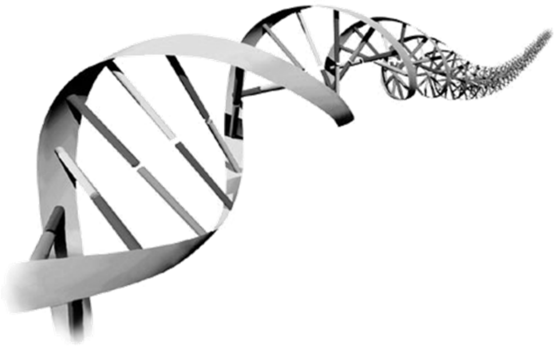


生物信息学

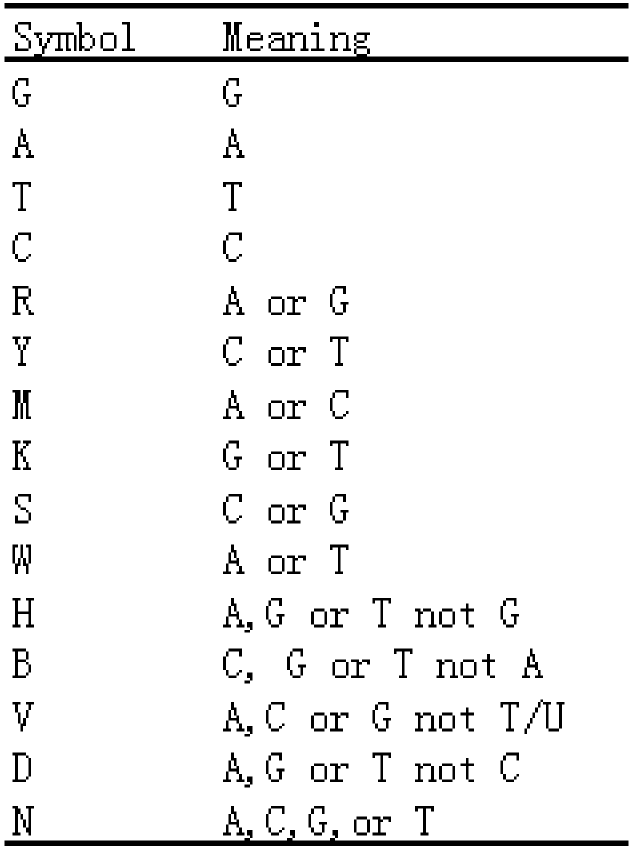
第三章 生物序列数据检索

生物序列数据的文件格式

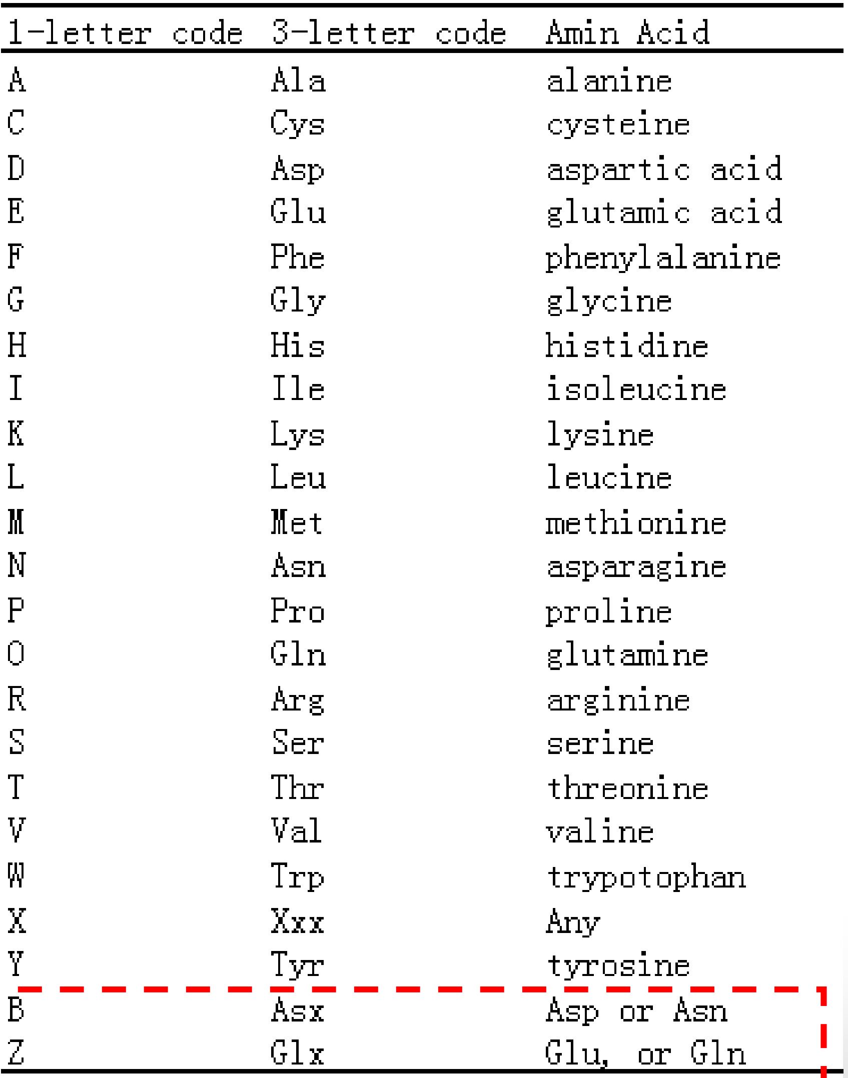
- DNA/RNA/氨基酸代码的标识
- GenBank数据格式
- UniProt
- FASTA

DNA代码

氨基酸代码

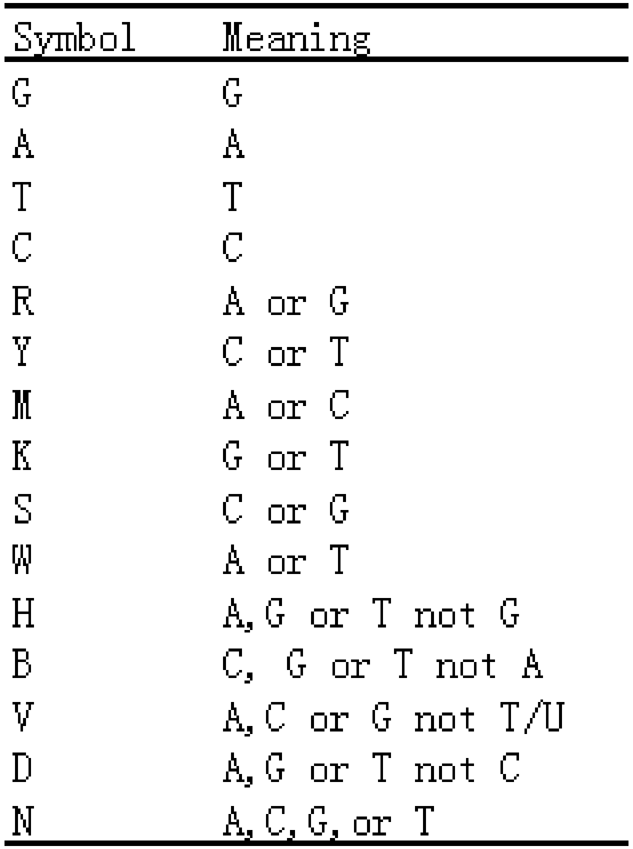


Symbol	Meaning
G	G
A	A
T	T
C	C
R	A or G
Y	C or T
M	A or C
K	G or T
S	C or G
W	A or T
H	A, G or T not G
B	C, G or T not A
V	A, C or G not T/U
D	A, G or T not C
N	A, C, G, or T



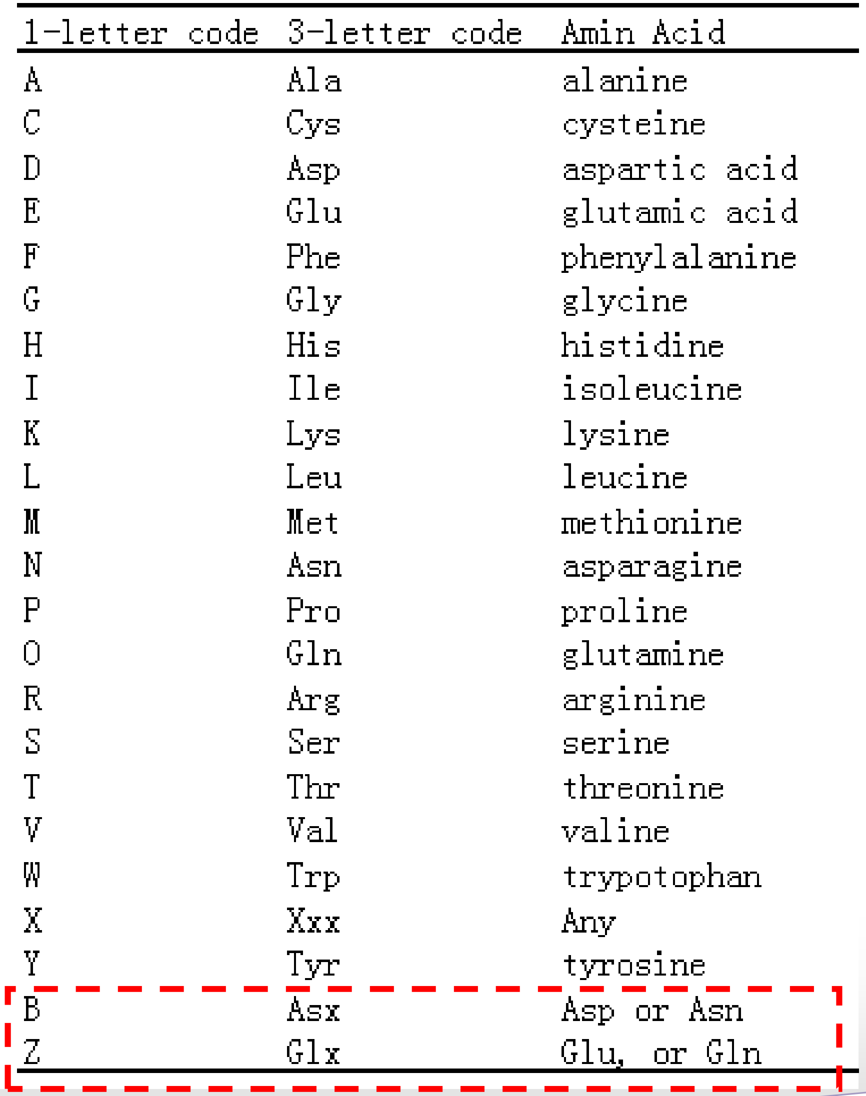
1-letter code	3-letter code	Amin Acid
A	Ala	alanine
C	Cys	cysteine
D	Asp	aspartic acid
E	Glu	glutamic acid
F	Phe	phenylalanine
G	Gly	glycine
H	His	histidine
I	Ile	isoleucine
K	Lys	lysine
L	Leu	leucine
M	Met	methionine
N	Asn	asparagine
P	Pro	proline
O	Gln	glutamine
R	Arg	arginine
S	Ser	serine
T	Thr	threonine
V	Val	valine
W	Trp	trypotophan
X	Xxx	Any
Y	Tyr	tyrosine
B	Asx	Asp or Asn
Z	Glx	Glu, or Gln

DNA代码



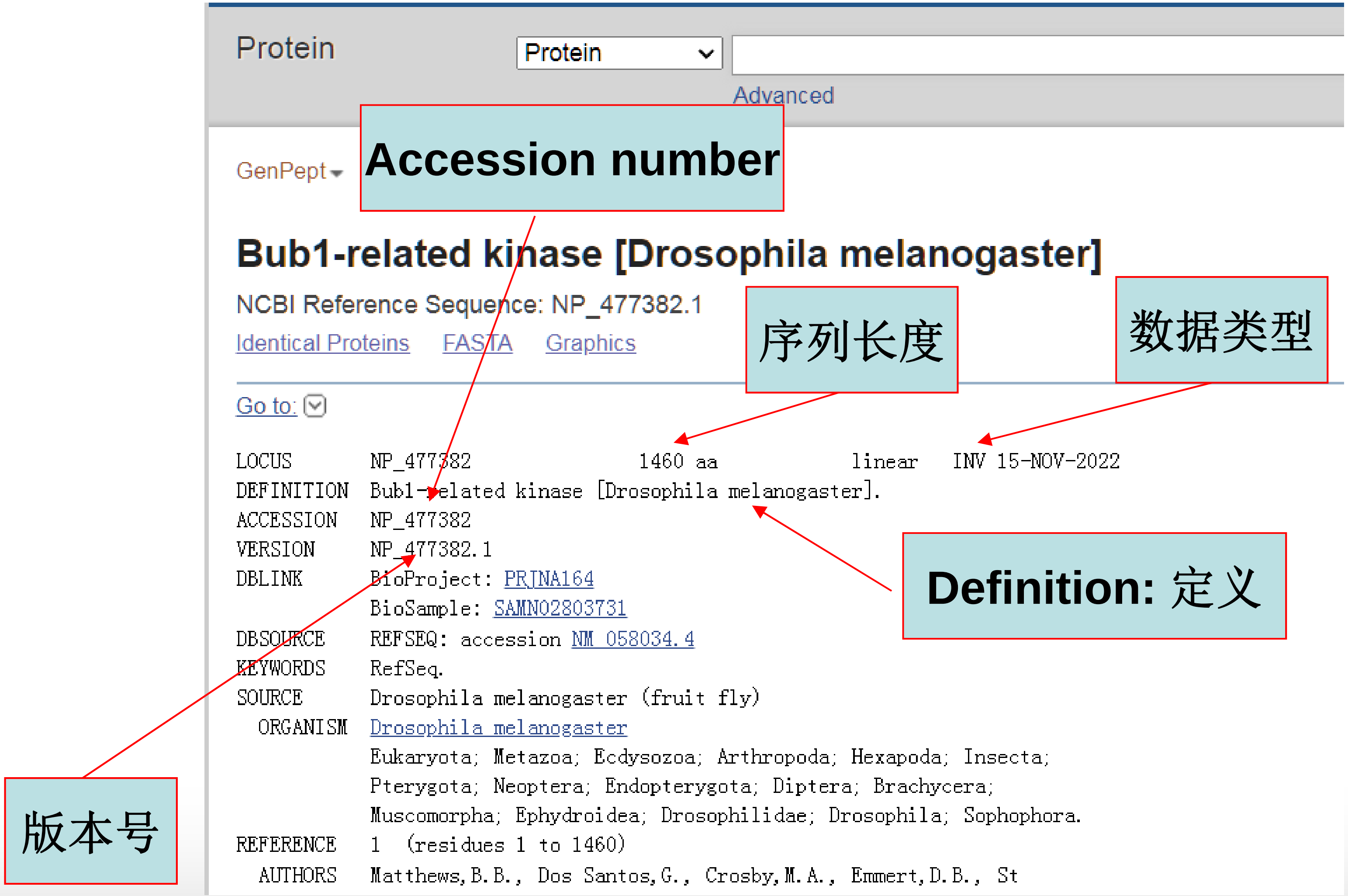
Symbol	Meaning
G	G
A	A
T	T
C	C
R	A or G
Y	C or T
M	A or C
K	G or T
S	C or G
W	A or T
H	A,G or T not G
B	C, G or T not A
V	A,C or G not T/U
D	A,G or T not C
N	A,C,G,or T

氨基酸代码



1-letter code	3-letter code	Amin Acid
A	Ala	alanine
C	Cys	cysteine
D	Asp	aspartic acid
E	Glu	glutamic acid
F	Phe	phenylalanine
G	Gly	glycine
H	His	histidine
I	Ile	isoleucine
K	Lys	lysine
L	Leu	leucine
M	Met	methionine
N	Asn	asparagine
P	Pro	proline
O	Gln	glutamine
R	Arg	arginine
S	Ser	serine
T	Thr	threonine
V	Val	valine
W	Trp	trypotophan
X	Xxx	Any
Y	Tyr	tyrosine
B	Asx	Asp or Asn
Z	Glx	Glu, or Gln

GenBank数据格式



Accession number

序列长度

数据类型

Definition: 定义

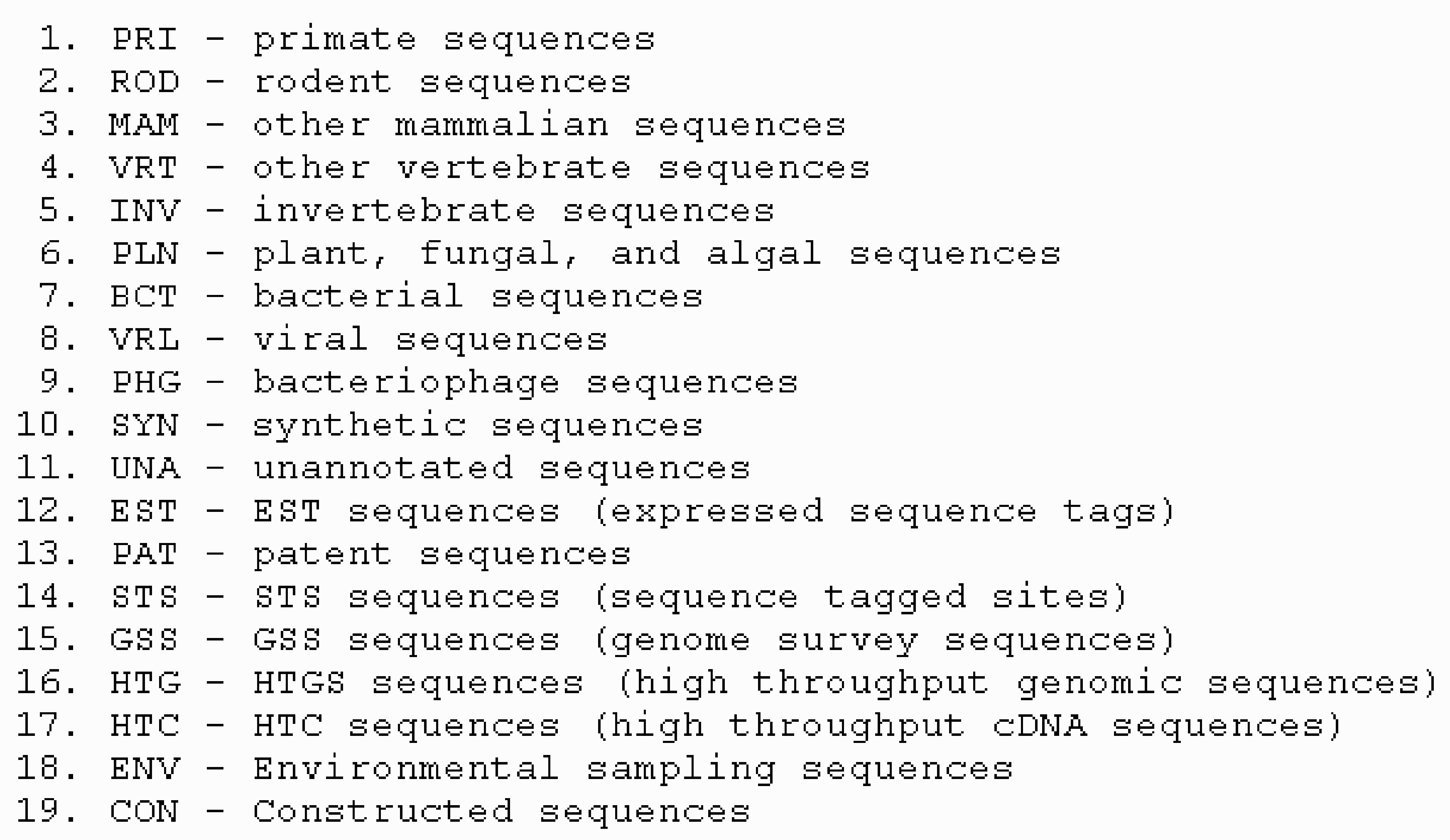
版本号

Bub1-related kinase [Drosophila melanogaster]

