

Module 2

Human and Cat INSR insulin receptor: Sequence comparison

•Objective

To teach students how to use NCBI tools for data search and how to use the tools for gene and protein sequence comparison.

•Provide students with INSR & have them find in Gene DB

- start with human (or cat)?
 - [Cat insulin receptor NCBI Gene- INSR insulin receptor *Felis catus* \(domestic cat\)](#) Gene ID: 100127108,
 - [Human Insulin Receptor](#) NCBI Gene

•Have them find additional INSR from different species

- have everyone use same subset
 - human, cat, dog, pig ??
 - allow them to add additional of their choice?

Gene

Gene

Advanced

Full Report

Send to

INSR insulin receptor [*Felis catus* (domestic cat)]

Download Datasets

Gene ID: 100127108, updated on 11-Apr-2024

Summary

Official Symbol

INSR

Official Full Name

insulin receptor

Primary source

VGNC:VGNC.67811

See related

EnsemblRapid:ENSEFTG000005016878

Gene type

protein coding

RefSeq status

MODEL

Organism

Felis catus

Lineage

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Feliformia; Felidae; Felinae; Felis

Orthologs

human mouse all

NEW

Try the new Gene table

Try the new Transcript table

find orthologs for INSR

Genomic context

Location:

chromosome: A2

See INSR in Genome Data Viewer

Exon count:

22

Annotation release	Status	Assembly	Chr	Location
105	current	F.catus_Fca126_mat1.0 (GCF_018350175.1)	A2	NC_058369.1 (6387620..6531220)
104	previous assembly	Felis_catus_9.0 (GCF_000181335.3)	A2	NC_018724.3 (6421801..6566365)

NCBI Orthologs [How was this calculated?](#)

0 items

SEARCH THE TAXONOMY TREE

Enter taxonomic name

jawed vertebrates

birds

turtles

alligators and others

lizards & snakes

mammals

amphibians

lungfishes

cartilaginous fishes

Select species of interest
e.g. human and cat

408 genes for: jawed vertebrates (*Gnathostomata*)

Add to cart Protein alignment Download

5 selected

				Previous	Next
Species	Gene	Architecture	aa		
<input checked="" type="checkbox"/> <i>Homo sapiens</i> human	INSR insulin receptor		1,382		▼
<input type="checkbox"/> <i>Mus musculus</i> house mouse	Insr insulin receptor		1,372		▼
<input type="checkbox"/> <i>Rattus norvegicus</i> Norway rat	Insr insulin receptor		1,384		▼
<input checked="" type="checkbox"/> <i>Bos taurus</i> cattle	INSR insulin receptor		1,382		▼
<input type="checkbox"/> <i>Gallus gallus</i> chicken	INSR insulin receptor		1,422		▼
<input checked="" type="checkbox"/> <i>Sus scrofa</i> pig	INSR insulin receptor		1,382		▼
<input type="checkbox"/> <i>Macaca mulatta</i>	INSR		1,388		▼

Sequence Viewer exploration

- Conduct INSR DNA BLAST & Comparative Genome Alignment

INSR alignment of Cat, Dog and Human using BLASTn

blastn

blastp

blastx

tblastn

tblastx

Align Sequences Nucleotide BLAST

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

Human INSR receptor No. AH002851

Query subrange [?](#)

From

To

Or, upload file No file chosen [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

☒ Align two or more sequences [?](#)

Enter Subject Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

Cat and Dog INSR receptor No. XM_023244792.2
XM_038428733

Subject subrange [?](#)

From

To

Or, upload file No file chosen [?](#)

Program Selection

Optimize for

☒ Highly similar sequences (megablast)

☐ More dissimilar sequences (discontiguous megablast)

☐ Somewhat similar sequences (blastn)

Choose a BLAST algorithm [?](#)

[< Edit Search](#)

[Save Search](#)

[Search Summary](#) [▼](#)

[? How to read this report?](#)

[▶ BLAST Help Videos](#)

[↶ Back to Traditional Results Page](#)

Job Title

AH002851:Homo sapiens insulin receptor (INSR)...

