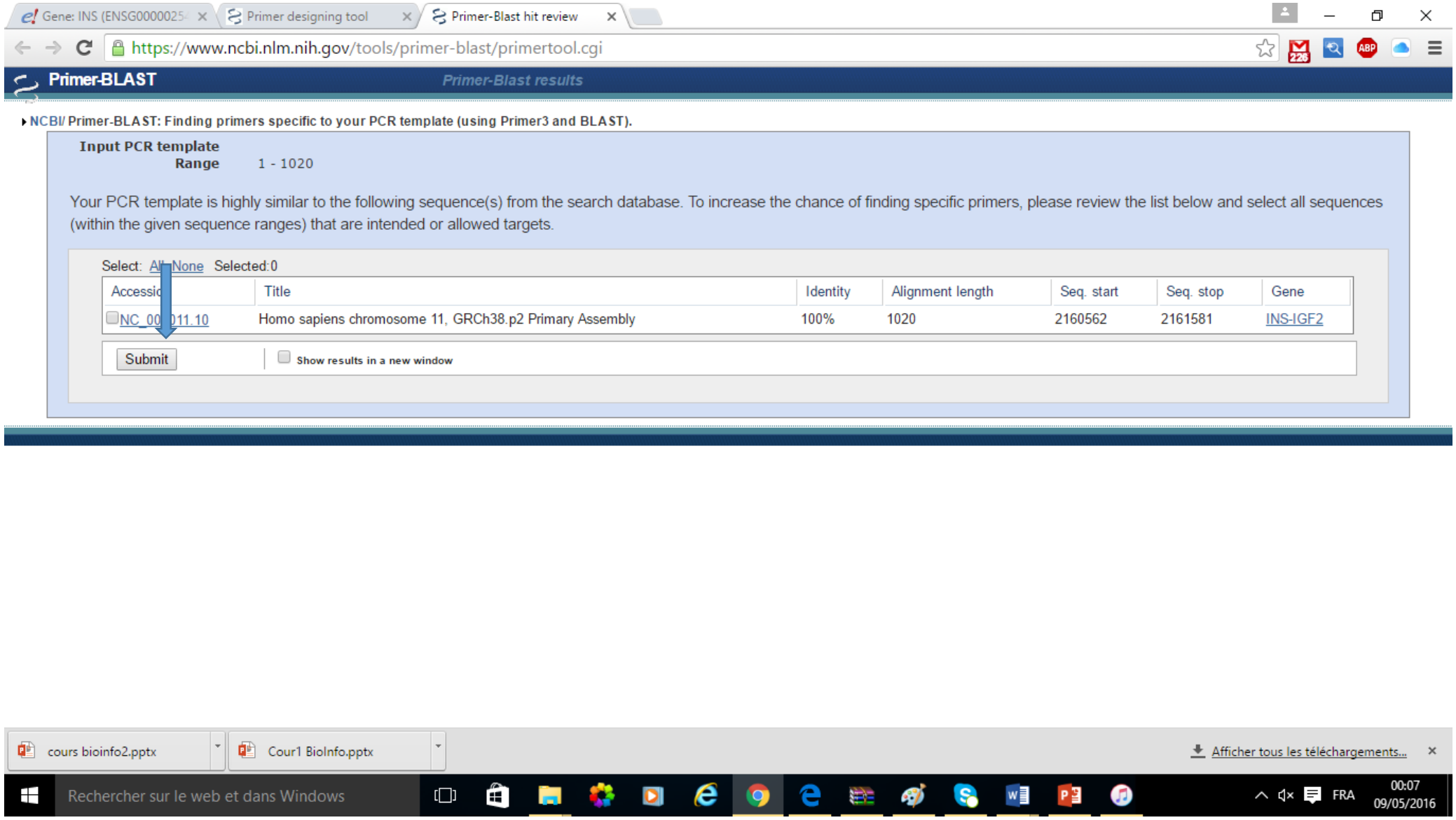
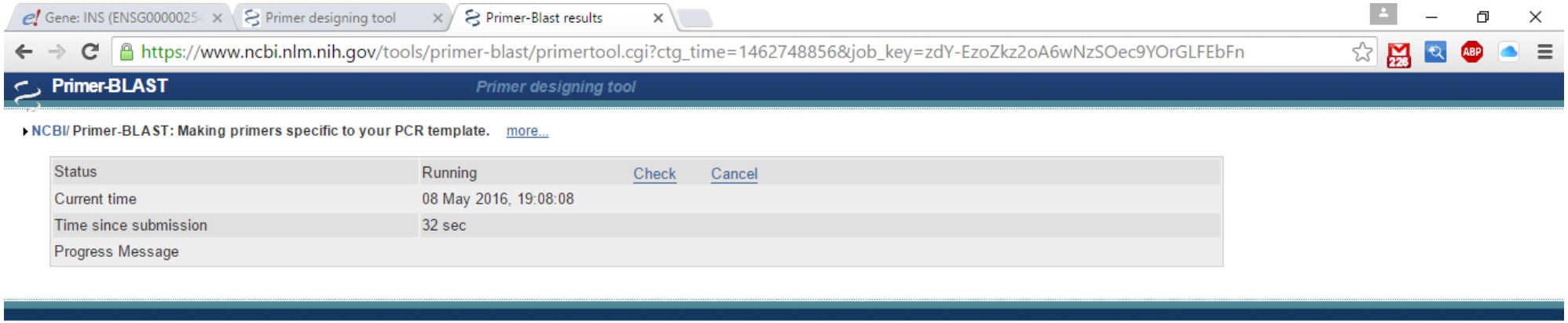
00:01
09/05/2016