NCBI Reference Sequence: NP_477382.1

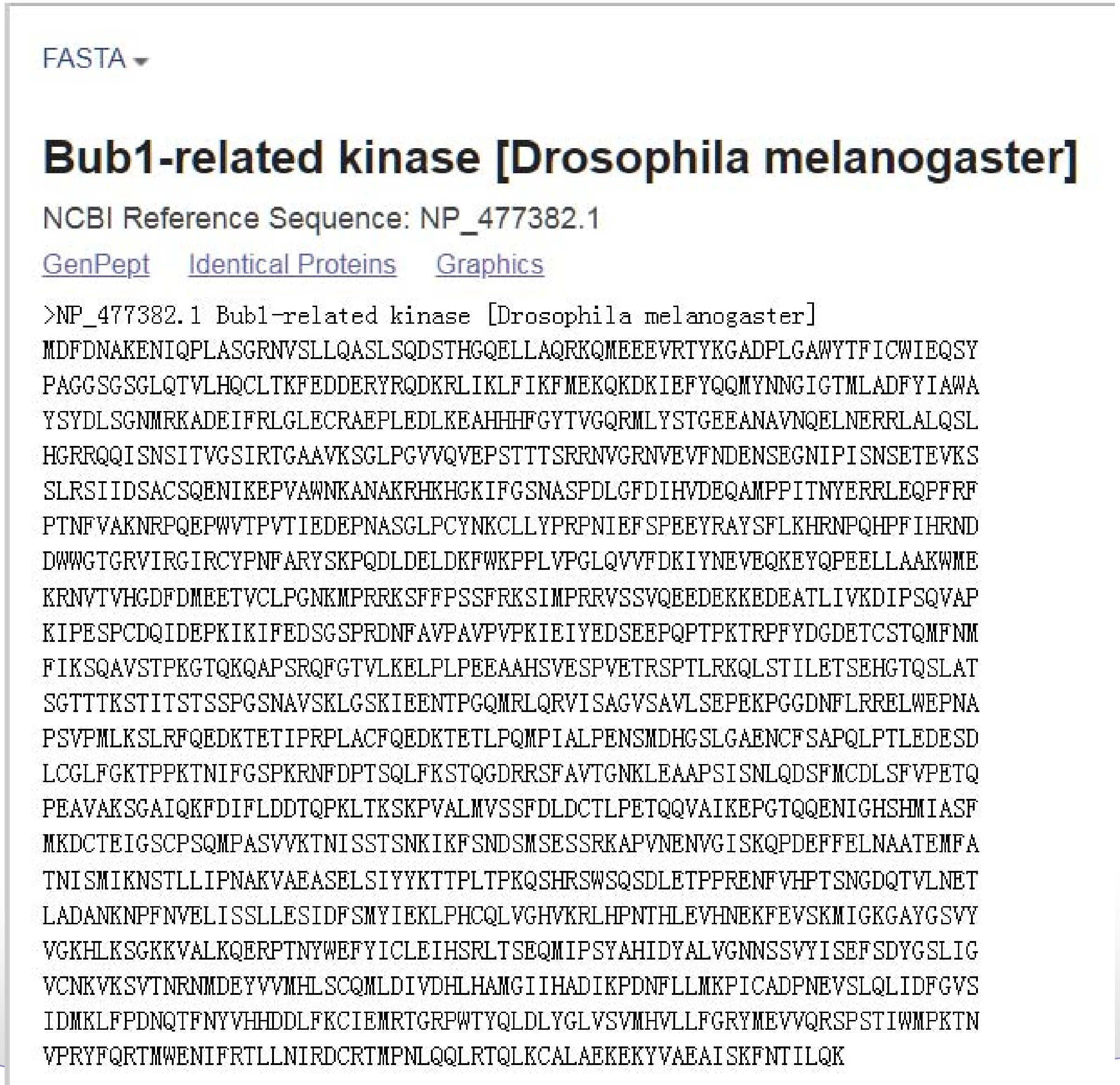
```
LOCUS       NP_477382               1460 aa            linear   INV 15-NOV-2022
DEFINITION  Bub1-related kinase [Drosophila melanogaster].
ACCESSION   NP_477382
VERSION     NP_477382.1
DBLINK      BioProject: PRJNA164
            BioSample: SAMN02803731
DBSOURCE    REFSEQ: accession NM_058034.4
KEYWORDS    RefSeq.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Sophophora.
REFERENCE   1  (residues 1 to 1460)
  AUTHORS   Matthews,B.B., Dos Santos,G., Crosby,M.A., Emmert,D.B., St
```

GenBank的数据类型



```
 1.  PRI - primate sequences
 2.  ROD - rodent sequences
 3.  MAM - other mammalian sequences
 4.  VRT - other vertebrate sequences
 5.  INV - invertebrate sequences
 6.  PLN - plant, fungal, and algal sequences
 7.  BCT - bacterial sequences
 8.  VRL - viral sequences
 9.  PHG - bacteriophage sequences
10.  SYN - synthetic sequences
11.  UNA - unannotated sequences
12.  EST - EST sequences (expressed sequence tags)
13.  PAT - patent sequences
14.  STS - STS sequences (sequence tagged sites)
15.  GSS - GSS sequences (genome survey sequences)
16.  HTG - HTGS sequences (high throughput genomic sequences)
17.  HTC - HTC sequences (high throughput cDNA sequences)
18.  ENV - Environmental sampling sequences
19.  CON - Constructed sequences
```

FASTA格式 - GenBank



Bub1-related kinase [Drosophila melanogaster]

NCBI Reference Sequence: NP_477382.1

```
>NP_477382.1 Bub1-related kinase [Drosophila melanogaster]
MDFDNAKENIQPLASGRNVSLLQASLSQDSTHGQELLAQRKQMEEEVRTYKGADPLGAWYTFICWIEQSY
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YSYDLSGNMRKADEIFRLGLECRAEPLEDLKEAHHHFGYTVGQRMLYSTGEEANAVNQELNERRLALQSL
HGRRQQISNSITVGSIRTGAAVKSGLPGVVQVEPSTTTSRRNVGRNVEVFNDENSEGNIPISNSETEVKS
SLRSIIDSACSQENIKEPVAWNKANAKRHKHGKIFGSNASPDLGFDIHVDEQAMPPITNYERRLEQPFRF
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FIKSQAVSTPKGTQKQAPSRQFGTVLKELPLPEEAAHSVESPVETRSPTLRKQLSTILETSEHGTQSLAT
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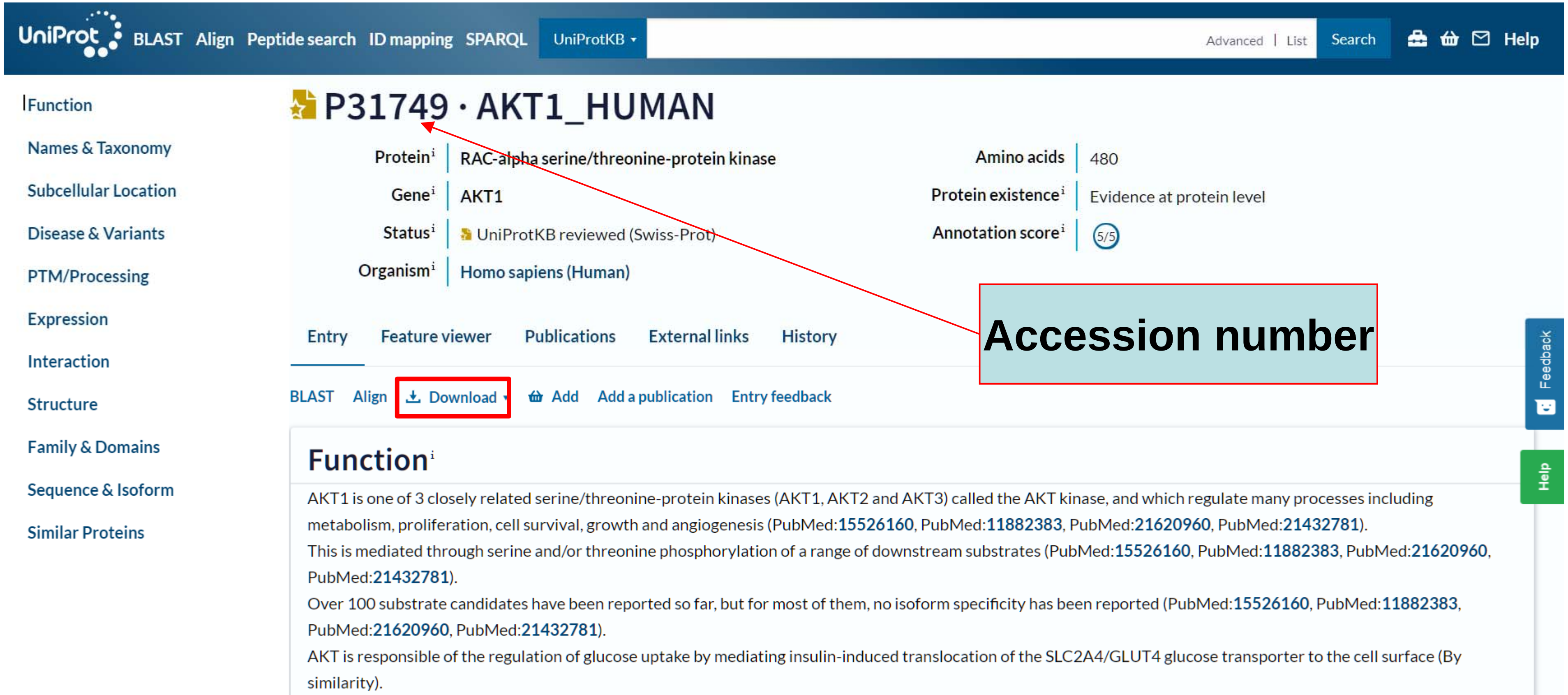
UniProt数据格式



P31749 · AKT1_HUMAN

Protein: RAC-alpha serine/threonine-protein kinase
Gene: AKT1
Status: UniProtKB reviewed (Swiss-Prot)
Organism: Homo sapiens (Human)
Amino acids: 480
Protein existence: Evidence at protein level
Annotation score: 5/5

Accession number

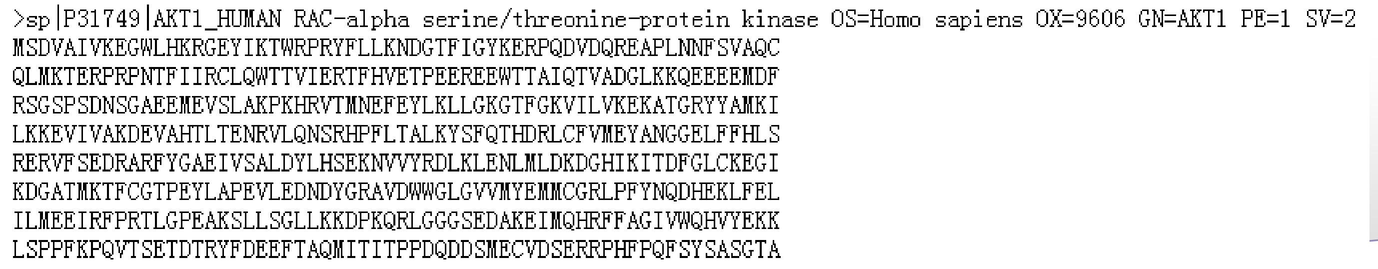
Function

AKT1 is one of 3 closely related serine/threonine-protein kinases (AKT1, AKT2 and AKT3) called the AKT kinase, and which regulate many processes including metabolism, proliferation, cell survival, growth and angiogenesis (PubMed:15526160, PubMed:11882383, PubMed:21620960, PubMed:21432781).

This is mediated through serine and/or threonine phosphorylation of a range of downstream substrates (PubMed:15526160, PubMed:11882383, PubMed:21620960, PubMed:21432781).

Over 100 substrate candidates have been reported so far, but for most of them, no isoform specificity has been reported (PubMed:15526160, PubMed:11882383, PubMed:21620960, PubMed:21432781).

AKT is responsible of the regulation of glucose uptake by mediating insulin-induced translocation of the SLC2A4/GLUT4 glucose transporter to the cell surface (By similarity).



```
>sp|P31749|AKT1_HUMAN RAC-alpha serine/threonine-protein kinase OS=Homo sapiens OX=9606 GN=AKT1 PE=1 SV=2
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RSGSPSDNSGAEEMEVSLAKPKHRVTMNEFEYLKLLGKGTFGKVILVKEKATGRYYAMKI
LKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLS
RERVFSEDRARFYGAEIVSALDYLHSEKNVVYRDLKLENLMLDKDGHIKITDFGLCKEGI
KDGATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFEL
ILMEEIRFPRTLGPEAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRFFAGIVWQHVYEKK
LSPPFKPQVTSETDTRYFDEEFTAQMITITPPDQDDSMECVDSERRPHFPQFSYSASGTA
```

生物序列数据检索

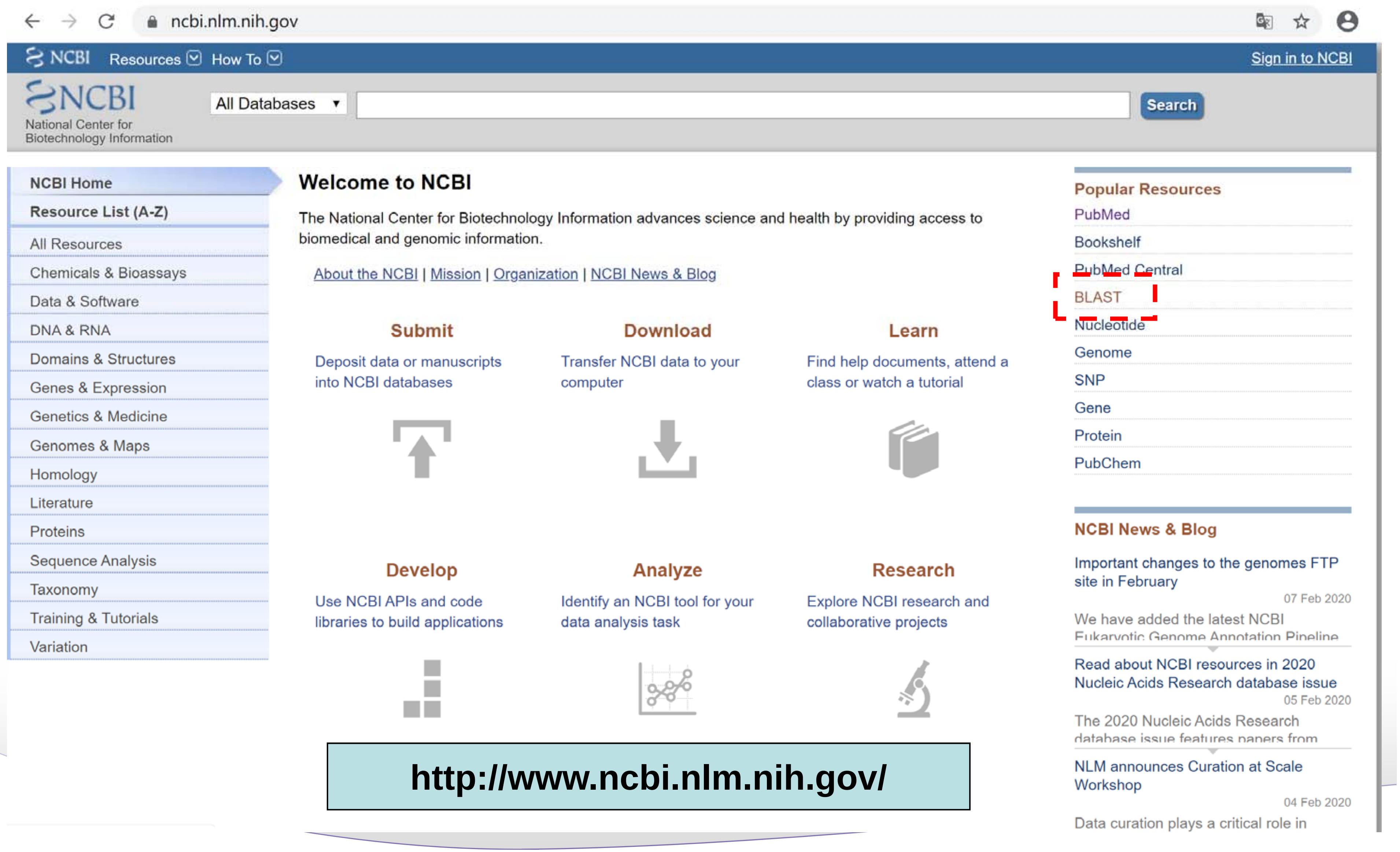
- **例：利用实验学方法（如RNA-Seq），发现了潜在参与调控细胞有丝分裂的某个基因，测序结果如下（genotype）：**

CCCCTGCCTGGCAGCCCTTTCTCAAGGACCACCGCATCTCTACATTCAAGA
ACTGGCCCTTCTTGGAGGGCTGCGCCTGCACCCCGGAGCGGATGGCCGA
GGCTGGCTTCATCCACTGCCCCACTGAGAACGAGCCAGACTTGGCCCAGT
GTTTCTTCTGCTTCAAGGAGCTGGAAGGCTGGGAGCCAGATGACGACCCC
ATAGAGGAACATAAAAAGCATTCGTCCGGTTGCGCTTTCCTTTCTGTCAAGA
AGCAGTTTGAAGAATTAACCCTTGGTGAATTTTTGAAACTGGACAGAGAAAG
AGCCAAGAACAAAATTGCAAAGGAAACCAACAATAAGAAGAAAGAATTTGAG
GAAACTGCGGAGAAAGTGCGCCGTGCCATCGAGCAGCTGGCTGCCATGGA
TTGAGGCCTCTGGC

问题：

- 这是哪个基因？
- 编码的蛋白质序列是怎样的？
- 有没有保守的功能结构域（domain）？
- 它的功能是怎样的？
- 它在真核生物中保守吗？
- 有没有三级结构信息？

NCBI: BLAST



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Important changes to the genomes FTP site in February

07 Feb 2020

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Read about NCBI resources in 2020 Nucleic Acids Research database issue

05 Feb 2020

The 2020 Nucleic Acids Research database issue features papers from

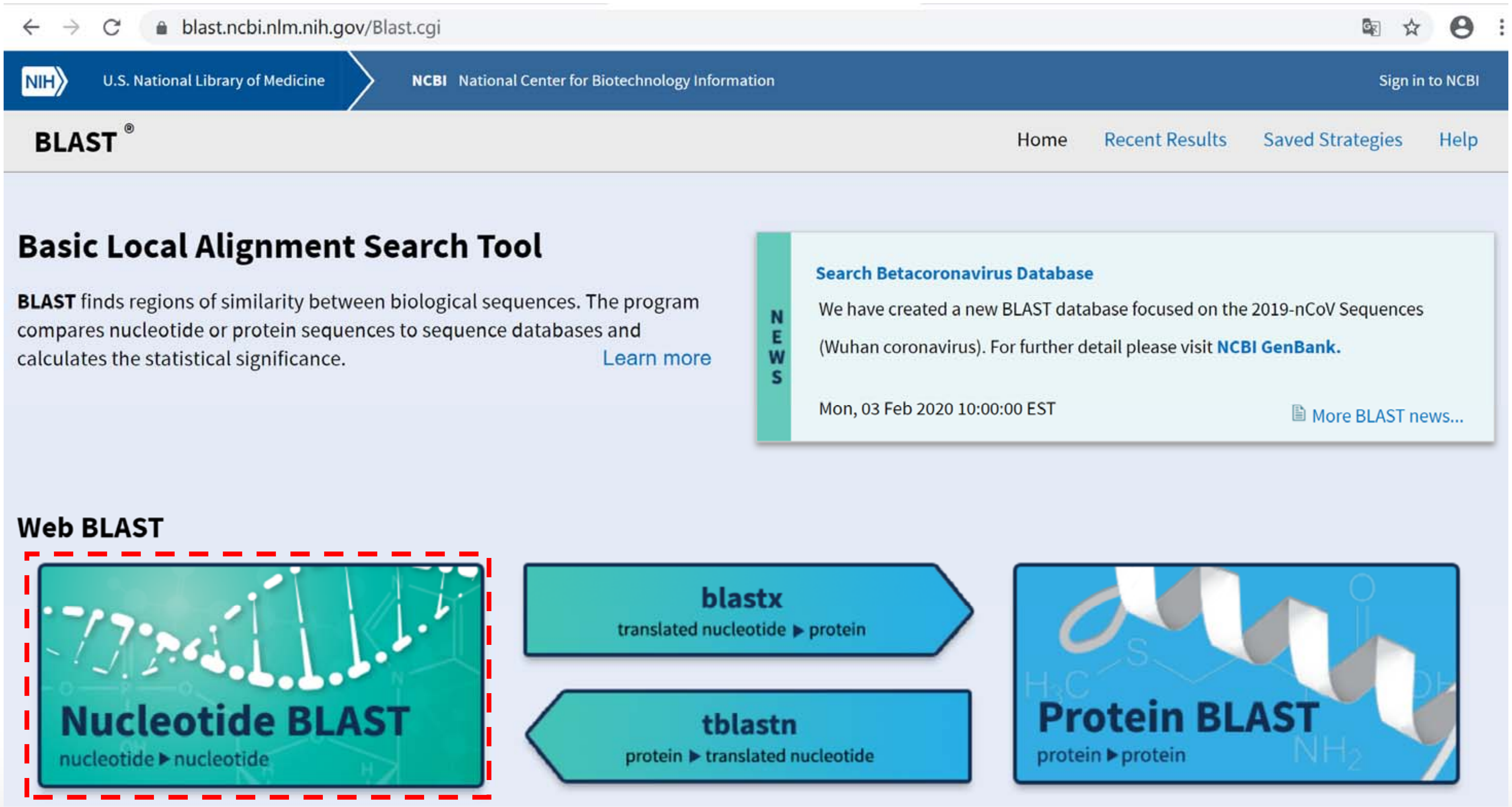
NLM announces Curation at Scale Workshop

04 Feb 2020

Data curation plays a critical role in

http://www.ncbi.nlm.nih.gov/

Nucleotide blast



Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. Learn more

Search Betacoronavirus Database

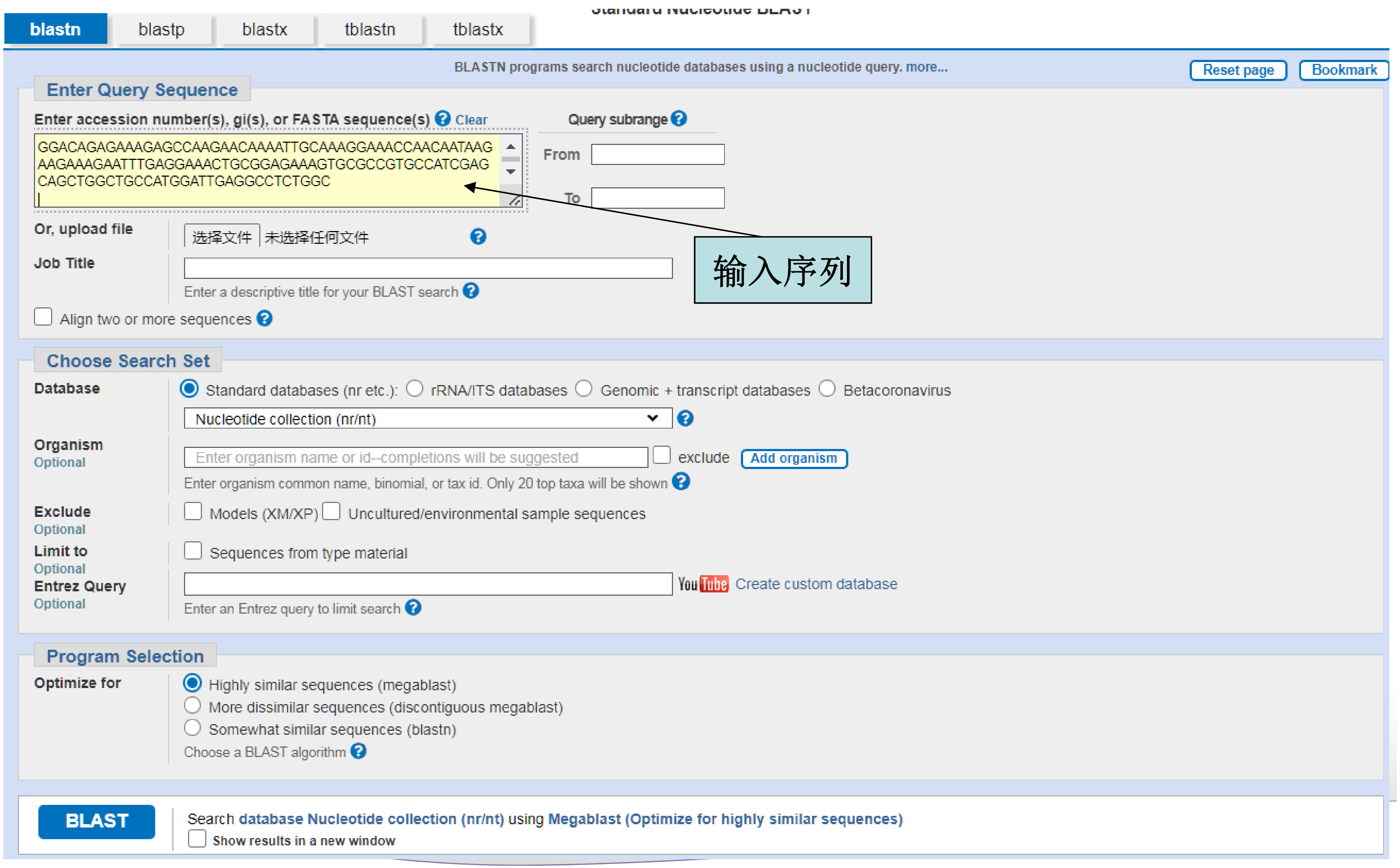
We have created a new BLAST database focused on the 2019-nCoV Sequences (Wuhan coronavirus). For further detail please visit **NCBI GenBank.**

Mon, 03 Feb 2020 10:00:00 EST

More BLAST news...

https://blast.ncbi.nlm.nih.gov/Blast.cgi

Megablast: 找基因序列



BLASTN programs search nucleotide databases using a nucleotide query. more...

Enter Query Sequence

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