RID

B7K4110D114 [Search expires on 08-09 03:35 am](#) [Download All](#) [▼](#)

Program

Blast 2 sequences [Citation](#) [▼](#)

Query ID

AH002851.2 (nucleic acid)

Query Descr

Homo sapiens insulin receptor (INSR) gene, complete cds

Query Length

14767

Subject ID

XM_023244792.2 and 1 more subject(s) (nucleic acid)

Subject Descr

[See details](#) [▼](#)

Subject Length

17482

Filter Results

Percent Identity

to

E value

to

Query Coverage

to

Descriptions

Graphic Summary

Alignments

Sequences producing significant alignments

[Download](#) [▼](#) [Select columns](#) [▼](#) [Show](#) [?](#)

☒ select all 2 sequences selected [GenBank](#) [Graphics](#) [Distance tree of results](#) [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	PREDICTED: Felis catus insulin receptor (INSR), transcript variant X1, mRNA	Felis catus	534	3441	21%	3e-153	79.55%	9160	XM_023244792.2
<input checked="" type="checkbox"/>	PREDICTED: Canis lupus familiaris insulin receptor (INSR), transcript variant X4, mRNA	Canis lupus familiaris	453	2592	12%	8e-129	91.72%	8322	XM_038428733.1

INSR alignment of Cat, Dog and Human using Comparative Genome viewer

[CGV Home](#) [Help](#) [Release Notes](#)

Comparative Genome Viewer

This tool allows you to compare two genomes based on assembly-assembly alignments provided by NCBI.

Set up your view

Make a selection in each of these four steps to view assembly comparison.

1. Select a species

Homo sapiens (human)

× | ▼

2. Select a second species

Felis catus (domestic cat)

× | ▼

3. Select an assembly

GRCh38.p14 (GCF_000001405.40)

× | ▼

4. Select a second assembly

F.catus_Fca126_mat1.0 (GCF_018350175.1)

× | ▼

Clear Form

View Comparison

Choose Species 1

Choose Orgn Species

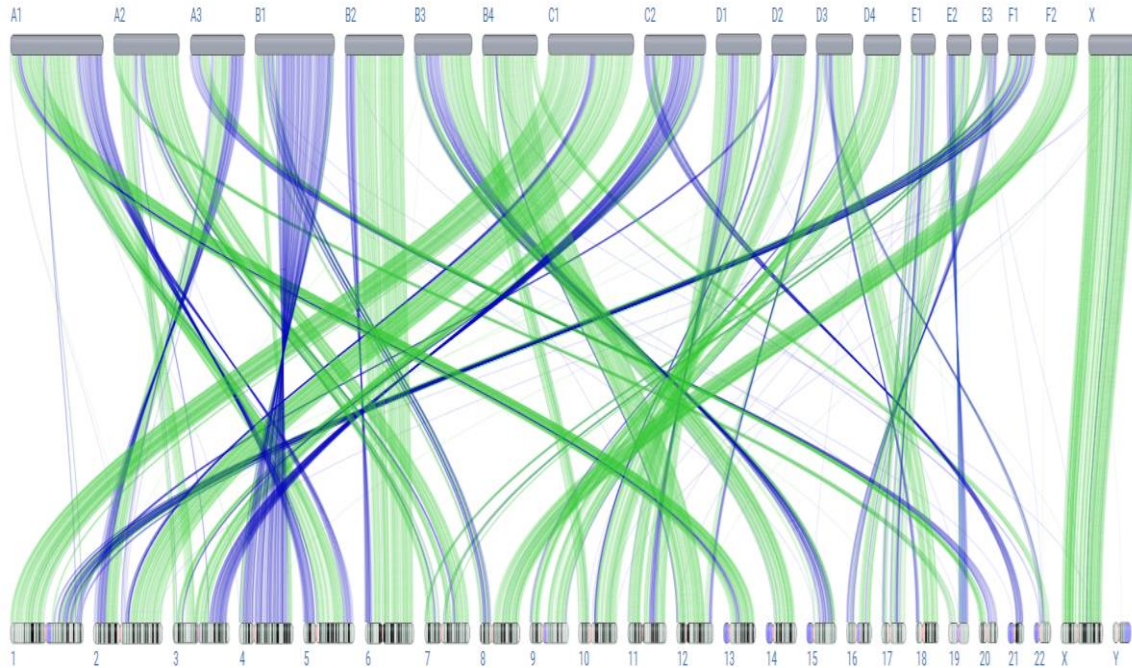
Choose Species 1 Refgenome

Choose Species 2 Refgenome

Click or press 'Enter'