Gene: INS (ENSG0000025
Primer designing tool
Primer-Blast hit review
https://www.ncbi.nlm.nih.gov/tools/primer-blast/primertool.cgi
Primer-BLAST
Primer-Blast results
NCBI/ Primer-BLAST: Finding primers specific to your PCR template (using Primer3 and BLAST).
Input PCR template
Range 1 - 1020
Your PCR template is highly similar to the following sequence(s) from the search database. To increase the chance of finding specific primers, please review the list below and select all sequences (within the given sequence ranges) that are intended or allowed targets.
Select: All None Selected:0
Accessio
Title
Identity
Alignment length
Seq. start
Seq. stop
Gene
NC_00 011.10
Homo sapiens chromosome 11, GRCh38.p2 Primary Assembly
100%
1020
2160562
2161581
INS-IGF2
Submit
Show results in a new window
cours bioinfo2.pptx
Cour1 BioInfo.pptx
Afficher tous les téléchargements...
Rechercher sur le web et dans Windows
FRA
00:07
09/05/2016


Gene: INS (ENSG0000025
Primer designing tool
Primer-Blast results
https://www.ncbi.nlm.nih.gov/tools/primer-blast/primertool.cgi?ctg_time=1462748856&job_key=zdY-EzoZkz2oA6wNzSOec9YOrGLFEbFn
Primer-BLAST
Primer designing tool
NCBI/ Primer-BLAST: Making primers specific to your PCR template.
more...
Status
Running
Check
Cancel
Current time
08 May 2016, 19:08:08
Time since submission
32 sec
Progress Message


cours bioinfo2.pptx
Cour1 BioInfo.pptx
Afficher tous les téléchargements...
Rechercher sur le web et dans Windows
FRA
00:08
09/05/2016

Gene: INS (ENSG0000025 | Primer designing tool | Primer-Blast results

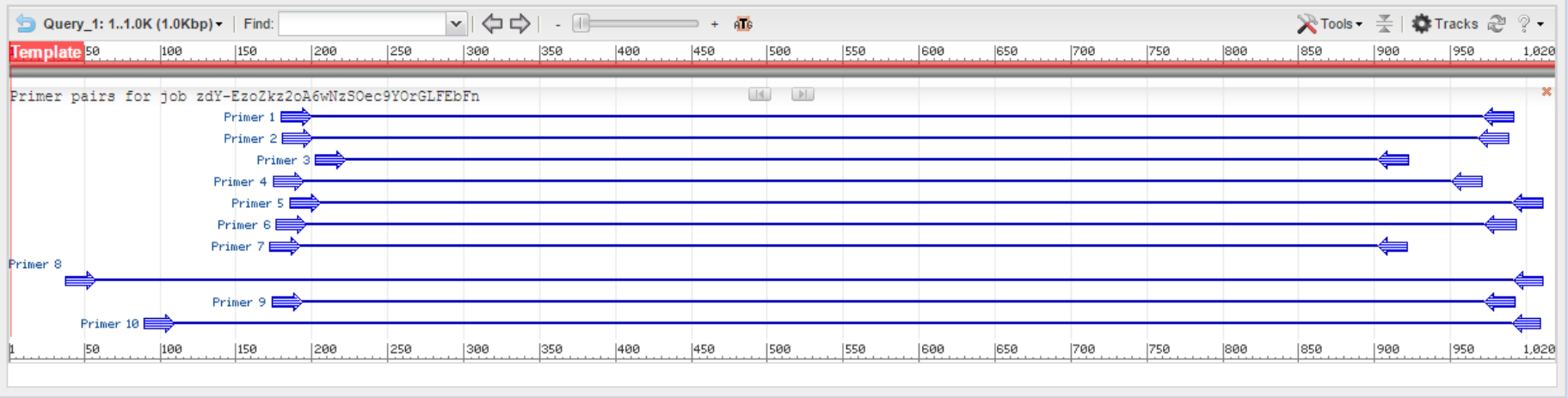
https://www.ncbi.nlm.nih.gov/tools/primer-blast/primertool.cgi?ctg_time=1462748856&job_key=zdY-EzoZkz2oA6wNzSOec9YOrGLFEbFn