```
GGACAGAGAAAGAGCCAAGAACAAAATTGCAAAGGAAACCAACAATAAG
AAGAAAGAATTTGAGGAAACTGCGGAGAAAGTGCGCCGTGCCATCGAG
CAGCTGGCTGCCATGGATTGAGGCCTCTGGC
```

Query subrange

From

To

输入序列

Or, upload file 选择文件 未选择任何文件

Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database ● Standard databases (nr etc.): ○ rRNA/ITS databases ○ Genomic + transcript databases ○ Betacoronavirus

Nucleotide collection (nr/nt)

Organism Optional

Enter organism name or id--completions will be suggested ☐ exclude Add organism

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

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

Limit to Optional ☐ Sequences from type material

Entrez Query Optional

YouTube Create custom database

Enter an Entrez query to limit search

Program Selection

Optimize for

● Highly similar sequences (megablast)
○ More dissimilar sequences (discontiguous megablast)
○ Somewhat similar sequences (blastn)

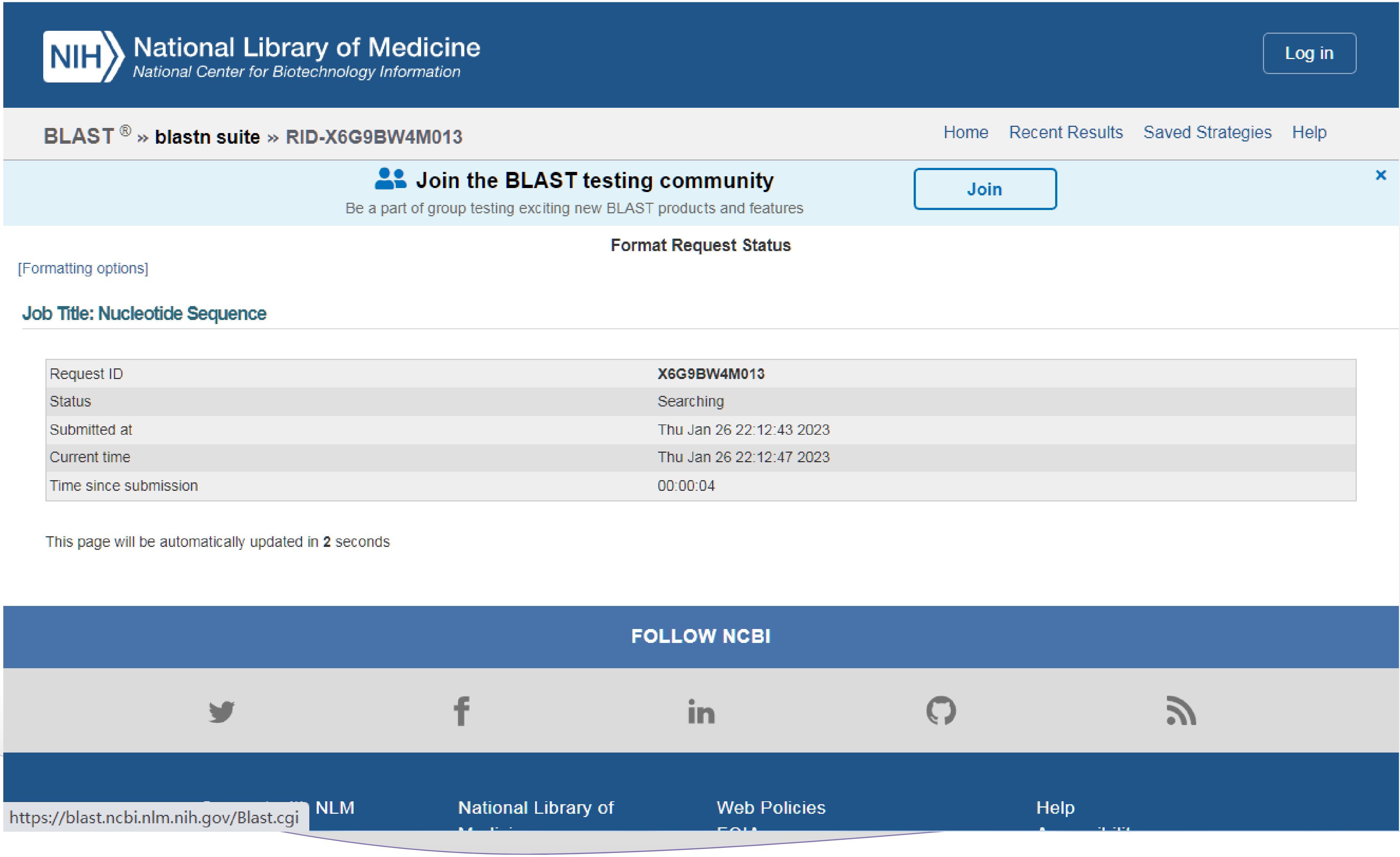
Choose a BLAST algorithm

BLAST

Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window

提交序列



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Format Request Status

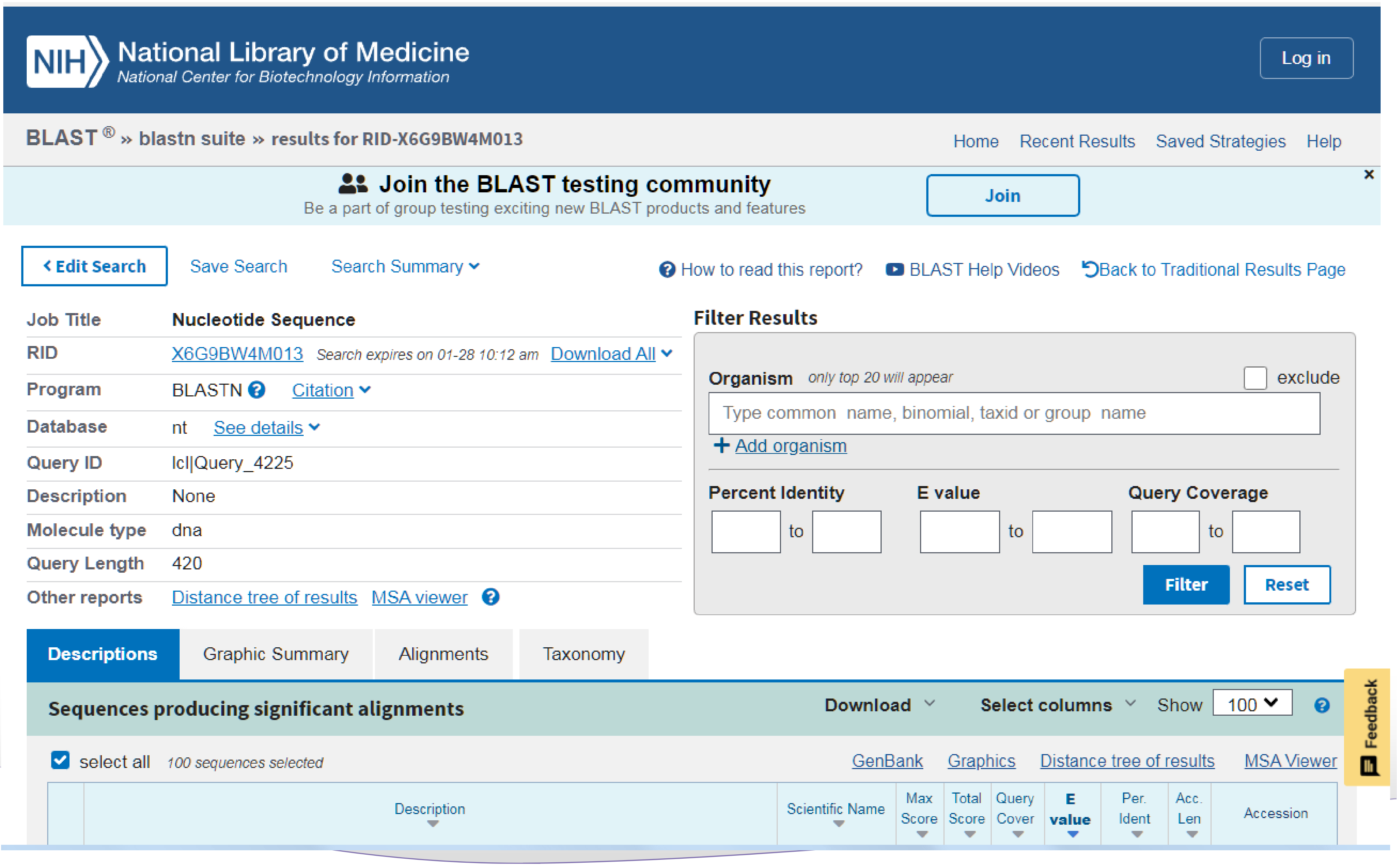
[Formatting options]

Job Title: Nucleotide Sequence

Request ID	**X6G9BW4M013**
Status	Searching
Submitted at	Thu Jan 26 22:12:43 2023
Current time	Thu Jan 26 22:12:47 2023
Time since submission	00:00:04

This page will be automatically updated in **2** seconds

结果页面



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BLAST ® » blastn suite » results for RID-X6G9BW4M013

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Job Title	**Nucleotide Sequence**
RID	X6G9BW4M013 *Search expires on 01-28 10:12 am* Download All
Program	BLASTN Citation
Database	nt See details
Query ID	lcl|Query_4225
Description	None
Molecule type	dna
Query Length	420
Other reports	Distance tree of results MSA viewer

Filter Results

Organism *only top 20 will appear* ☐ exclude

Type common name, binomial, taxid or group name

+ Add organism

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

Filter Reset

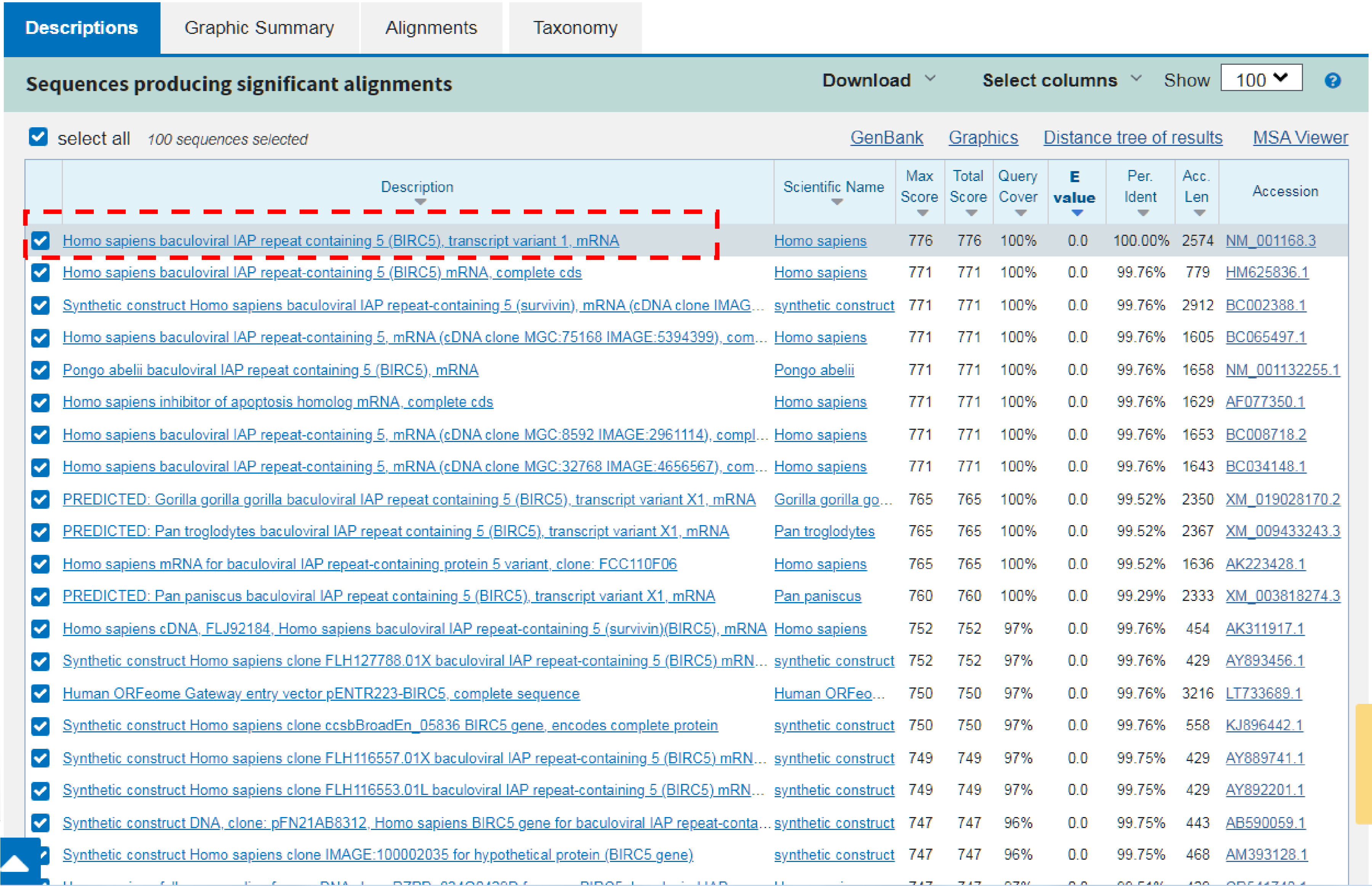
Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments Download Select columns Show 100

☑ select all *100 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

NM_001168.3：BIRC5 (Survivin)

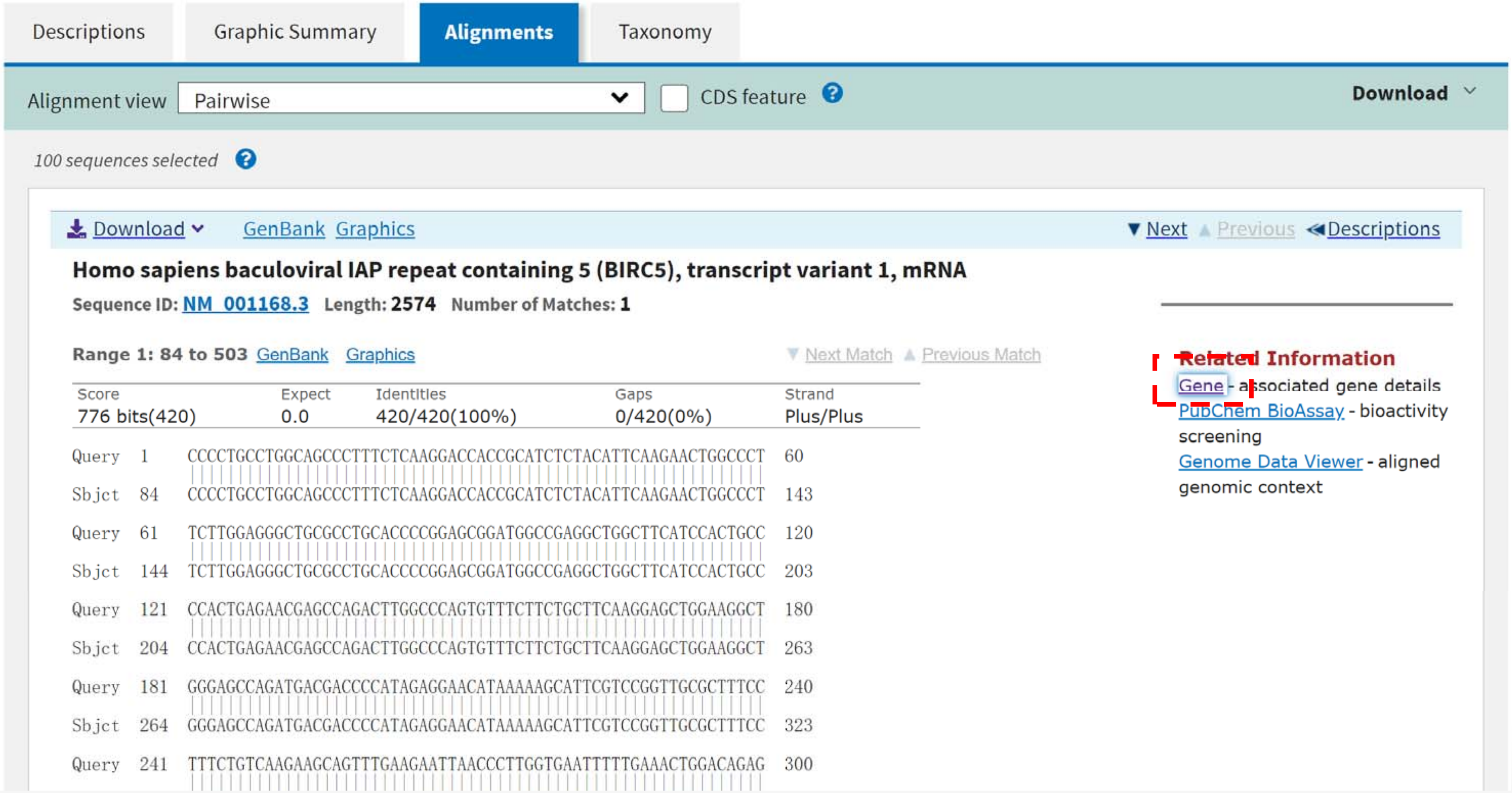


Sequences producing significant alignments

☑ select all *100 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	Homo sapiens baculoviral IAP repeat containing 5 (BIRC5), transcript variant 1, mRNA	Homo sapiens	776	776	100%	0.0	100.00%	2574	NM_001168.3
☑	Homo sapiens baculoviral IAP repeat-containing 5 (BIRC5) mRNA, complete cds	Homo sapiens	771	771	100%	0.0	99.76%	779	HM625836.1
☑	Synthetic construct Homo sapiens baculoviral IAP repeat-containing 5 (survivin), mRNA (cDNA clone IMAG...	synthetic construct	771	771	100%	0.0	99.76%	2912	BC002388.1
☑	Homo sapiens baculoviral IAP repeat-containing 5, mRNA (cDNA clone MGC:75168 IMAGE:5394399), com...	Homo sapiens	771	771	100%	0.0	99.76%	1605	BC065497.1
☑	Pongo abelii baculoviral IAP repeat containing 5 (BIRC5), mRNA	Pongo abelii	771	771	100%	0.0	99.76%	1658	NM_001132255.1
☑	Homo sapiens inhibitor of apoptosis homolog mRNA, complete cds	Homo sapiens	771	771	100%	0.0	99.76%	1629	AF077350.1
☑	Homo sapiens baculoviral IAP repeat-containing 5, mRNA (cDNA clone MGC:8592 IMAGE:2961114), compl...	Homo sapiens	771	771	100%	0.0	99.76%	1653	BC008718.2
☑	Homo sapiens baculoviral IAP repeat-containing 5, mRNA (cDNA clone MGC:32768 IMAGE:4656567), com...	Homo sapiens	771	771	100%	0.0	99.76%	1643	BC034148.1
☑	PREDICTED: Gorilla gorilla gorilla baculoviral IAP repeat containing 5 (BIRC5), transcript variant X1, mRNA	Gorilla gorilla go...	765	765	100%	0.0	99.52%	2350	XM_019028170.2
☑	PREDICTED: Pan troglodytes baculoviral IAP repeat containing 5 (BIRC5), transcript variant X1, mRNA	Pan troglodytes	765	765	100%	0.0	99.52%	2367	XM_009433243.3
☑	Homo sapiens mRNA for baculoviral IAP repeat-containing protein 5 variant, clone: FCC110F06	Homo sapiens	765	765	100%	0.0	99.52%	1636	AK223428.1
☑	PREDICTED: Pan paniscus baculoviral IAP repeat containing 5 (BIRC5), transcript variant X1, mRNA	Pan paniscus	760	760	100%	0.0	99.29%	2333	XM_003818274.3
☑	Homo sapiens cDNA, FLJ92184, Homo sapiens baculoviral IAP repeat-containing 5 (survivin)(BIRC5), mRNA	Homo sapiens	752	752	97%	0.0	99.76%	454	AK311917.1
☑	Synthetic construct Homo sapiens clone FLH127788.01X baculoviral IAP repeat-containing 5 (BIRC5) mRN...	synthetic construct	752	752	97%	0.0	99.76%	429	AY893456.1
☑	Human ORFeome Gateway entry vector pENTR223-BIRC5, complete sequence	Human ORFeo...	750	750	97%	0.0	99.76%	3216	LT733689.1
☑	Synthetic construct Homo sapiens clone ccsbBroadEn_05836 BIRC5 gene, encodes complete protein	synthetic construct	750	750	97%	0.0	99.76%	558	KJ896442.1
☑	Synthetic construct Homo sapiens clone FLH116557.01X baculoviral IAP repeat-containing 5 (BIRC5) mRN...	synthetic construct	749	749	97%	0.0	99.75%	429	AY889741.1
☑	Synthetic construct Homo sapiens clone FLH116553.01L baculoviral IAP repeat-containing 5 (BIRC5) mRN...	synthetic construct	749	749	97%	0.0	99.75%	429	AY892201.1
☑	Synthetic construct DNA, clone: pFN21AB8312, Homo sapiens BIRC5 gene for baculoviral IAP repeat-conta...	synthetic construct	747	747	96%	0.0	99.75%	443	AB590059.1
☑	Synthetic construct Homo sapiens clone IMAGE:100002035 for hypothetical protein (BIRC5 gene)	synthetic construct	747	747	96%	0.0	99.75%	468	AM393128.1

BIRC5 Gene



100 sequences selected

Homo sapiens baculoviral IAP repeat containing 5 (BIRC5), transcript variant 1, mRNA

Sequence ID: NM_001168.3 **Length:** 2574 **Number of Matches:** 1

Range 1: 84 to 503 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
776 bits(420)	0.0	420/420(100%)	0/420(0%)	Plus/Plus