Results

Felis catus F.catus_Fca126_mat1.0 (GCF_018350175.1)



Homo sapiens GRCh38.p14 (GCF_000001405.40)



Searching for specific gene

Find a gene in this alignment

INSR Insulin receptor

Search

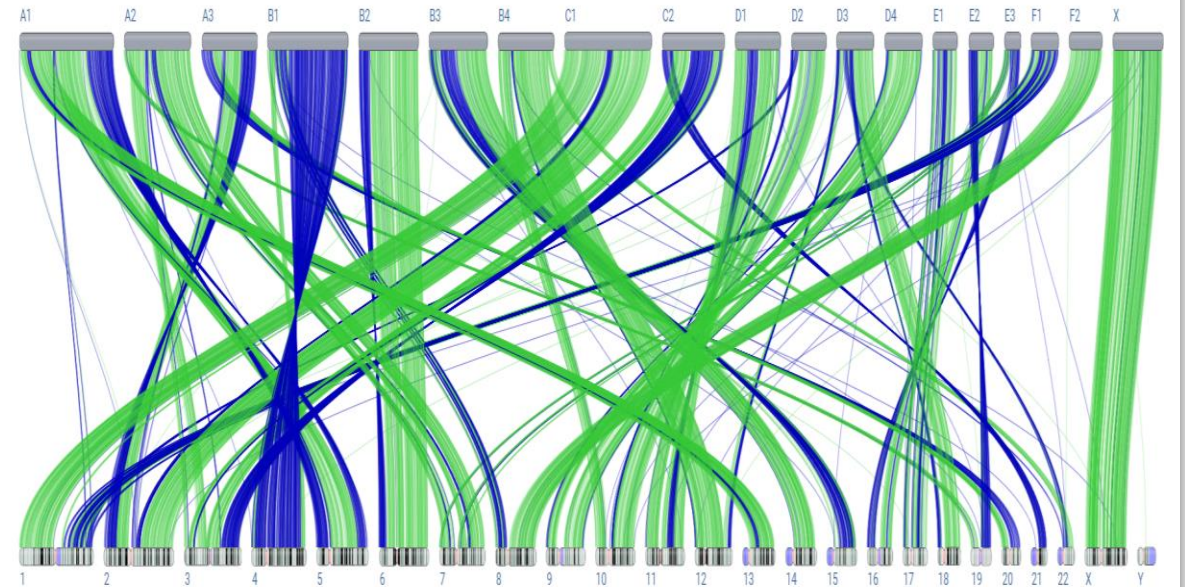
[Go to dotplot view](#)

Reset to genome view



Search for INSR Insulin receptor

Felis catus F.catus_Fca126_mat1.0 (GCF_018350175.1)



Comparative Genome Viewer

You are ready to explore whole genome alignment between *Felis catus*

F.catus_Fca126_mat1.0 (GCF_018350175.1) and *Homo sapiens* GRCh38.p14

(GCF_000001405.40). [🔗](#)