Primer-BLAST *Primer-Blast results*

NCBI/ Primer-BLAST : results: Job id=zdY-EzoZkz2oA6wNzSOec9YOrGLFEbFn more...

Input PCR template
Range 1 - 1020
Specificity of primers primers may **not** be specific to the input PCR template as targets were found in selected database:Genome database (reference assembly only) for selected species (Organism limited to Homo sapiens)...help on specific primers
Other reports ▷ Search Summary

Graphical view of primer pairs



Detailed primer reports

Primer pair 1

cours bioinfo2.pptx | Cour1 BioInfo.pptx | Afficher tous les téléchargements...

Rechercher sur le web et dans Windows

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Detailed primer reports

Primer pair 1

	Sequence (5'->3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	GAAGAGGTGCTGACGACCAA	Plus	20	180	199	59.97	55.00	3.00	0.00
Reverse primer	GGCTGAGATTCTGACTGGGC	Minus	20	991	972	60.46	60.00	5.00	2.00
Product length	812								

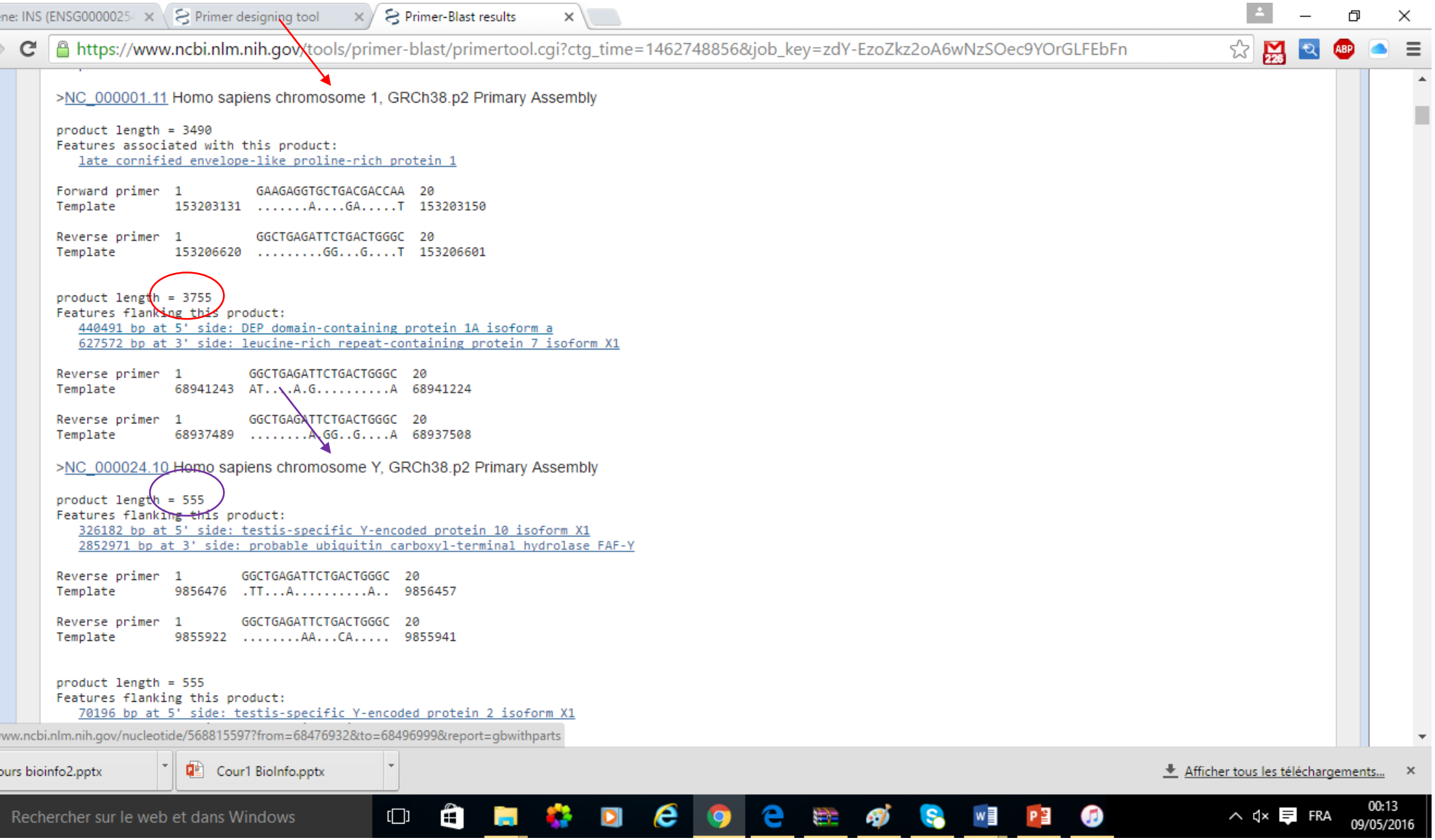
Products on potentially unintended templates