```
Query  1    CCCCTGCCTGGCAGCCCTTTCTCAAGGACCACCGCATCTCTACATTCAAGAACTGGCCCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  84   CCCCTGCCTGGCAGCCCTTTCTCAAGGACCACCGCATCTCTACATTCAAGAACTGGCCCT  143

Query  61   TCTTGGAGGGCTGCGCCTGCACCCCGGAGCGGATGGCCGAGGCTGGCTTCATCCACTGCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  144  TCTTGGAGGGCTGCGCCTGCACCCCGGAGCGGATGGCCGAGGCTGGCTTCATCCACTGCC  203

Query  121  CCACTGAGAACGAGCCAGACTTGGCCCAGTGTTTCTTCTGCTTCAAGGAGCTGGAAGGCT  180
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Query  181  GGGAGCCAGATGACGACCCCATAGAGGAACATAAAAAGCATTCGTCCGGTTGCGCTTTCC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query  241  TTTCTGTCAAGAAGCAGTTTGAAGAATTAACCCTTGGTGAATTTTTGAAACTGGACAGAG  300
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```

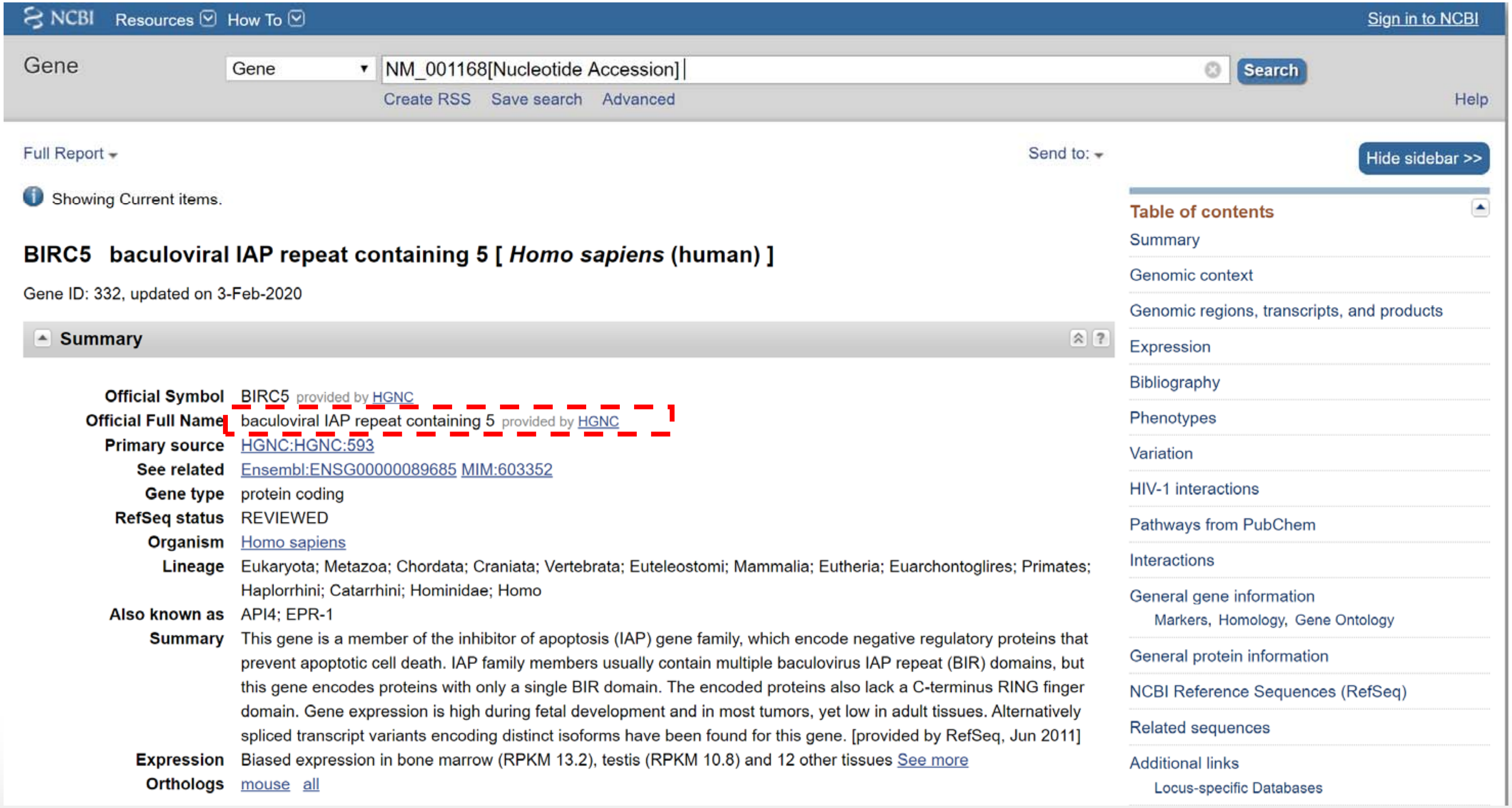
Related Information

Gene - associated gene details

PubChem BioAssay - bioactivity screening

Genome Data Viewer - aligned genomic context

BIRC5 gene information



Showing Current items.

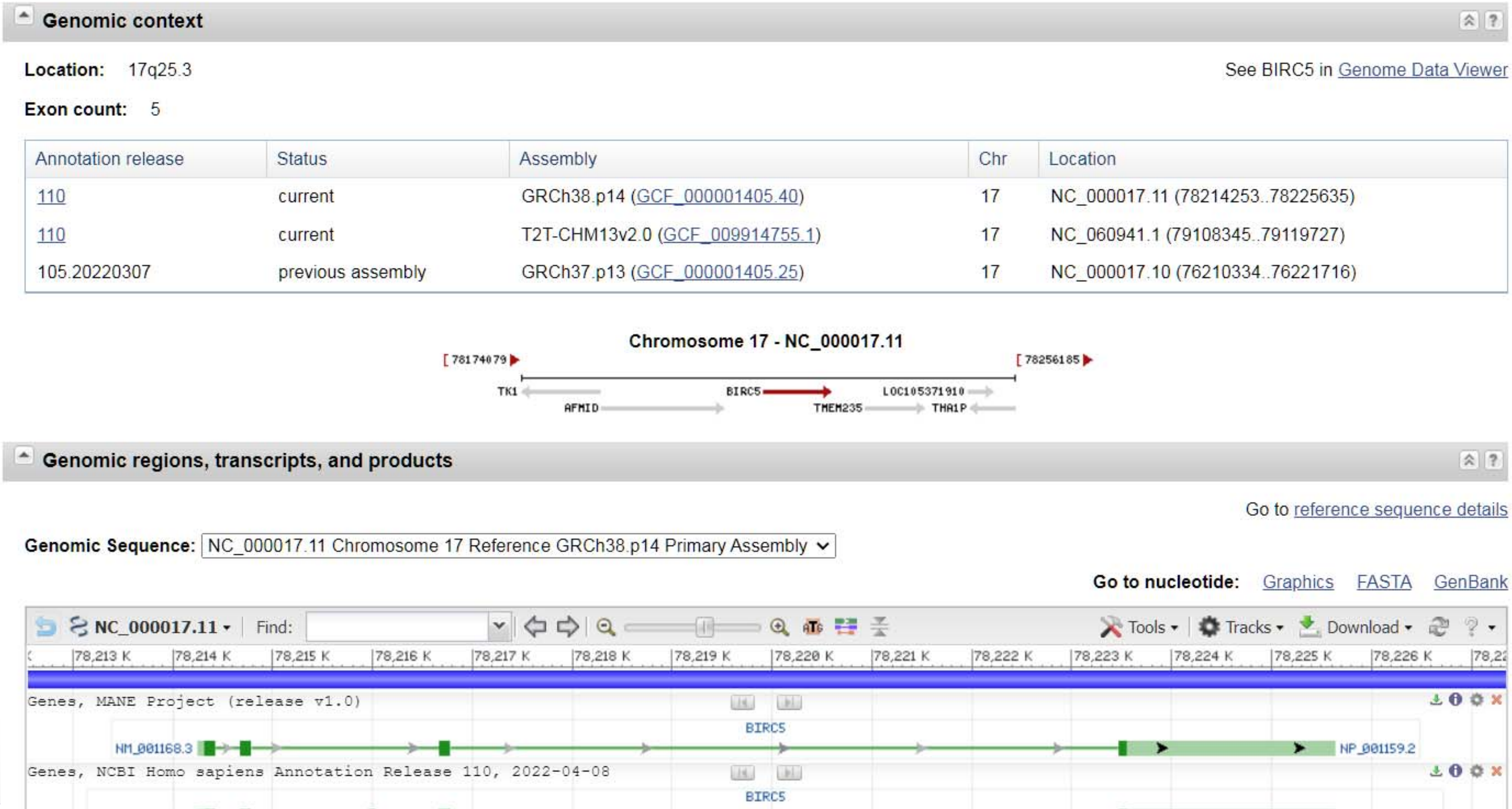
BIRC5 baculoviral IAP repeat containing 5 [*Homo sapiens* (human)]

Gene ID: 332, updated on 3-Feb-2020

Summary

Official Symbol	BIRC5 provided by HGNC
Official Full Name	baculoviral IAP repeat containing 5 provided by HGNC
Primary source	HGNC:HGNC:593
See related	Ensembl:ENSG00000089685 MIM:603352
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	API4; EPR-1
Summary	This gene is a member of the inhibitor of apoptosis (IAP) gene family, which encode negative regulatory proteins that prevent apoptotic cell death. IAP family members usually contain multiple baculovirus IAP repeat (BIR) domains, but this gene encodes proteins with only a single BIR domain. The encoded proteins also lack a C-terminus RING finger domain. Gene expression is high during fetal development and in most tumors, yet low in adult tissues. Alternatively spliced transcript variants encoding distinct isoforms have been found for this gene. [provided by RefSeq, Jun 2011]
Expression	Biased expression in bone marrow (RPKM 13.2), testis (RPKM 10.8) and 12 other tissues See more
Orthologs	mouse all

基因信息：17号染色体



Genomic context

Location: 17q25.3

See BIRC5 in Genome Data Viewer

Exon count: 5

Annotation release	Status	Assembly	Chr	Location
110	current	GRCh38.p14 (GCF_000001405.40)	17	NC_000017.11 (78214253..78225635)
110	current	T2T-CHM13v2.0 (GCF_009914755.1)	17	NC_060941.1 (79108345..79119727)
105.20220307	previous assembly	GRCh37.p13 (GCF_000001405.25)	17	NC_000017.10 (76210334..76221716)

Chromosome 17 - NC_000017.11

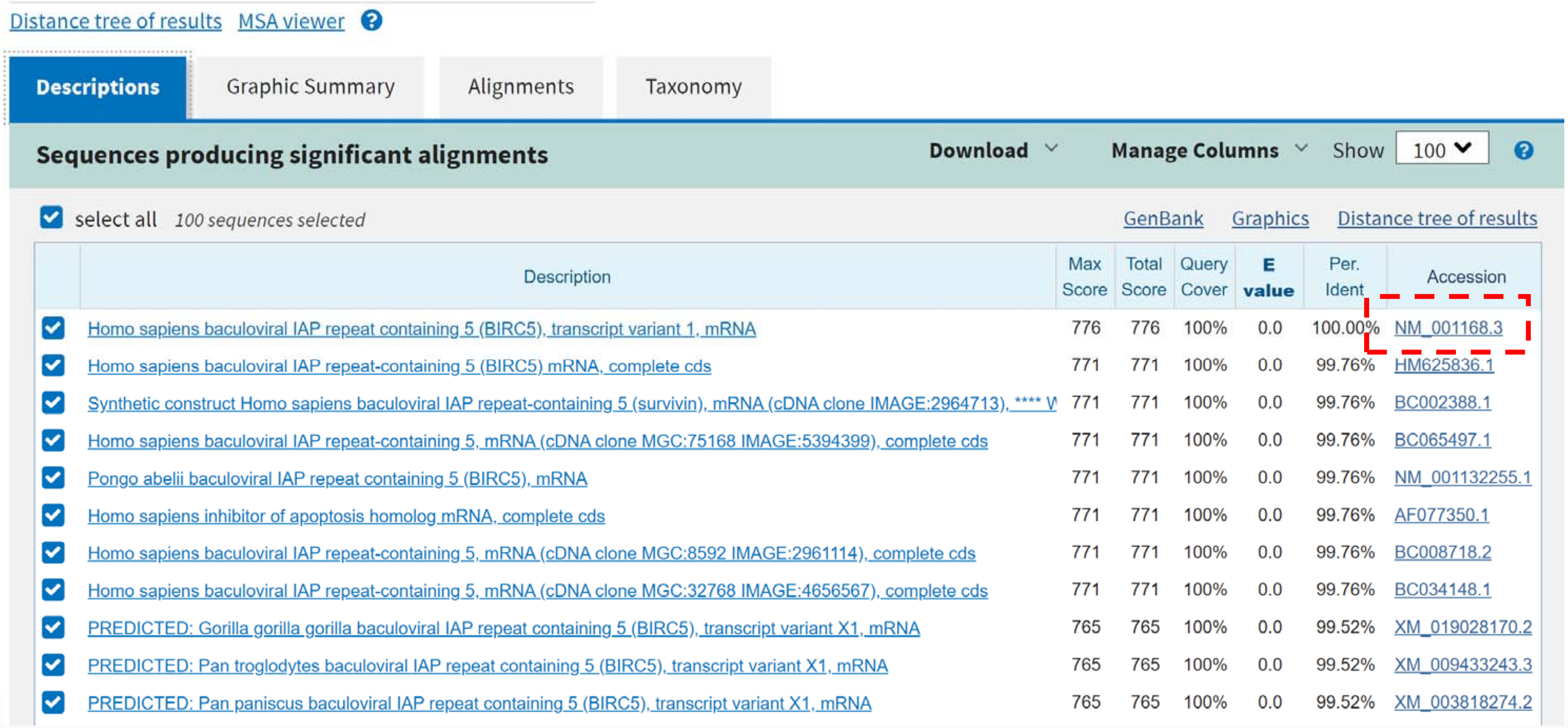
Genomic regions, transcripts, and products

Go to reference sequence details

Genomic Sequence: NC_000017.11 Chromosome 17 Reference GRCh38.p14 Primary Assembly

Go to nucleotide: Graphics FASTA GenBank

NM_001168.3：BIRC5

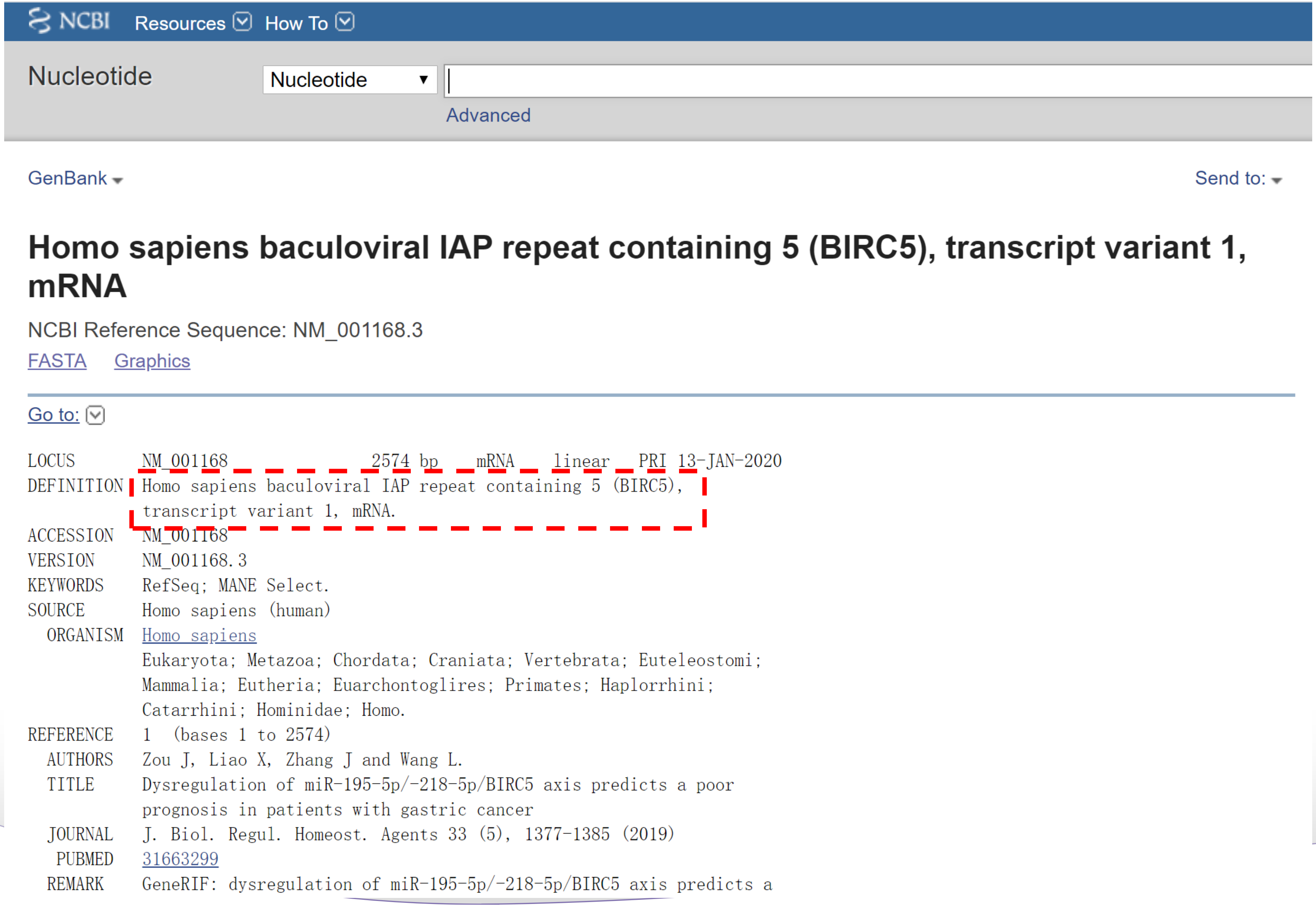


Sequences producing significant alignments

☑ select all *100 sequences selected*

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
☑	Homo sapiens baculoviral IAP repeat containing 5 (BIRC5), transcript variant 1, mRNA	776	776	100%	0.0	100.00%	NM_001168.3
☑	Homo sapiens baculoviral IAP repeat-containing 5 (BIRC5) mRNA, complete cds	771	771	100%	0.0	99.76%	HM625836.1
☑	Synthetic construct Homo sapiens baculoviral IAP repeat-containing 5 (survivin), mRNA (cDNA clone IMAGE:2964713), **** W	771	771	100%	0.0	99.76%	BC002388.1
☑	Homo sapiens baculoviral IAP repeat-containing 5, mRNA (cDNA clone MGC:75168 IMAGE:5394399), complete cds	771	771	100%	0.0	99.76%	BC065497.1
☑	Pongo abelii baculoviral IAP repeat containing 5 (BIRC5), mRNA	771	771	100%	0.0	99.76%	NM_001132255.1
☑	Homo sapiens inhibitor of apoptosis homolog mRNA, complete cds	771	771	100%	0.0	99.76%	AF077350.1
☑	Homo sapiens baculoviral IAP repeat-containing 5, mRNA (cDNA clone MGC:8592 IMAGE:2961114), complete cds	771	771	100%	0.0	99.76%	BC008718.2
☑	Homo sapiens baculoviral IAP repeat-containing 5, mRNA (cDNA clone MGC:32768 IMAGE:4656567), complete cds	771	771	100%	0.0	99.76%	BC034148.1
☑	PREDICTED: Gorilla gorilla gorilla baculoviral IAP repeat containing 5 (BIRC5), transcript variant X1, mRNA	765	765	100%	0.0	99.52%	XM_019028170.2
☑	PREDICTED: Pan troglodytes baculoviral IAP repeat containing 5 (BIRC5), transcript variant X1, mRNA	765	765	100%	0.0	99.52%	XM_009433243.3
☑	PREDICTED: Pan paniscus baculoviral IAP repeat containing 5 (BIRC5), transcript variant X1, mRNA	765	765	100%	0.0	99.52%	XM_003818274.2

Human BIRC5 !