Find a gene in this alignment

× Search

Search results ⌵

Assembly F.catus_Fca126_mat1.0 - 2 genes shown

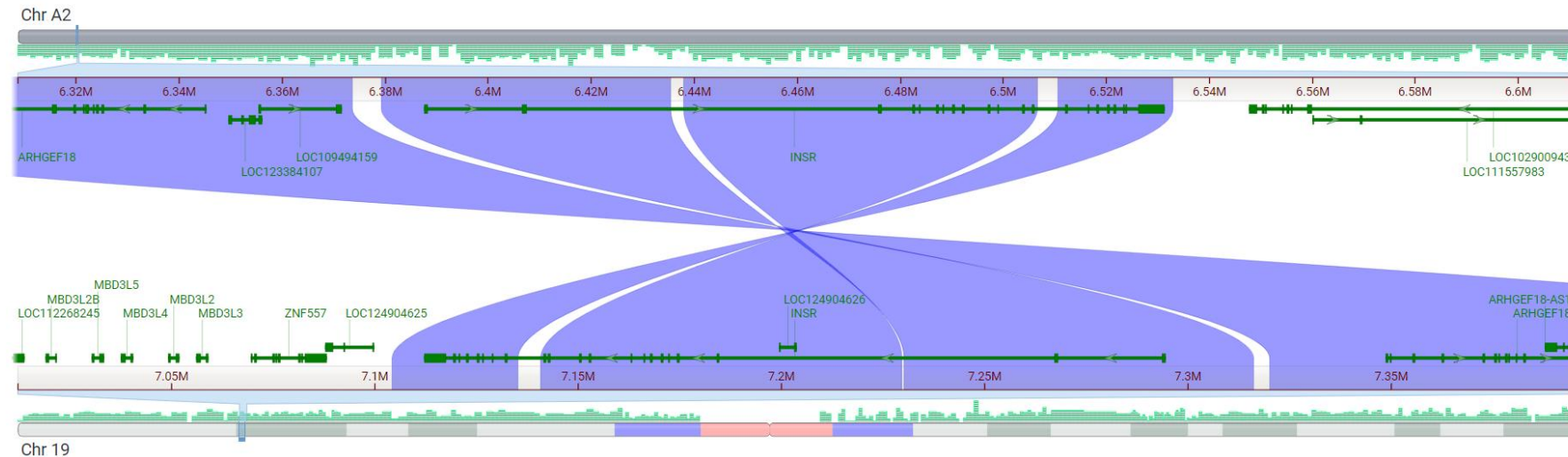
Gene ⬆	Description	⬆ Location	⬆
INSR	insulin receptor	ChrA2: 6387620..6531220	
INSRR	insulin receptor related receptor	ChrF1: 66784504..66800100	

Assembly GRCh38.p14 - 7 genes shown

Gene ⬆	Description	⬆ Location	⬆
INSR	insulin receptor	Chr19: 7112265..7294414	
IRS1	insulin receptor substrate 1	Chr2: 226731312..226799820	
IRS2	insulin receptor substrate 2	Chr13: 109752695..109786583	

Click on Insulin receptor

Felis catus F.catus_Fca126_mat1.0 ([GCF_018350175.1](#))



Homo sapiens GRCh38.p14 ([GCF_000001405.40](#))



Conduct
protein
alignment for
dog, cat and
human using
Cobalt!

COBALT Constraint-based Multiple Alignment Tool Home Recent Results Help

COBALT computes a multiple protein sequence alignment using conserved domain and local sequence similarity information. [Reset page](#)

Enter Query Sequences

Enter at least 2 protein accessions, gis, or FASTA sequences [Clear](#)

NP_000199.2
XP_038284657.1
XP_023100560.2

Or, upload FASTA file [Choose File](#) [Upload](#)

Job Title

Align ☐ Show results in a new window

[Advanced parameters](#)

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Graphical Overview

Find: [Tools](#) [Columns](#) [Rows](#) [Download](#) [Coloring](#) [?](#)

Sequence ID	Start	1	100	300	400	500	600	700	800	900	1000	1100	1200	1300	1382	End	Organism
NP_000199.2	1															1,382	Homo sapiens
XP_038284657.1	1															1,344	Canis lupus familiaris
XP_023100560.2	1															1,381	Felis catus

Alignments ☒ Select All [Re-align](#) [Mouse over the sequence identifier for sequence title](#)

View Format: [Compact](#) [Full](#) Conservation Setting: [Identity](#) [Similarity](#)