>NC_000011.10 Homo sapiens chromosome 11, GRCh38.p2 Primary Assembly

```
product length = 812
Features associated with this product:
   insulin, isoform 2 precursor

   insulin preproprotein

Forward primer  1        GAAGAGGTGCTGACGACCAA  20
Template        2161402  ....................  2161383

Reverse primer  1        GGCTGAGATTCTGACTGGGC  20
Template        2160591  ....................  2160610
```

>NC_000001.11 Homo sapiens chromosome 1, GRCh38.p2 Primary Assembly

```
product length = 3490
Features associated with this product:
   late cornified envelope-like proline-rich protein 1

Forward primer  1          GAAGAGGTGCTGACGACCAA  20
Template        153203131  .......A....GA.....T  153203150
```


Primer designing tool
Primer-Blast results
https://www.ncbi.nlm.nih.gov/tools/primer-blast/primertool.cgi?ctg_time=1462748856&job_key=zdY-EzoZkz2oA6wNzSOec9YOrGLFEbFn
>NC_000001.11 Homo sapiens chromosome 1, GRCh38.p2 Primary Assembly
product length = 3490
Features associated with this product:
late cornified envelope-like proline-rich protein 1
Forward primer 1 GAAGAGGTGCTGACGACCAA 20
Template 153203131 .....A....GA.....T 153203150
Reverse primer 1 GGCTGAGATTCTGACTGGGC 20
Template 153206620 .....GG...G....T 153206601
product length = 3755
Features flanking this product:
440491 bp at 5' side: DEP domain-containing protein 1A isoform a
627572 bp at 3' side: leucine-rich repeat-containing protein 7 isoform X1
Reverse primer 1 GGCTGAGATTCTGACTGGGC 20
Template 68941243 AT...A.G.....A 68941224
Reverse primer 1 GGCTGAGATTCTGACTGGGC 20
Template 68937489 .....A.GG..G....A 68937508
>NC_000024.10 Homo sapiens chromosome Y, GRCh38.p2 Primary Assembly
product length = 555
Features flanking this product:
326182 bp at 5' side: testis-specific Y-encoded protein 10 isoform X1
2852971 bp at 3' side: probable ubiquitin carboxyl-terminal hydrolase FAF-Y
Reverse primer 1 GGCTGAGATTCTGACTGGGC 20
Template 9856476 .TT...A.....A.. 9856457
Reverse primer 1 GGCTGAGATTCTGACTGGGC 20
Template 9855922 .....AA...CA..... 9855941
product length = 555
Features flanking this product:
70196 bp at 5' side: testis-specific Y-encoded protein 2 isoform X1
www.ncbi.nlm.nih.gov/nucleotide/568815597?from=68476932&to=68496999&report=gbwithparts
ours bioinfo2.pptx
Cour1 BioInfo.pptx
Afficher tous les téléchargements...
Rechercher sur le web et dans Windows
FRA
00:13
09/05/2016