Homo sapiens baculoviral IAP repeat containing 5 (BIRC5), transcript variant 1, mRNA

NCBI Reference Sequence: NM_001168.3

FASTA Graphics

Go to:

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LOCUS       NM_001168               2574 bp    mRNA    linear   PRI 13-JAN-2020
DEFINITION  Homo sapiens baculoviral IAP repeat containing 5 (BIRC5),
            transcript variant 1, mRNA.
ACCESSION   NM_001168
VERSION     NM_001168.3
KEYWORDS    RefSeq; MANE Select.
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 2574)
  AUTHORS   Zou J, Liao X, Zhang J and Wang L.
  TITLE     Dysregulation of miR-195-5p/-218-5p/BIRC5 axis predicts a poor
            prognosis in patients with gastric cancer
  JOURNAL   J. Biol. Regul. Homeost. Agents 33 (5), 1377-1385 (2019)
   PUBMED   31663299
  REMARK    GeneRIF: dysregulation of miR-195-5p/-218-5p/BIRC5 axis predicts a
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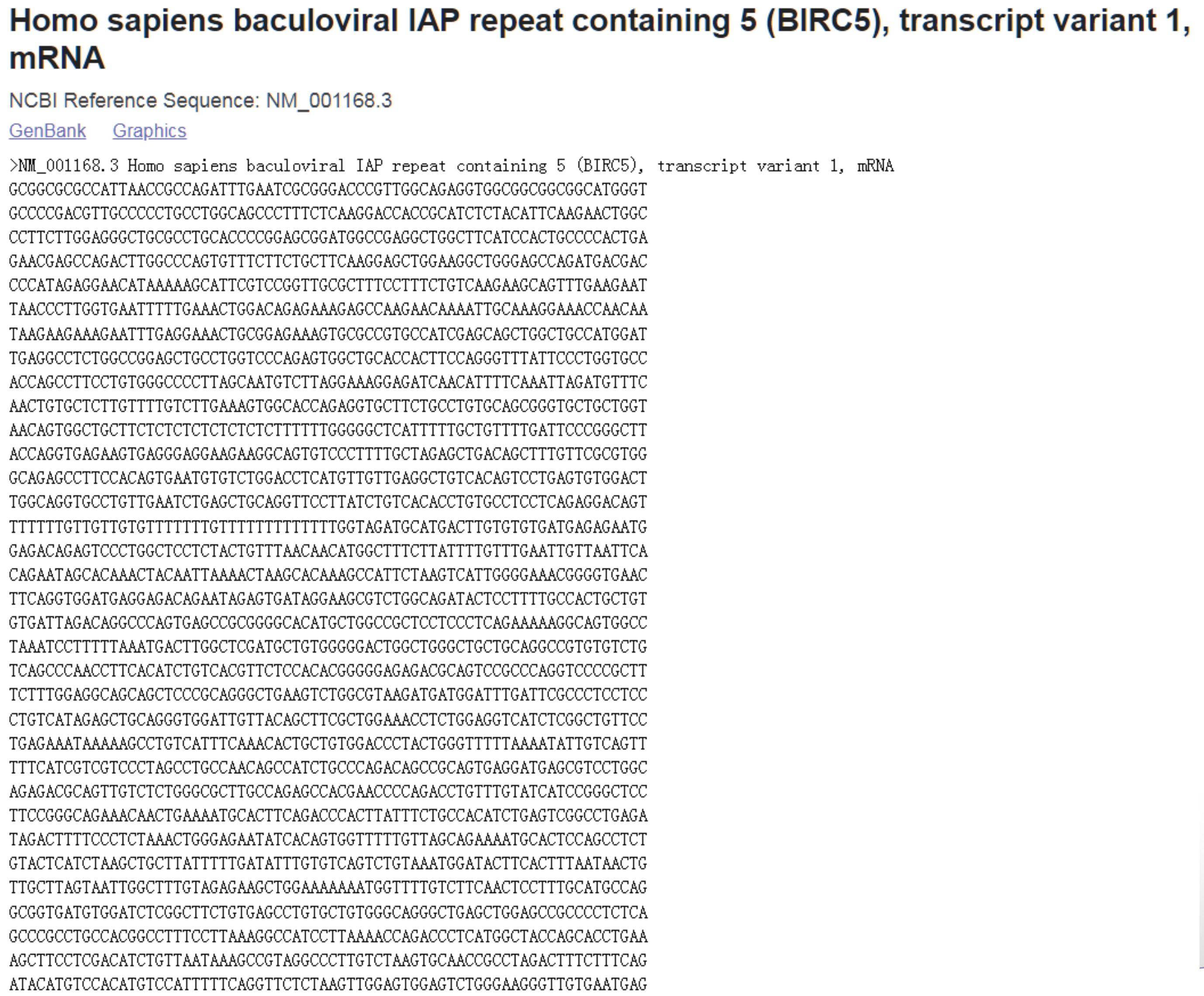
Human BIRC5的核酸序列



Homo sapiens baculoviral IAP repeat containing 5 (BIRC5), transcript variant 1, mRNA

NCBI Reference Sequence: NM_001168.3

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>NM_001168.3 Homo sapiens baculoviral IAP repeat containing 5 (BIRC5), transcript variant 1, mRNA
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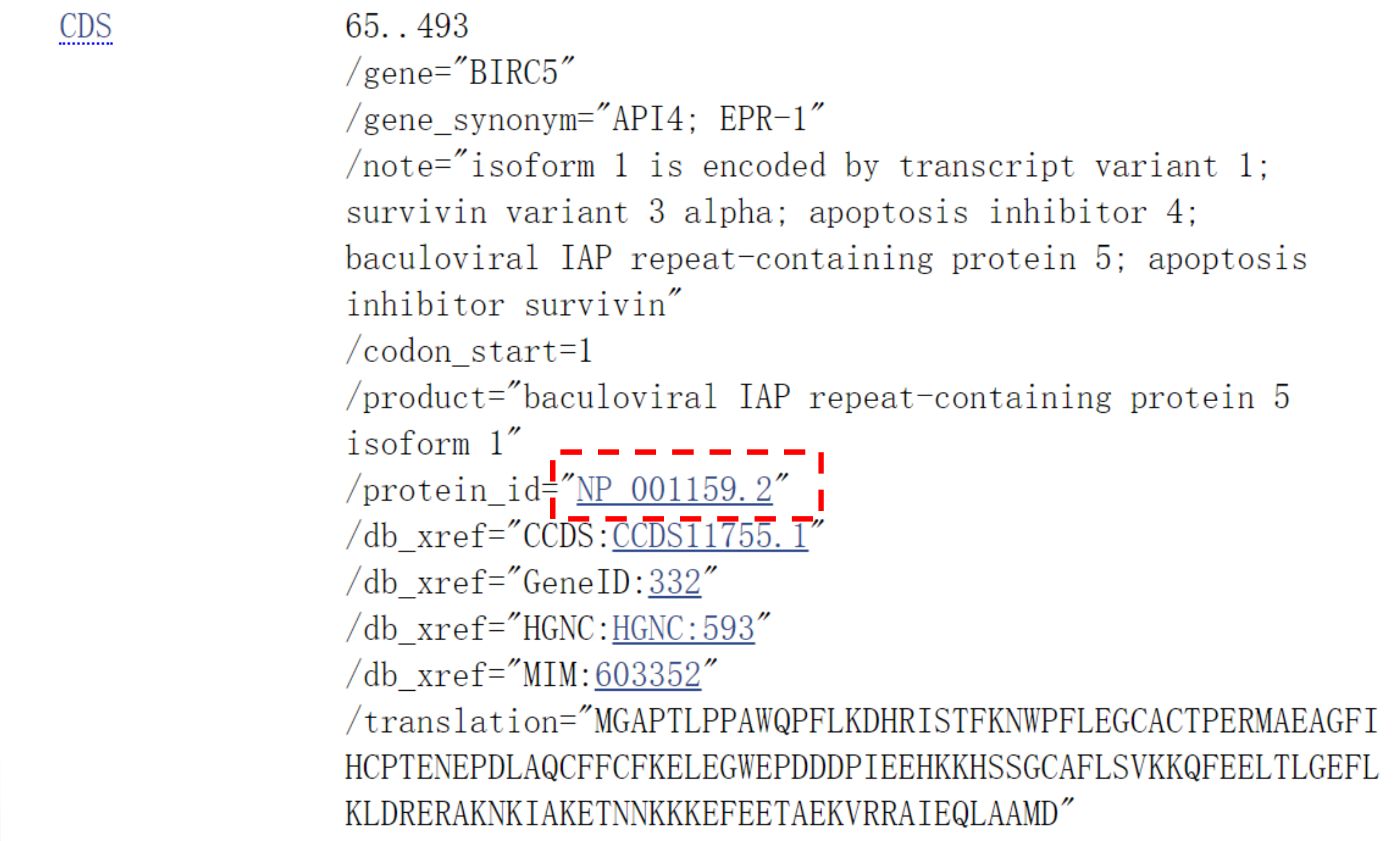
获取蛋白质的序列信息



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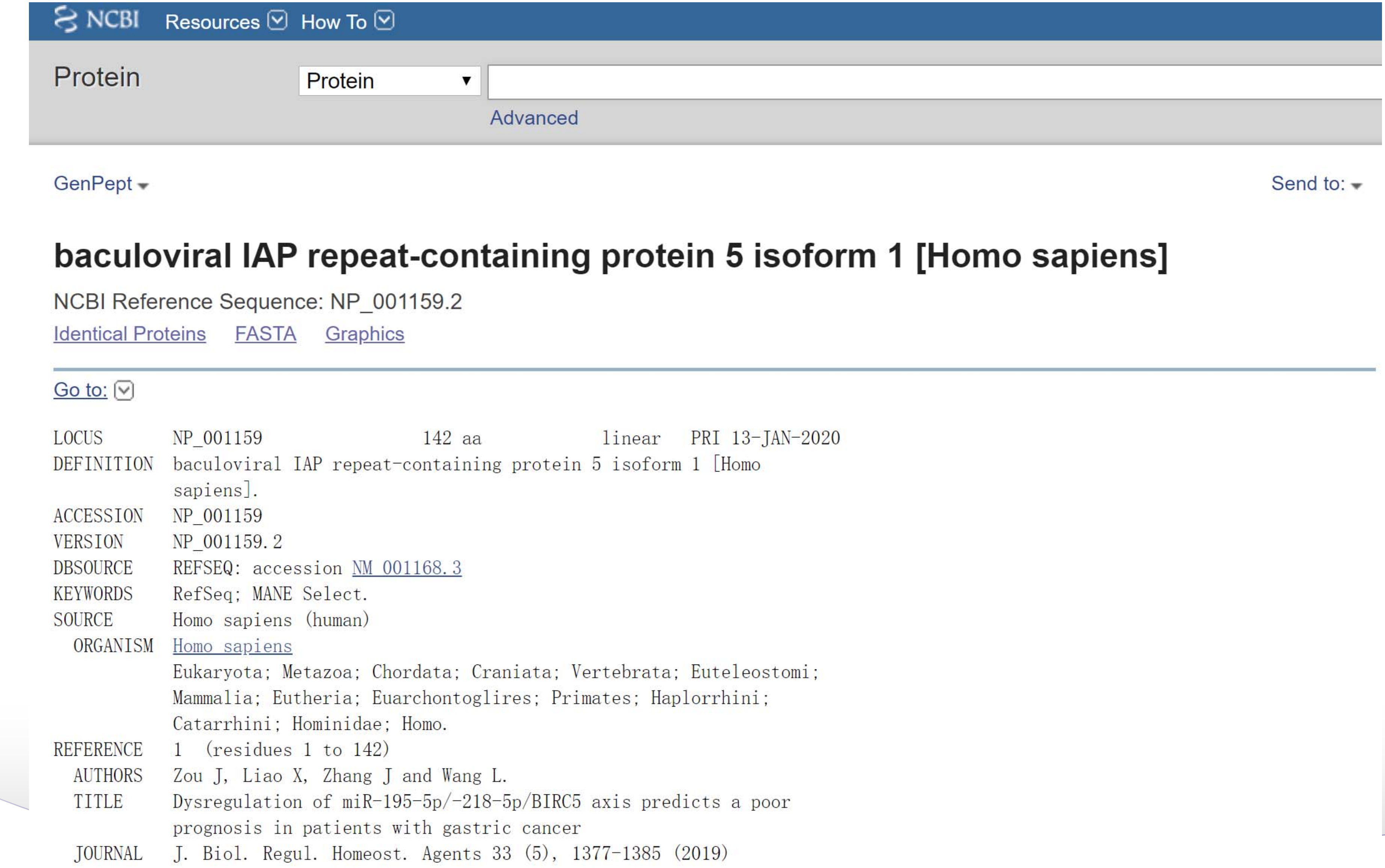
BIRC5：142aa



baculoviral IAP repeat-containing protein 5 isoform 1 [Homo sapiens]

NCBI Reference Sequence: NP_001159.2

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DEFINITION  baculoviral IAP repeat-containing protein 5 isoform 1 [Homo
            sapiens].
ACCESSION   NP_001159
VERSION     NP_001159.2
DBSOURCE    REFSEQ: accession NM_001168.3
KEYWORDS    RefSeq; MANE Select.
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 142)
  AUTHORS   Zou J, Liao X, Zhang J and Wang L.
  TITLE     Dysregulation of miR-195-5p/-218-5p/BIRC5 axis predicts a poor
            prognosis in patients with gastric cancer
  JOURNAL   J. Biol. Regul. Homeost. Agents 33 (5), 1377-1385 (2019)
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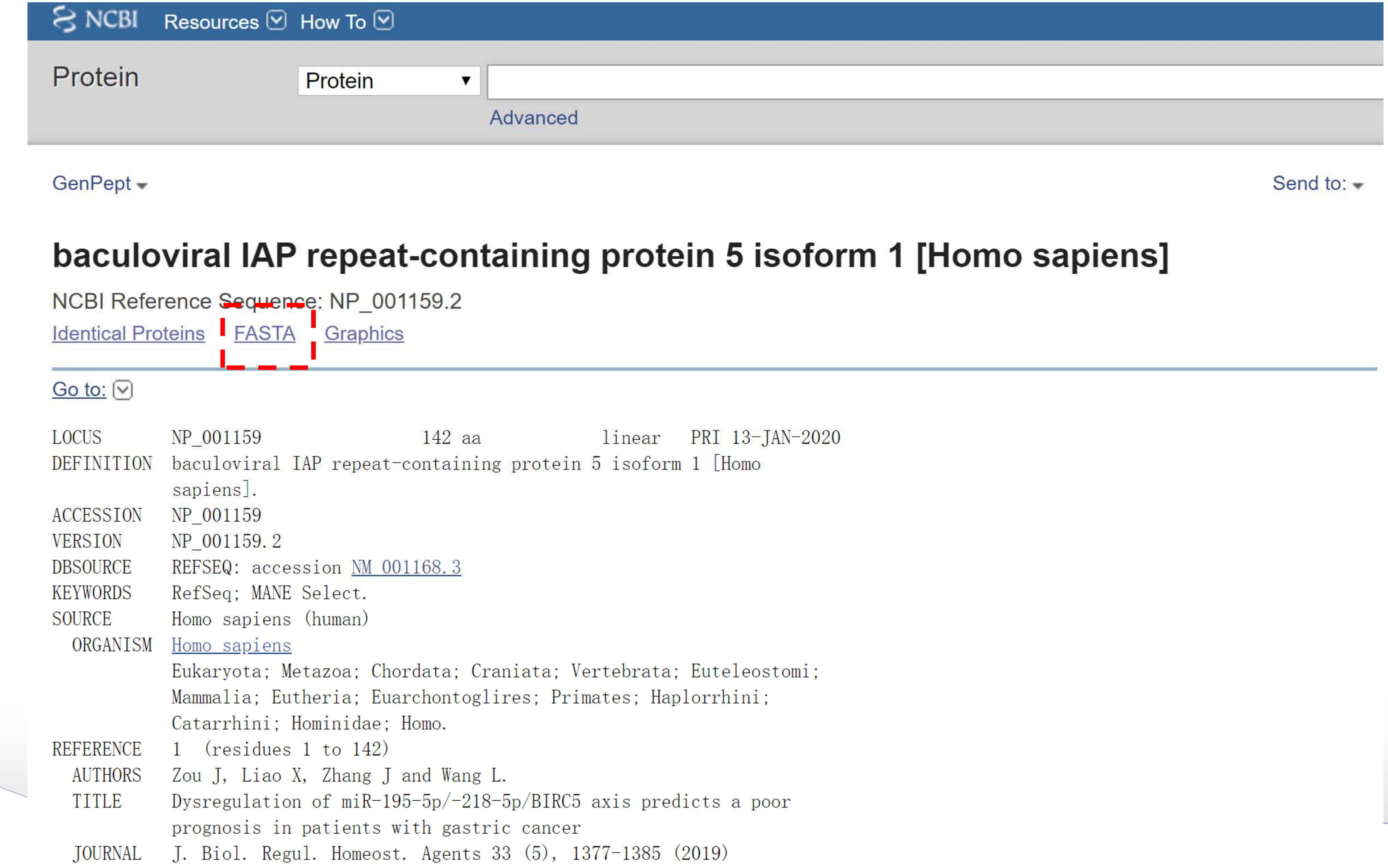
获取FASTA序列



baculoviral IAP repeat-containing protein 5 isoform 1 [Homo sapiens]