Sequence ID	Start	End	Sequence	Score
NP_000199.2	1	80	MATGGRGAAAAAPLLVAVAAALLGAAGHLYPGEVCPGMDIRNNLTRLHELNCSVIEGHLQILLMFKTRPEDFRDLSFPK	80
XP_038284657.1	1	43	-----MDIRNNLTRLHELNCSVIEGHLQILLMFKTRPEDFRDLSFPK	43
XP_023100560.2	1	80	MGAGAGRGAATAPLLVAVAAALLGAAGHLYPGEVCPGMDIRNNLTRLHELNCSVIEGHLQILLMFKTRPEDFRDLSFPK	80
NP_000199.2	81	160	LIMITDYLLLFVRYGLESKDLFPNLTVIRGSRLFFNYALVIFEMVHLKELGLYLMNITRGSVRIEKNNELCYLATIDW	160
XP_038284657.1	44	123	LIMITDYLLLFVRYGLESKDLFPNLTVIRGSRLFFNYALVIFEMVHLKELGLYLMNITRGSVRIEKNNELCYLATIDW	123
XP_023100560.2	81	160	LVMITDYLLLFVRYGLESKDLFPNLTVIRGSRLFFNYALVVFEMVHLKELGLYLMNITRGSVRIEKNNELCYLATIDW	160
NP_000199.2	161	240	SRILDSVEDNYIVLNKDDNEECGDI PCGTAKGKTNC PATVINGQFVERC WTHSHCQKVCPTICKSHGCTAEGLCCHSECL	240
XP_038284657.1	124	203	SRILDSVEDNYIVLNKDDNEECGDI PCGTAKGKTNC PATVINGQFVERC WTHSHCQKVCPTICKSHGCTAEGLCCHSECL	203
XP_023100560.2	161	240	SRILDSVEDNYIVLNKDDNEECGDI PCGTAKGKTNC PATVINGQFVERC WTHGHCQKVCPTVCKSHGCTADGLCCHSECL	240
NP_000199.2	241	320	GNCSQPDPTKCVACRNFYLDGR CVETCPPPYHFDQWRCVNF SFCQDLHNKCKNSRRQGCHQYVIHNNKCIPECPSGYT	320
XP_038284657.1	204	283	GNCSQPDPTKCVACRNFYLDGR CVETCPPPYHFDQWRCVNF SFCQDLHNKCKNSRRQGCHQYVIHNNKCIPECPSGYT	283
XP_023100560.2	241	320	GNCSQPDPTKCVACRNFYLDGR CVETCPPPYHFDQWRCVNF SFCQDLHNKCKNSRRQGCHQYVIHNNKCIPECPSGYT	320
NP_000199.2	321	400	MNSSNLCTPCLGPCPKVCHILEGEKTIDSVTSAQELRGCTVINGSLIINIRGGNNLAAELEANLGLIEEISGYLKIRRS	400
XP_038284657.1	284	363	MNSSNLCTPCLGPCPKVCHILEGEKTIDSVTSAQELRGCTVINGSLIINIRGGNNLAAELEANLGLIEEISGYLKIRRS	363
XP_023100560.2	321	400	MNSSNLCTPCLGPCPKVCHILEGEKTIDSVTSAQELRGCTVINGSLIINIRGGNNLAAELEANLGLIEEISGYLKIRRS	400

Phylogenetic Tree

Phylogenetic Tree Edit and Resubmit Download

- Cobalt RID BA5U4UP1212 (3 seqs)

Graphical Overview Click

Sequence ID Start 1 100 200 300 400 500 600 700 800 900 1000 1100 1200 1300 1382 End Organism

Sequence ID	Start	End	Organism
NP_000199.2	1	1,382	Homo sapiens
XP_038284657.1	1	1,344	Canis lupus familiaris
XP_023100560.2	1	1,381	Felis catus

Tree method: Fast Minimum Evolution Max Seq Difference: 0.85 Distance: Grishin (protein) Sequence Label: Sequence Title (if avail)

Tools Columns Rows Download Coloring

insulin receptor isoform Long preproprotein [Homo sapiens]

insulin receptor isoform X1 [Canis lupus familiaris]

Click on Tools

Click on Tools

Edit labels

Choose common name

Labels Custom Labels

Feature

- label
- dist
- seq-id
- organism
- seq-title
- accession-nbr
- blast-name
- align-index
- node-info
- leaf-label
- common-name

Set Maximum Label Length

Click here to see help about labels format

OK Cancel

Cobalt RID BA5U4UP1212 Number of Seqs 3

Tree method: Fast Minimum Evolution Max Seq Difference: 0.85 Distance: Grishin (protein) Sequence Label: Sequence Title (if avail)

Find: all

human

dog

domestic cat

Success Nodes 5/0 selected View port at (0.0) of 1352x368