NCBI Reference Sequence: NP_001159.2

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LOCUS       NP_001159                142 aa            linear   PRI 13-JAN-2020
DEFINITION  baculoviral IAP repeat-containing protein 5 isoform 1 [Homo
            sapiens].
ACCESSION   NP_001159
VERSION     NP_001159.2
DBSOURCE    REFSEQ: accession NM_001168.3
KEYWORDS    RefSeq; MANE Select.
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 142)
  AUTHORS   Zou J, Liao X, Zhang J and Wang L.
  TITLE     Dysregulation of miR-195-5p/-218-5p/BIRC5 axis predicts a poor
            prognosis in patients with gastric cancer
  JOURNAL   J. Biol. Regul. Homeost. Agents 33 (5), 1377-1385 (2019)
```

FASTA格式的序列

baculoviral IAP repeat-containing protein 5 isoform 1 [Homo sapiens]

NCBI Reference Sequence: NP_001159.2

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>NP_001159.2 baculoviral IAP repeat-containing protein 5 isoform 1 [Homo sapiens]
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MD
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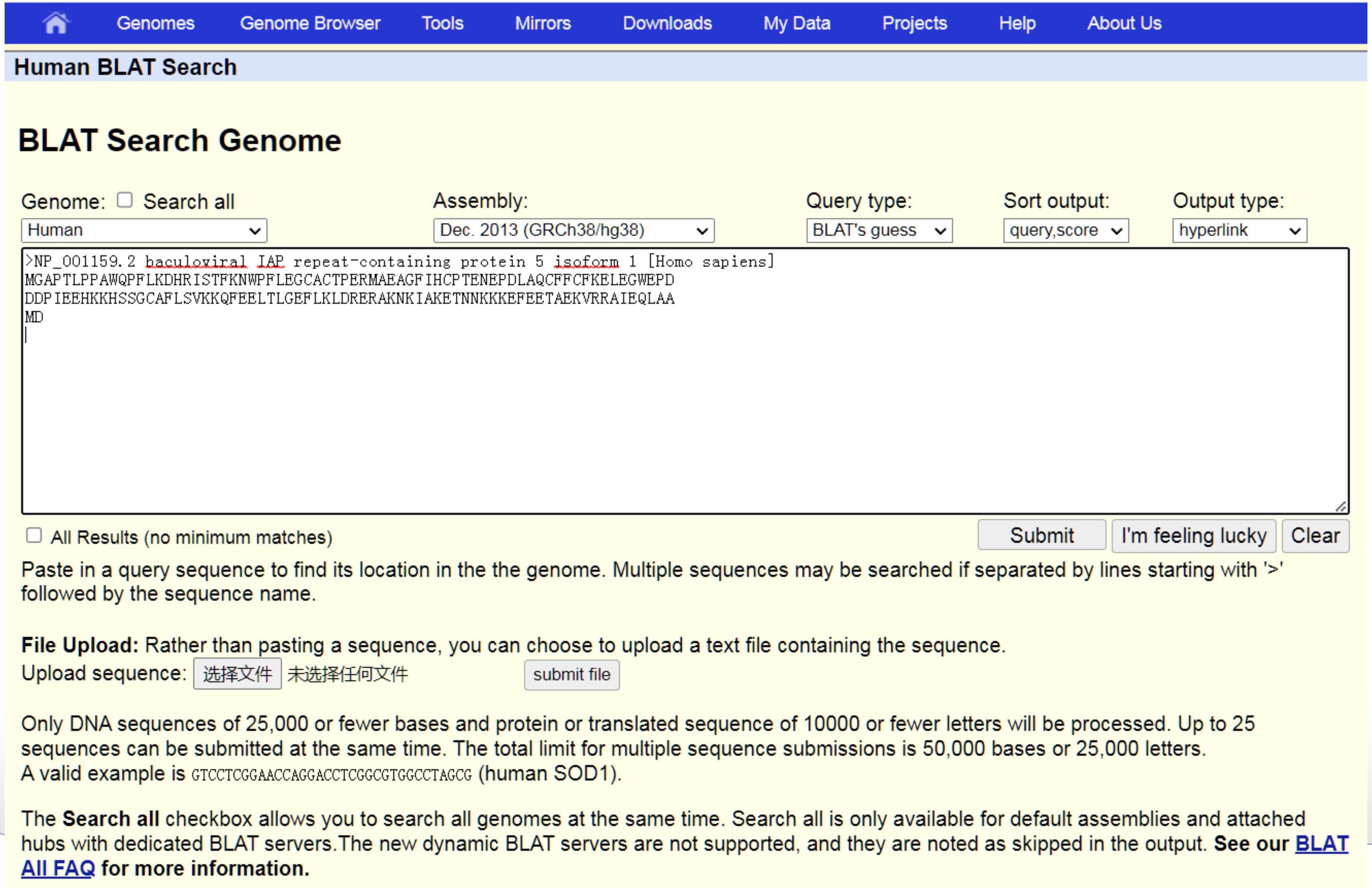
UCSC BLAT

- ❐ http://genome.ucsc.edu/cgi-bin/hgBlat



Human BLAT Search

BLAT Search Genome

Genome: ☐ Search all — Human

Assembly: Dec. 2013 (GRCh38/hg38)

Query type: BLAT's guess

Sort output: query,score

Output type: hyperlink

```
>NP_001159.2 baculoviral IAP repeat-containing protein 5 isoform 1 [Homo sapiens]
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DDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNKKKEFEETAEKVRRAIEQLAA
MD
```

☐ All Results (no minimum matches)

Paste in a query sequence to find its location in the the genome. Multiple sequences may be searched if separated by lines starting with '>' followed by the sequence name.

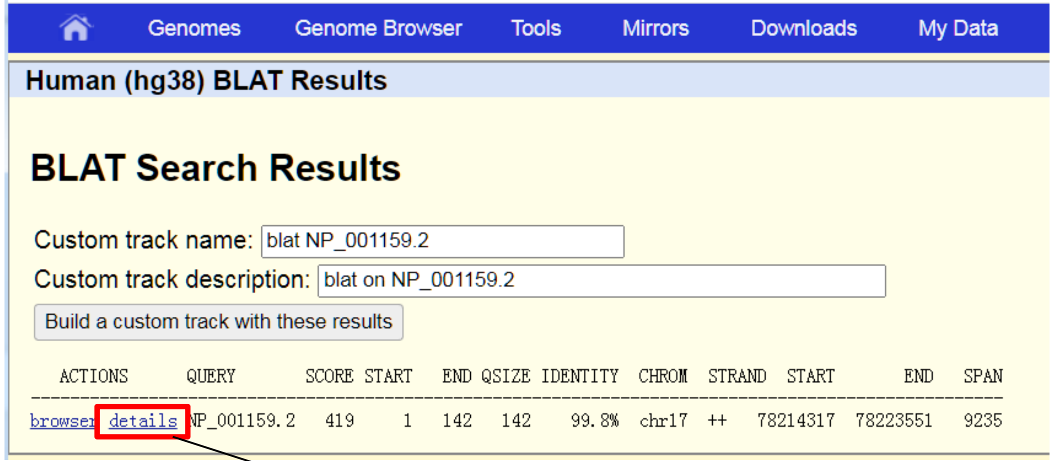
File Upload: Rather than pasting a sequence, you can choose to upload a text file containing the sequence.

Upload sequence: 选择文件 未选择任何文件 submit file

Only DNA sequences of 25,000 or fewer bases and protein or translated sequence of 10000 or fewer letters will be processed. Up to 25 sequences can be submitted at the same time. The total limit for multiple sequence submissions is 50,000 bases or 25,000 letters.
A valid example is GTCCTCGGAACCAGGACCTCGGCGTGGCCTAGCG (human SOD1).

The **Search all** checkbox allows you to search all genomes at the same time. Search all is only available for default assemblies and attached hubs with dedicated BLAT servers.The new dynamic BLAT servers are not supported, and they are noted as skipped in the output. **See our BLAT All FAQ for more information.**

BLAT结果



Human (hg38) BLAT Results

BLAT Search Results

Custom track name: blat NP_001159.2

Custom track description: blat on NP_001159.2

Build a custom track with these results

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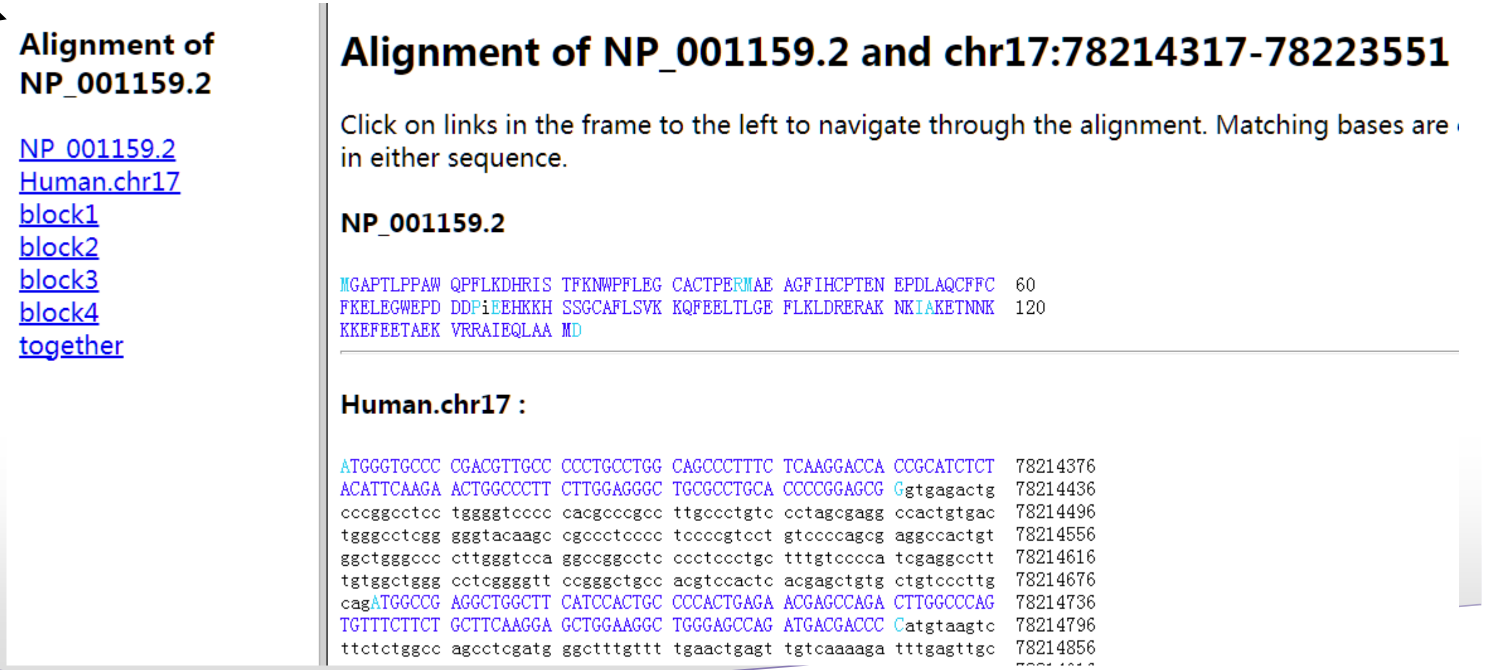

Alignment of NP_001159.2

NP_001159.2
Human.chr17
block1
block2
block3
block4
together

Alignment of NP_001159.2 and chr17:78214317-78223551

Click on links in the frame to the left to navigate through the alignment. Matching bases are
in either sequence.

NP_001159.2

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MGAPTLPPAW QPFLKDHRIS TFKNWPFLEG CACTPERMAE AGFIHCPTEN EPDLAQCFFC  60
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KKEFEETAEK VRRAIEQLAA MD
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Human.chr17 :

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ATGGGTGCCC CGACGTTGCC CCCTGCCTGG CAGCCCTTTC TCAAGGACCA CCGCATCTCT  78214376
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本体论 (Ontology)

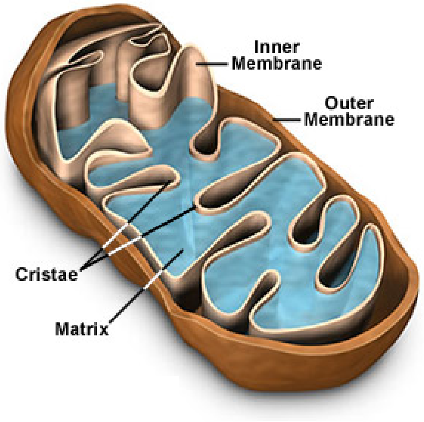
- 本体论
  - 形而上学 (metaphysics) 的一个分支
  - 关注自然及相关的存在
- Barry Smith (基督传教士)：本体论
  - 物体是什么、类型、结构、特性、事件、过程以及关联等
- 本体包括:
  - 一系列术语的词汇
  - 定义
  - 相互之间逻辑关系的定义

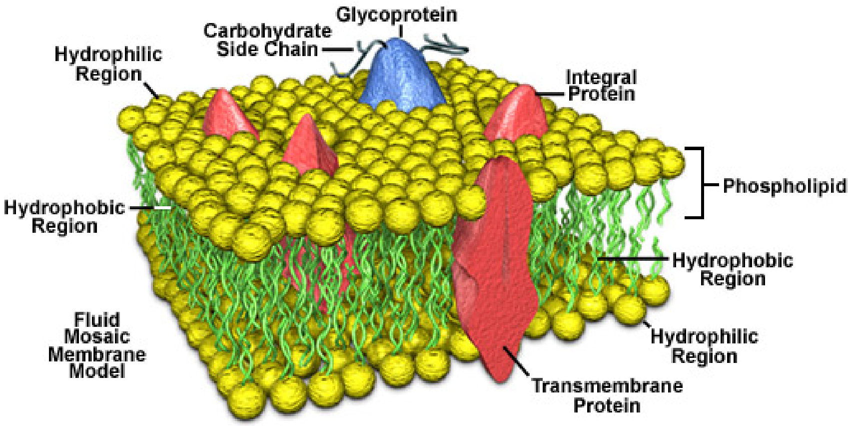
基因本体GO

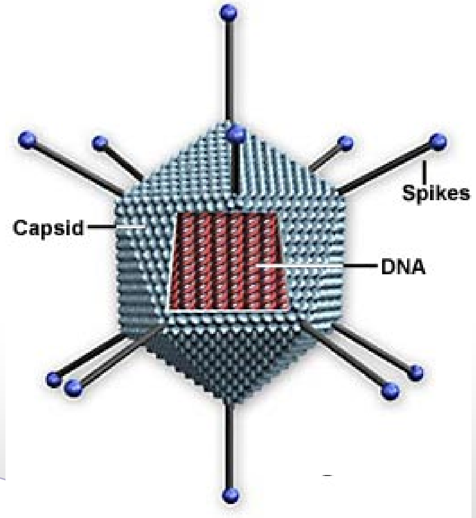
- 描述基因/蛋白质的功能：将已知的生物学知识进行分类表示
- 三类术语 (Term):
  - Cellular component: 在哪里？
    - 亚细胞结构、定位以及大分子复合物
    - *Nucleus*, *telomere*和*RNA polymerase II holoenzyme*
  - Molecular function：我是谁？
    - 基本的活性或任务
    - *Carbohydrate binding*和 *ATPase activity*
  - Biological process: 干什么？
    - 生物学目标或目的
    - *Mitosis*或*purine metabolism*

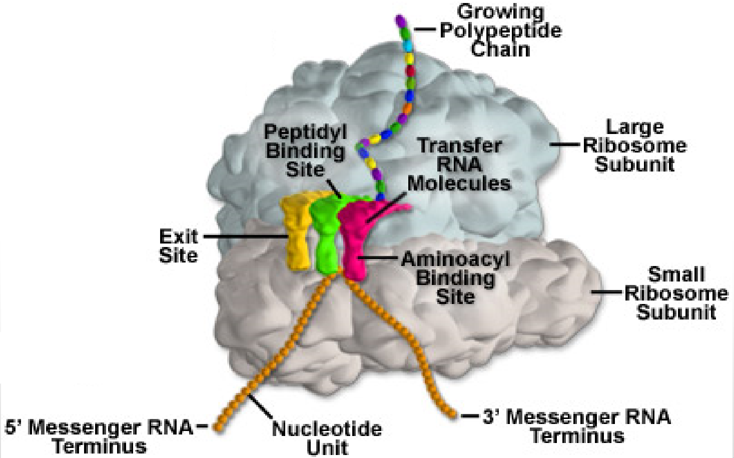
Cellular Component

基因产物在哪里？



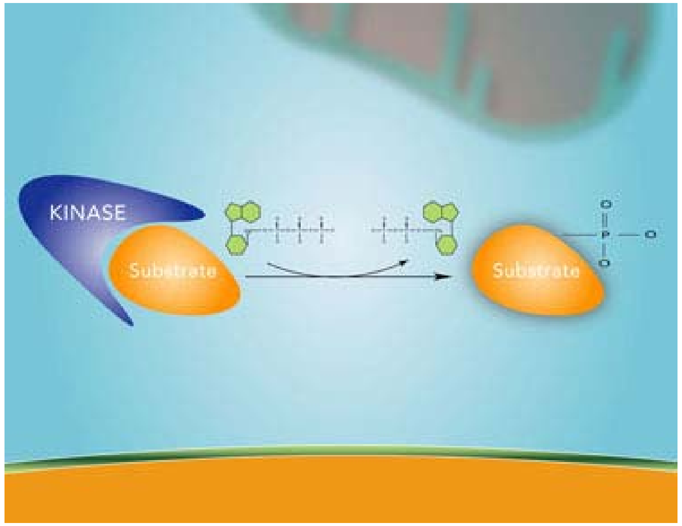




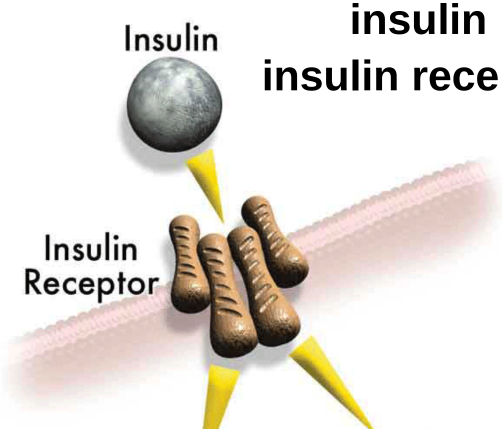


Molecular Function

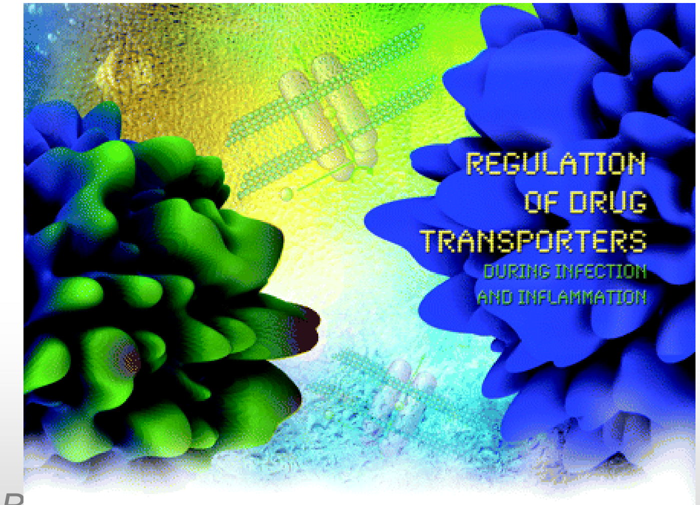
基因产物的活性或任务



Kinase activity

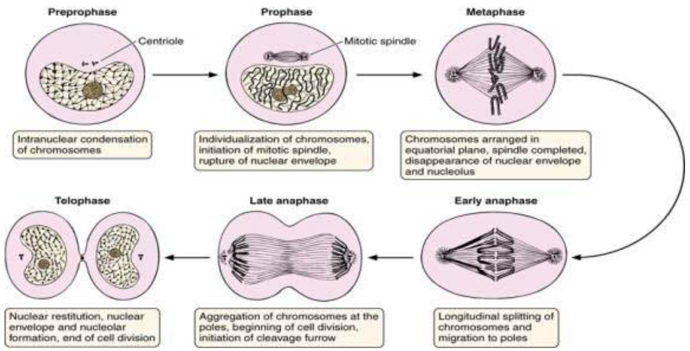


insulin binding
insulin receptor activity

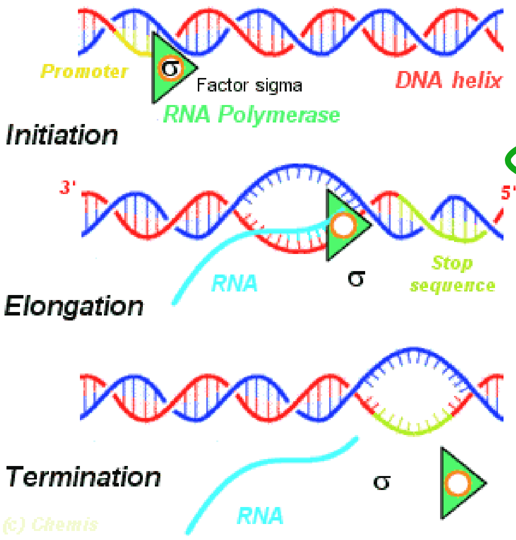


drug transporter activity

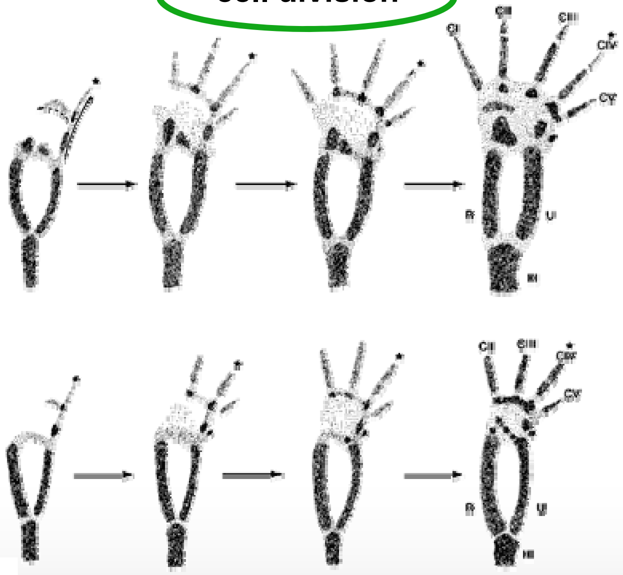
Biological Process



cell division



transcription



limb development

Courtship behavior

GO术语包含的内容

- **term**: gluconeogenesis (糖原异生)
- **id**: GO:0006094
- **definition**: The formation of glucose from noncarbohydrate precursors, such as pyruvate, amino acids and glycerol.
- **Synonym**: glucose biosynthesis (葡萄糖生物合成)

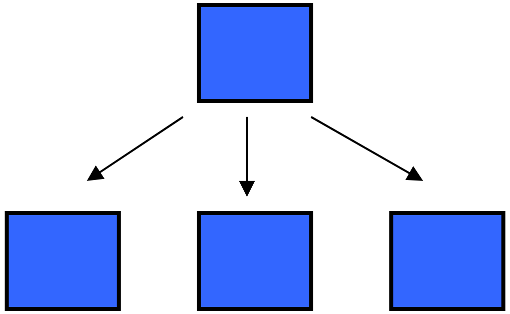
GO术语不包含的内容

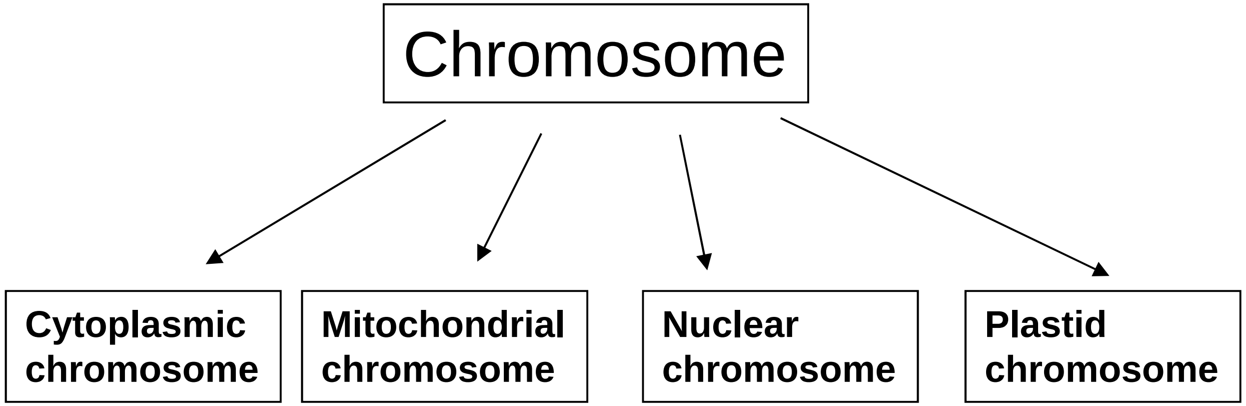
- GO仅包括正常的功能和过程
  - 不包括疾病过程
  - 不包括实验条件
- 不考虑进化关系
- 不包括基因产物本身
- 不是基因命名的体系

基因本体的结构

- 基因本体被组织为层次性的有向非循环图 **(Directed acyclic graph, DAG)**
- 每个术语
  - 可以有一个多个父亲术语
  - **0**个，**1**个或多个孩子术语
- 术语通过两类关系连接
  - is-a
  - part-of

父子关系





Chromosome

Cytoplasmic chromosome

Mitochondrial chromosome

Nuclear chromosome

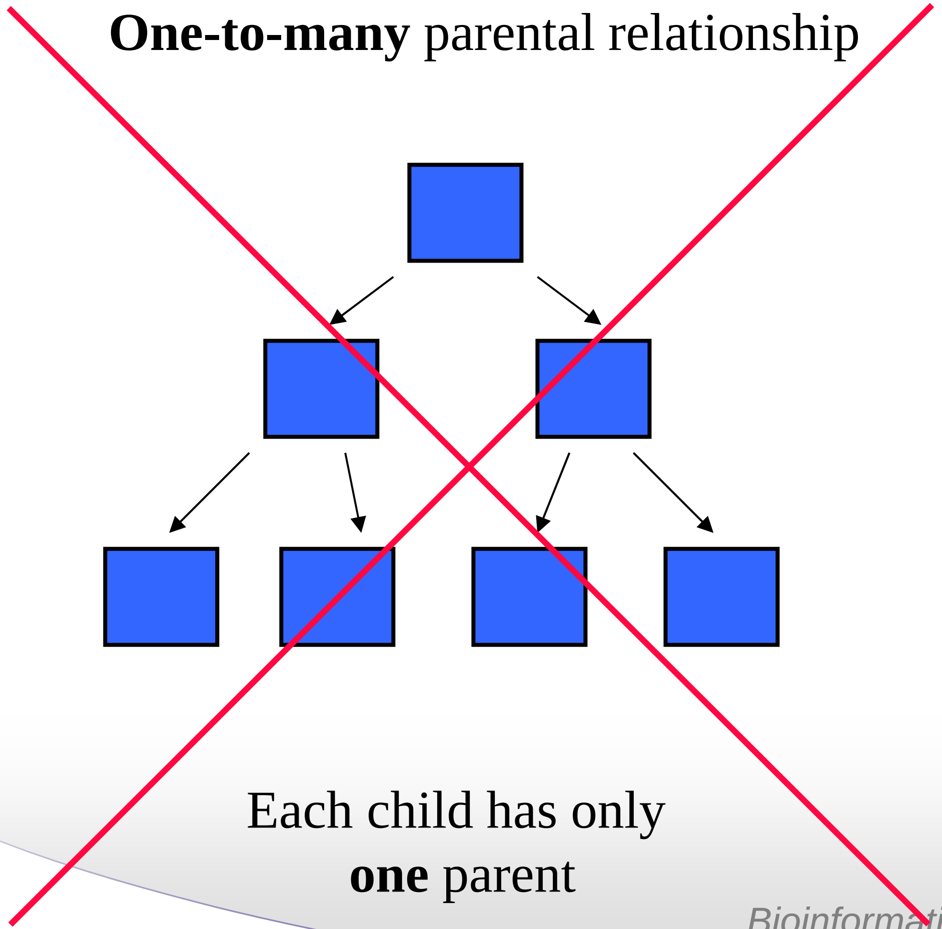
Plastid chromosome

孩子术语是父亲术语的一个子集或实例

父子关系

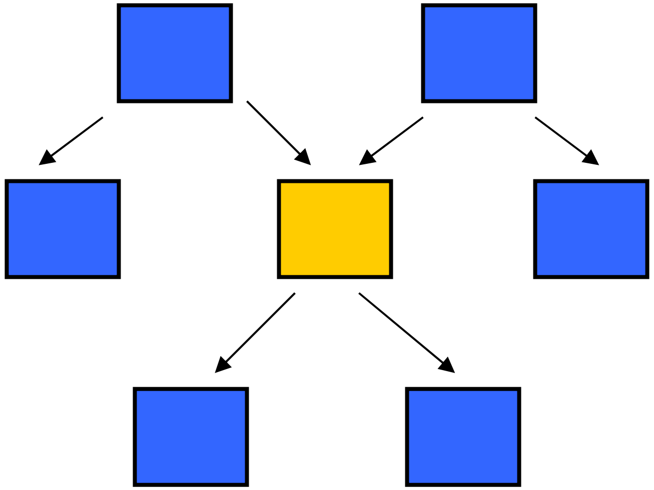
DAG: Directed Acyclic Graph

One-to-many parental relationship



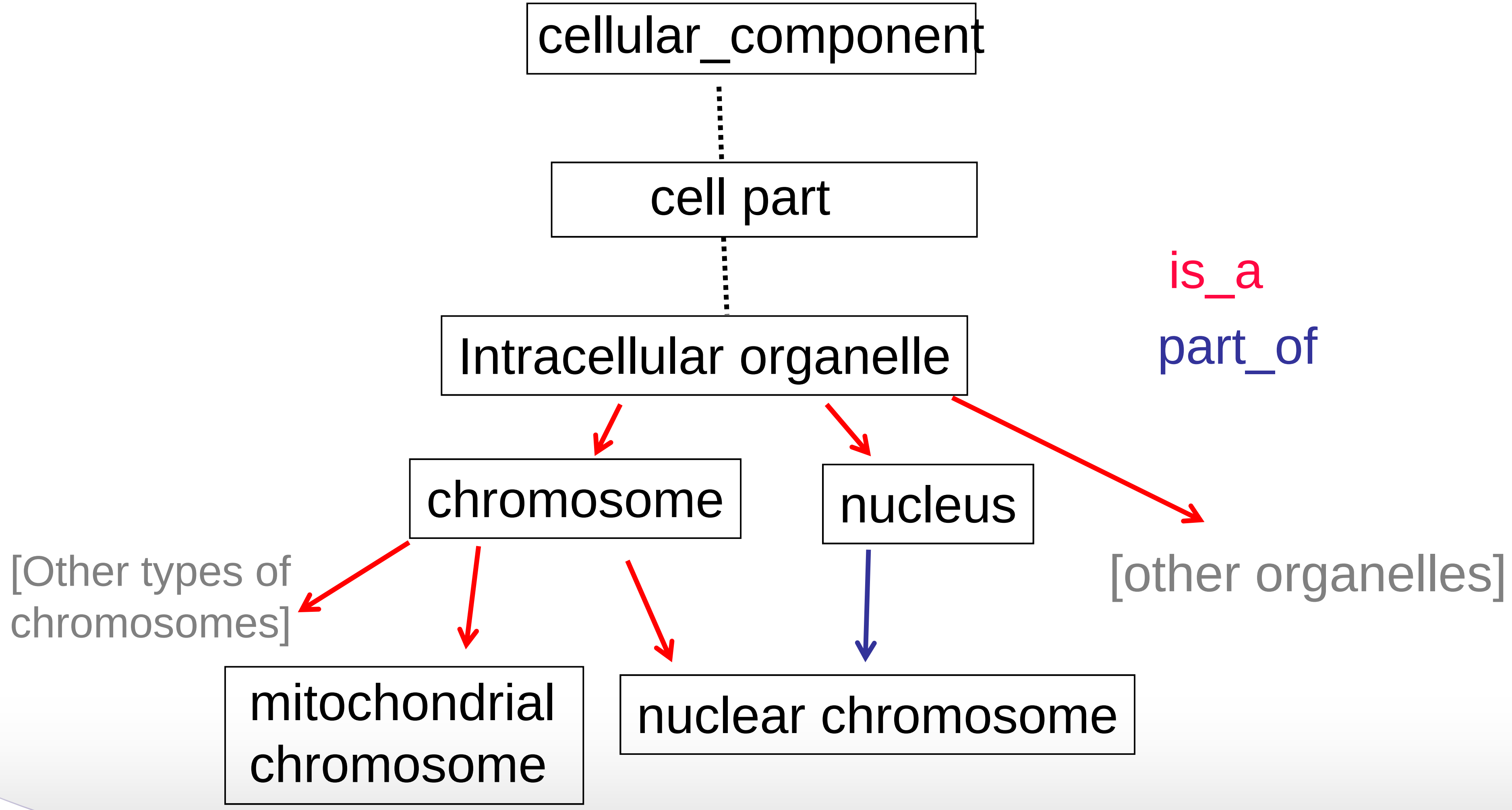
Each child has only
one parent

Many-to-many parental relationship



Each child may have
one or more parents

有向非循环图的实例



cellular_component

cell part

Intracellular organelle

chromosome

nucleus

[other organelles]

[Other types of chromosomes]

mitochondrial chromosome

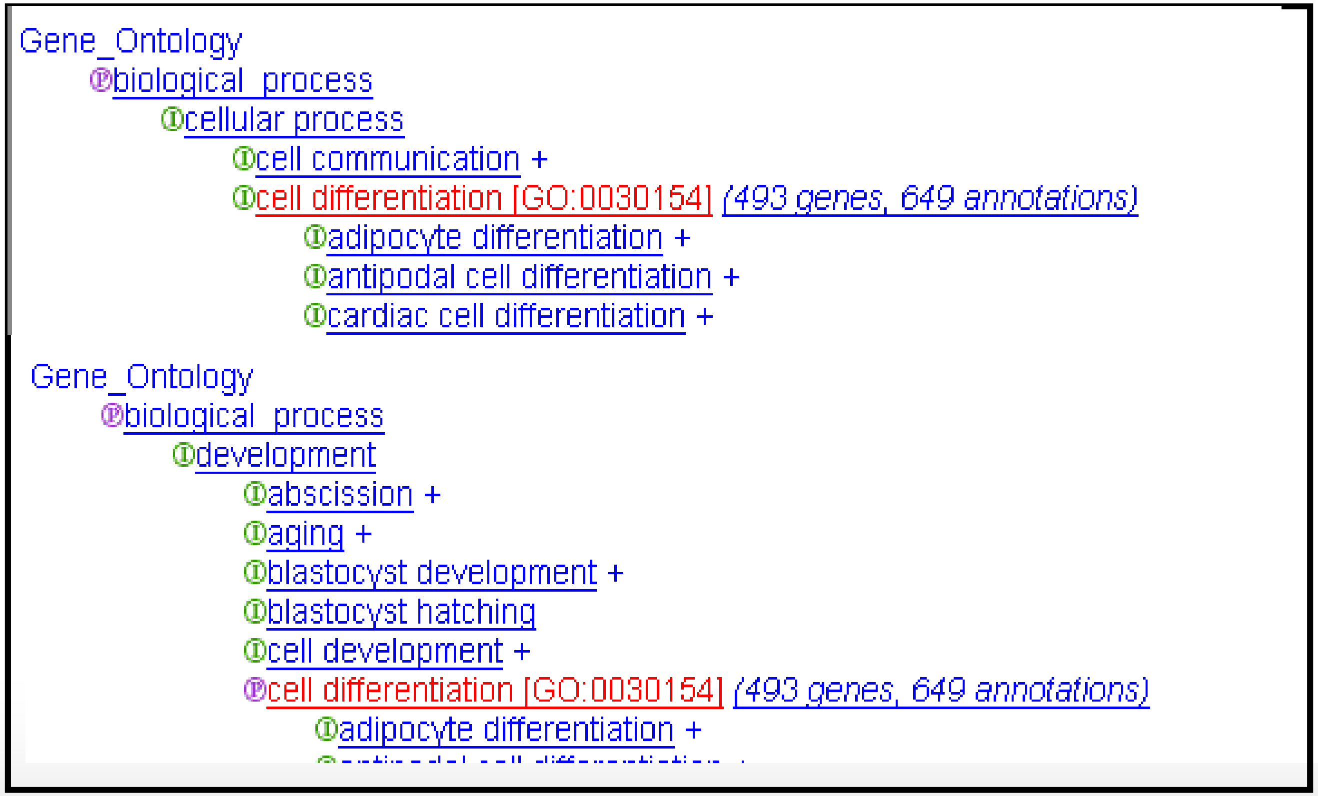
nuclear chromosome

is_a

part_of

True Path Rule

❐ 从孩子术语到上层的父亲术语的路径必须是真实的



Gene_Ontology
  Ⓟbiological_process
    Ⓘcellular process
      Ⓘcell communication +
      Ⓘcell differentiation [GO:0030154] (493 genes, 649 annotations)
        Ⓘadipocyte differentiation +
        Ⓘantipodal cell differentiation +
        Ⓘcardiac cell differentiation +

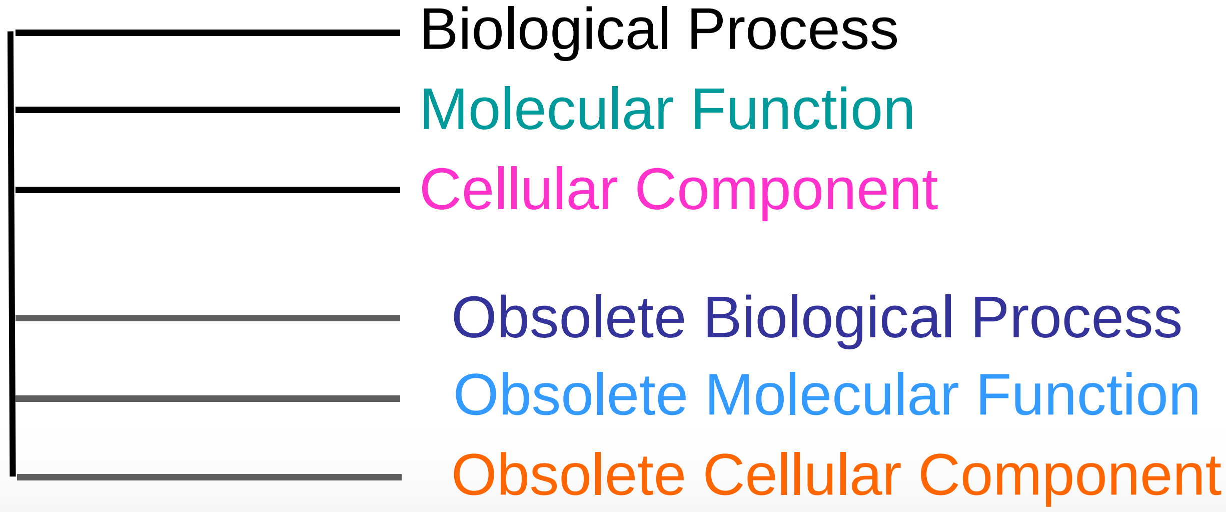
Gene_Ontology
  Ⓟbiological_process
    Ⓘdevelopment
      Ⓘabscission +
      Ⓘaging +
      Ⓘblastocyst development +
      Ⓘblastocyst hatching
      Ⓘcell development +
      Ⓟcell differentiation [GO:0030154] (493 genes, 649 annotations)
        Ⓘadipocyte differentiation +

is-a Ⓘ

part-of Ⓟ

基因本体的维护

- 废弃 (Obsolete): 术语被去除或重新定义
- 基因本体的ID永不删除
- 对每一个废弃的术语，需要说明为何该术语废弃



Biological Process

Molecular Function

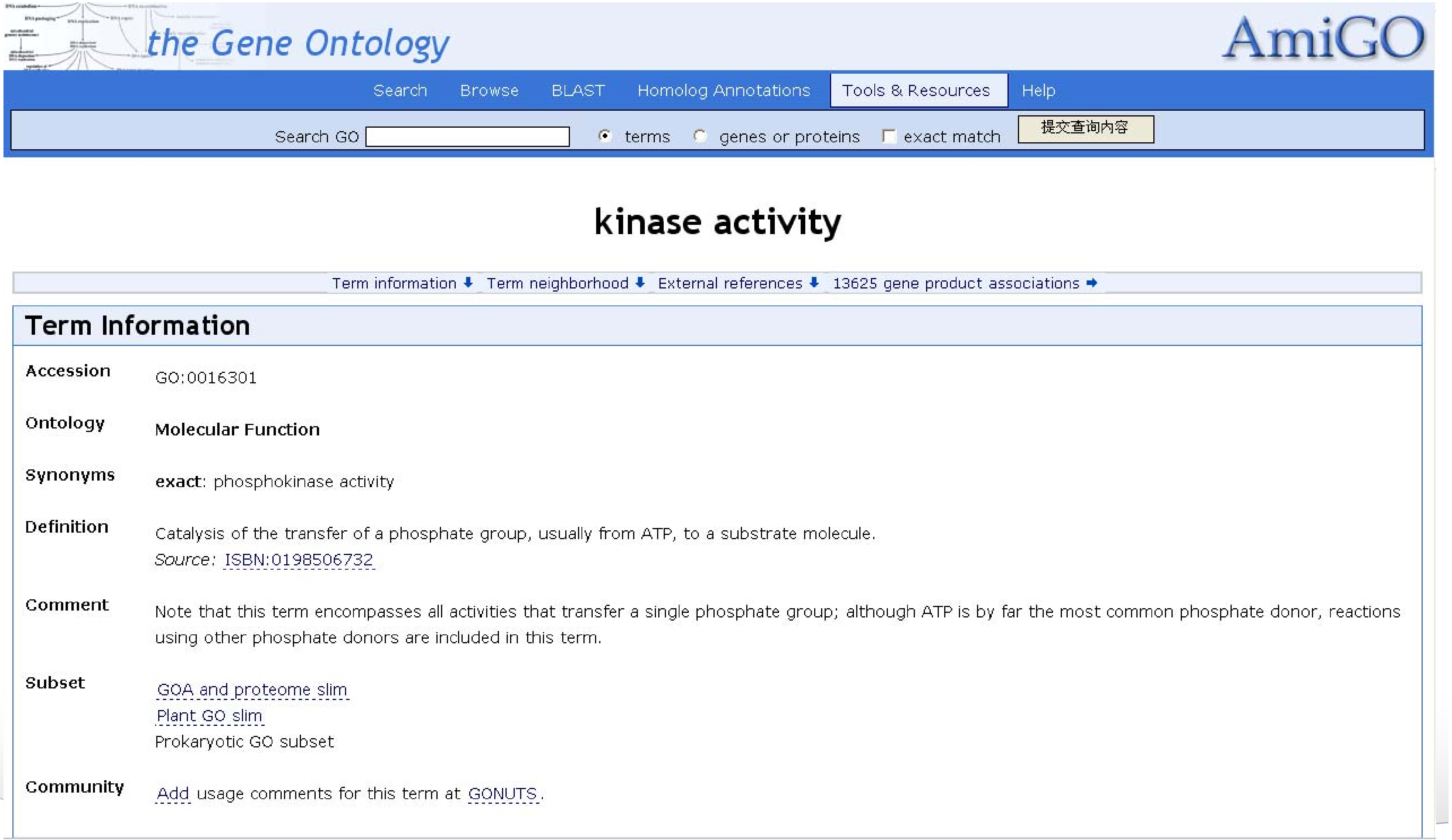
Cellular Component

Obsolete Biological Process

Obsolete Molecular Function

Obsolete Cellular Component

AmiGO

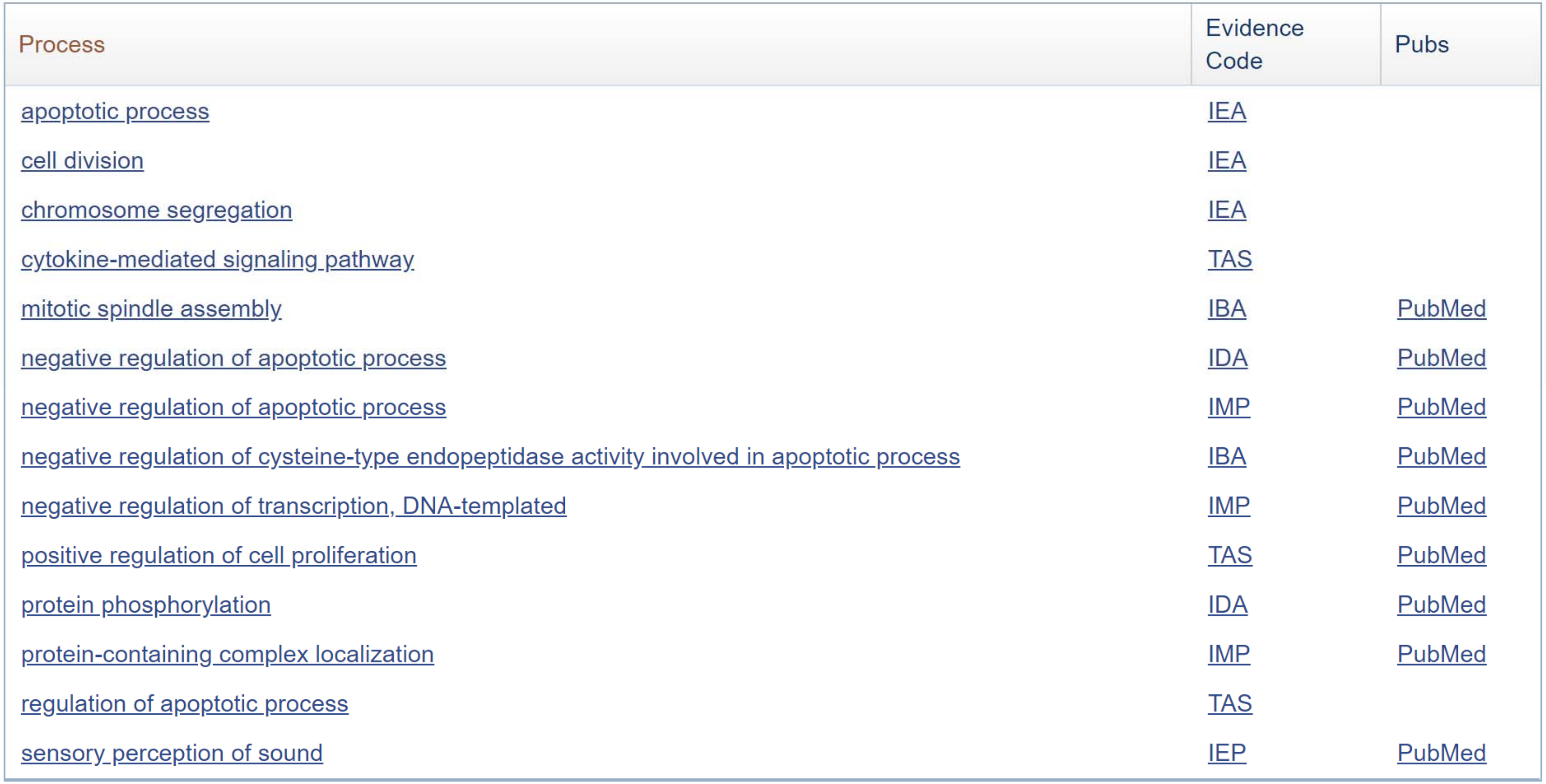


kinase activity

Term Information

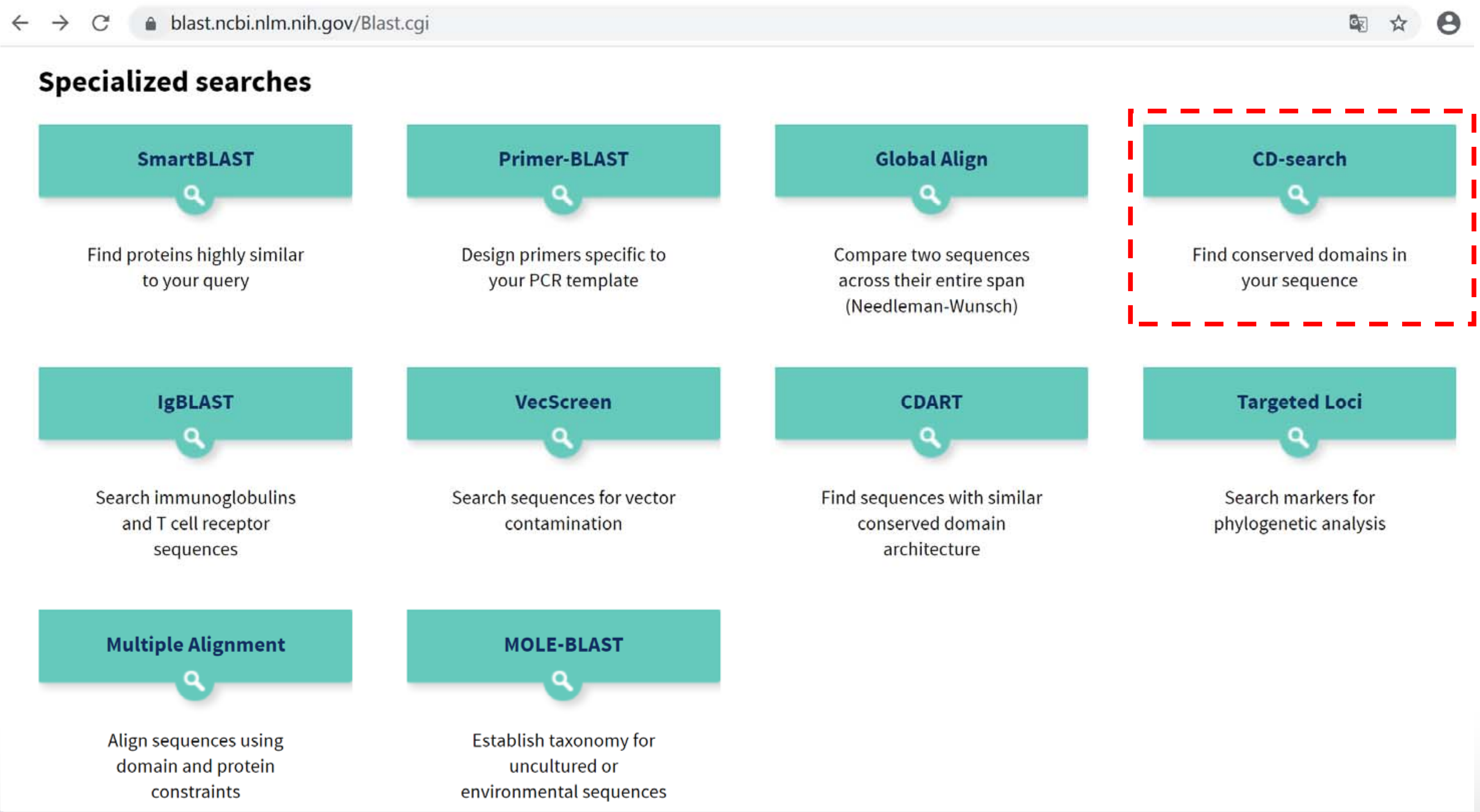
Accession	GO:0016301
Ontology	**Molecular Function**
Synonyms	**exact**: phosphokinase activity
Definition	Catalysis of the transfer of a phosphate group, usually from ATP, to a substrate molecule. *Source:* ISBN:0198506732
Comment	Note that this term encompasses all activities that transfer a single phosphate group; although ATP is by far the most common phosphate donor, reactions using other phosphate donors are included in this term.
Subset	GOA and proteome slim Plant GO slim Prokaryotic GO subset
Community	Add usage comments for this term at GONUTS.

功能注释：Gene Ontology



Process	Evidence Code	Pubs
apoptotic process	IEA	
cell division	IEA	
chromosome segregation	IEA	
cytokine-mediated signaling pathway	TAS	
mitotic spindle assembly	IBA	PubMed
negative regulation of apoptotic process	IDA	PubMed
negative regulation of apoptotic process	IMP	PubMed
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	IBA	PubMed
negative regulation of transcription, DNA-templated	IMP	PubMed
positive regulation of cell proliferation	TAS	PubMed
protein phosphorylation	IDA	PubMed
protein-containing complex localization	IMP	PubMed
regulation of apoptotic process	TAS	
sensory perception of sound	IEP	PubMed

PHI-BLAST: find domain



Specialized searches

SmartBLAST

Find proteins highly similar to your query

Primer-BLAST

Design primers specific to your PCR template

Global Align

Compare two sequences across their entire span (Needleman-Wunsch)

CD-search

Find conserved domains in your sequence

IgBLAST

Search immunoglobulins and T cell receptor sequences

VecScreen

Search sequences for vector contamination

CDART

Find sequences with similar conserved domain architecture

Targeted Loci

Search markers for phylogenetic analysis

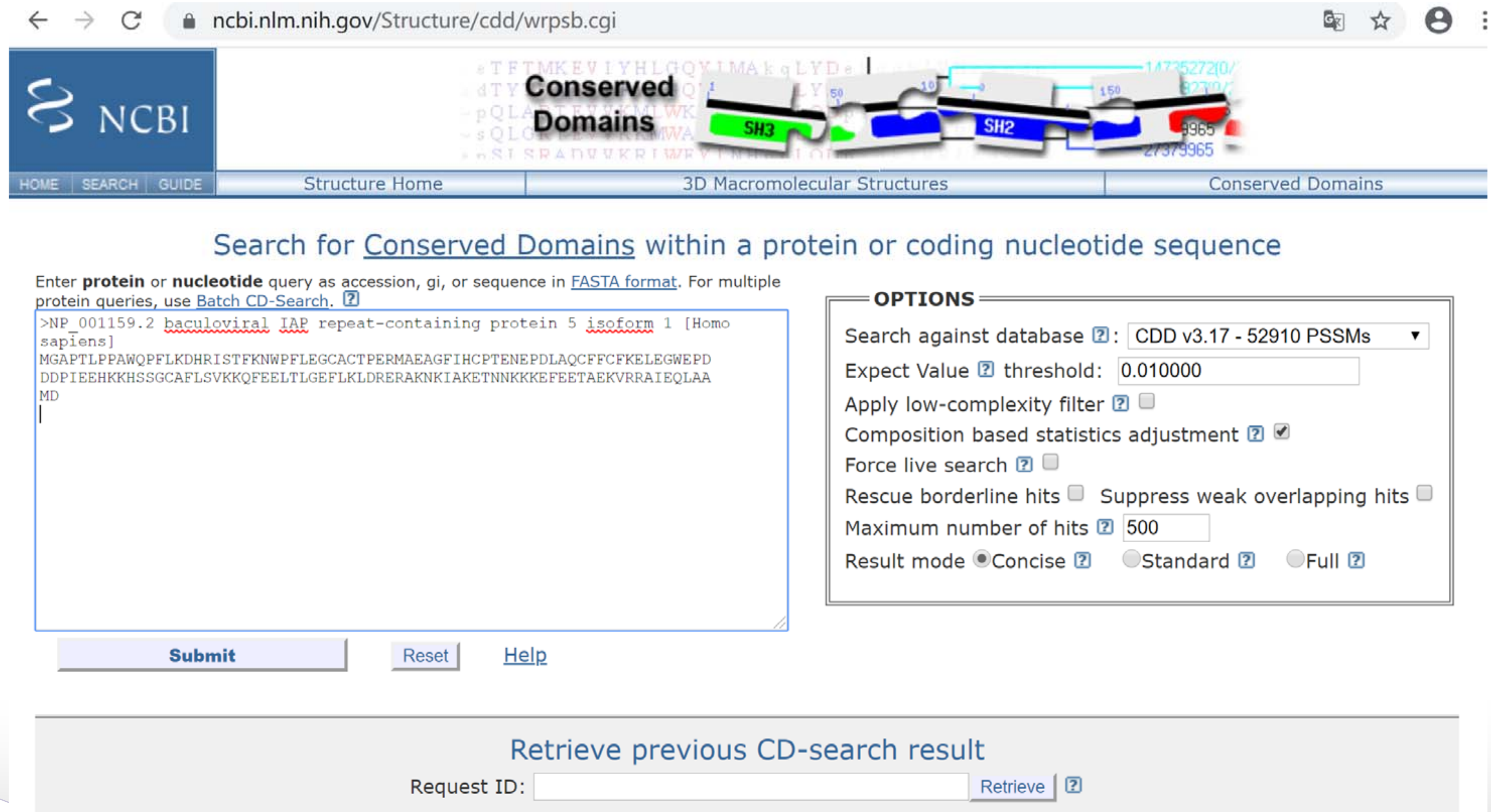
Multiple Alignment

Align sequences using domain and protein constraints

MOLE-BLAST

Establish taxonomy for uncultured or environmental sequences

填入蛋白质的FASTA序列



Search for Conserved Domains within a protein or coding nucleotide sequence

Enter **protein** or **nucleotide** query as accession, gi, or sequence in FASTA format. For multiple protein queries, use Batch CD-Search.

```
>NP_001159.2 baculoviral IAP repeat-containing protein 5 isoform 1 [Homo
sapiens]
MGAPTLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEPD
DDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNKKKEFEETAEKVRRAIEQLAA
MD
```

OPTIONS

Search against database: CDD v3.17 - 52910 PSSMs

Expect Value threshold: 0.010000

Apply low-complexity filter ☐

Composition based statistics adjustment ☑

Force live search ☐

Rescue borderline hits ☐ Suppress weak overlapping hits ☐

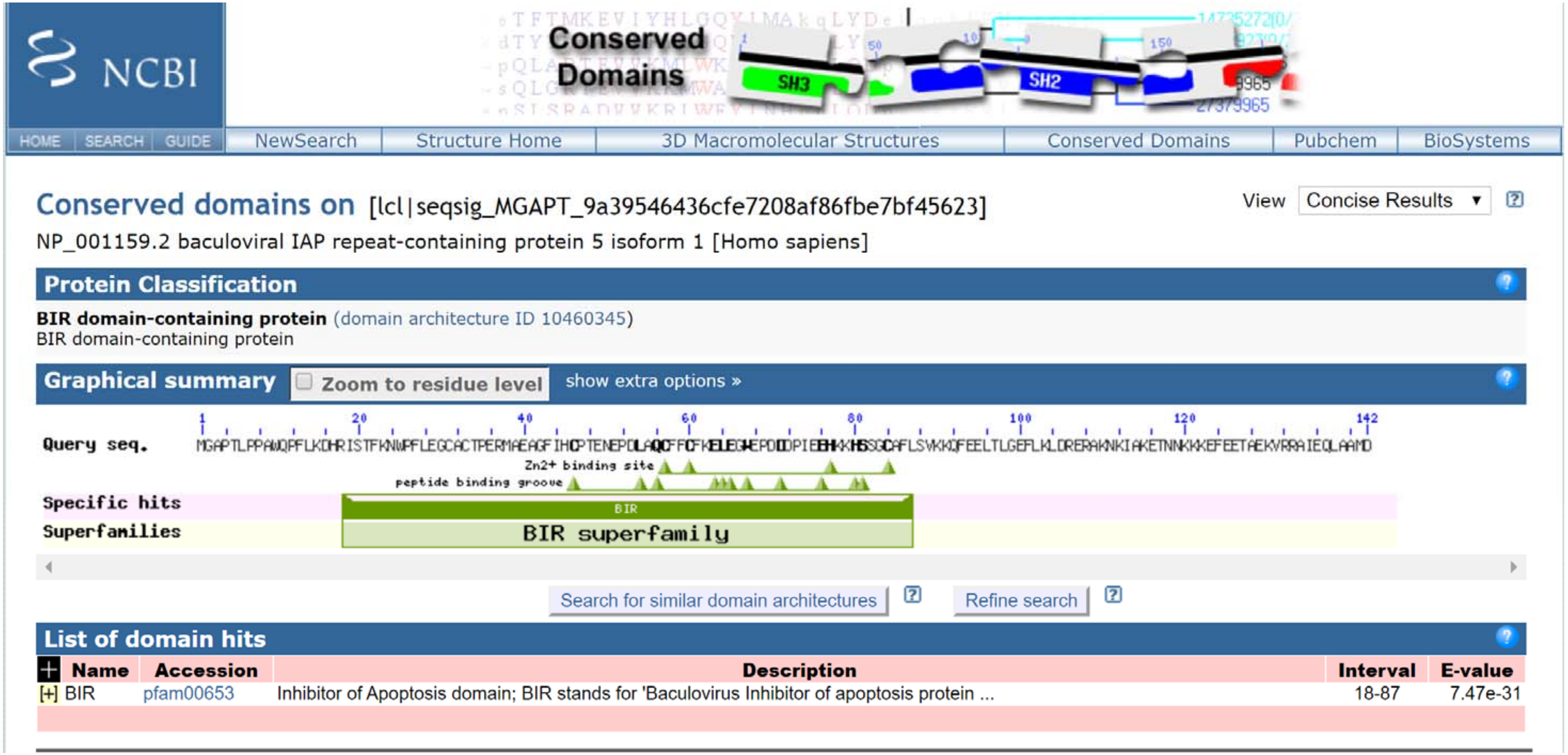
Maximum number of hits 500

Result mode ● Concise ○ Standard ○ Full

Retrieve previous CD-search result

Request ID:

BIR domain



Conserved domains on [lcl|seqsig_MGAPT_9a39546436cfe7208af86fbe7bf45623]

View: Concise Results ▾

NP_001159.2 baculoviral IAP repeat-containing protein 5 isoform 1 [Homo sapiens]

Protein Classification

BIR domain-containing protein (domain architecture ID 10460345)
BIR domain-containing protein

Graphical summary ☐ Zoom to residue level   show extra options »

Search for similar domain architectures   Refine search

List of domain hits

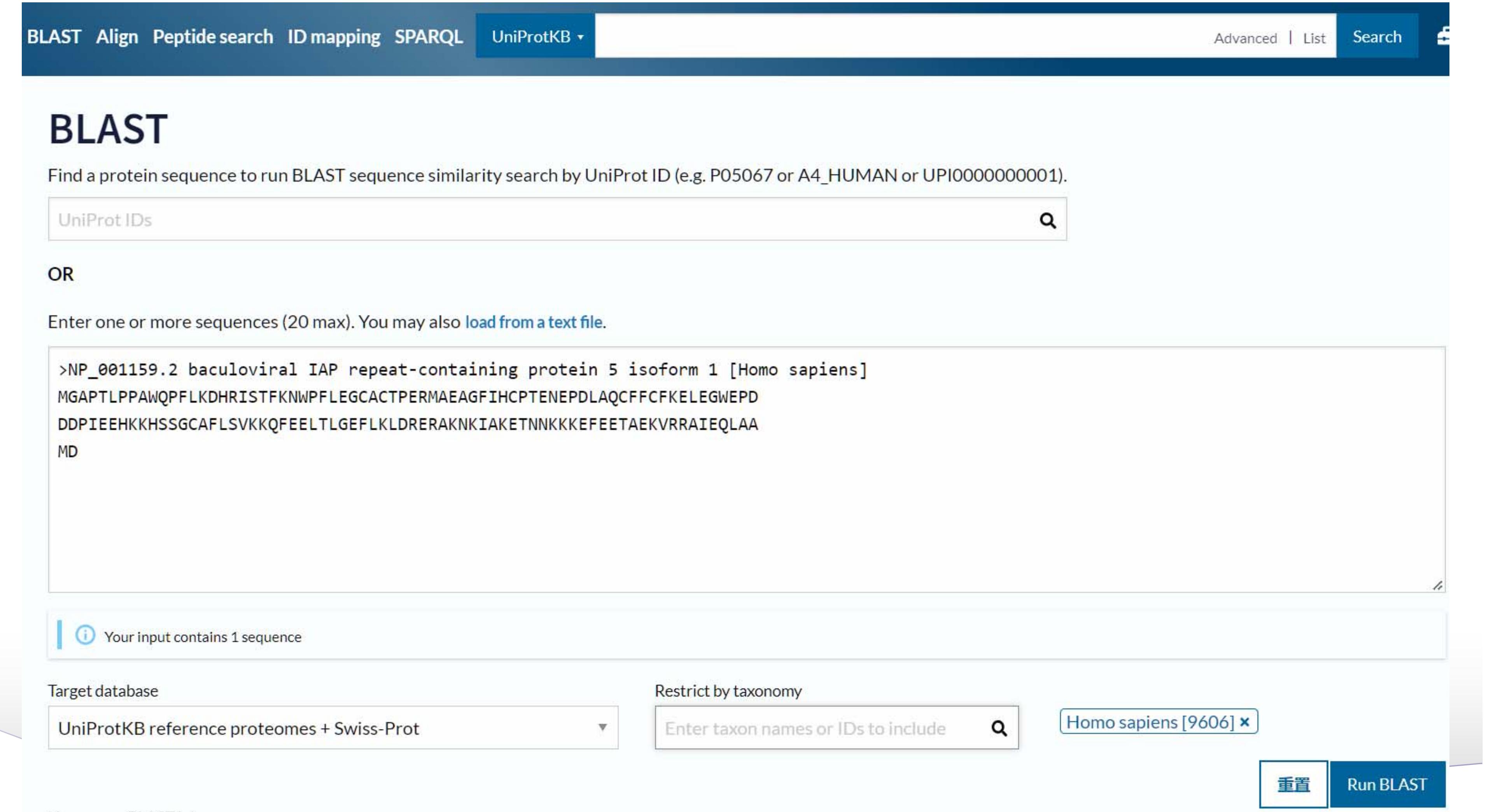
Name	Accession	Description	Interval	E-value
[+] BIR	pfam00653	Inhibitor of Apoptosis domain; BIR stands for 'Baculovirus Inhibitor of apoptosis protein ...	18-87	7.47e-31

结论1

- **核酸序列标识符：NM_001168.3**
- **该基因为人类BIRC5基因**
- **人类BIRC5蛋白质包含142个氨基酸，序列标识符为：NP_001159.2**
- **染色体定位：17q25.3**
- **基因组坐标：78214253-78225635/ 78214317-78223551（BLAT）**
- **功能分析：凋亡、细胞分裂、染色体分离等**
- **BIRC5具有保守的功能结构域BIR**

UniProt BLAST

- ❐ https://www.uniprot.org/blast



BLAST

Find a protein sequence to run BLAST sequence similarity search by UniProt ID (e.g. P05067 or A4_HUMAN or UPI0000000001).

OR

Enter one or more sequences (20 max). You may also load from a text file.

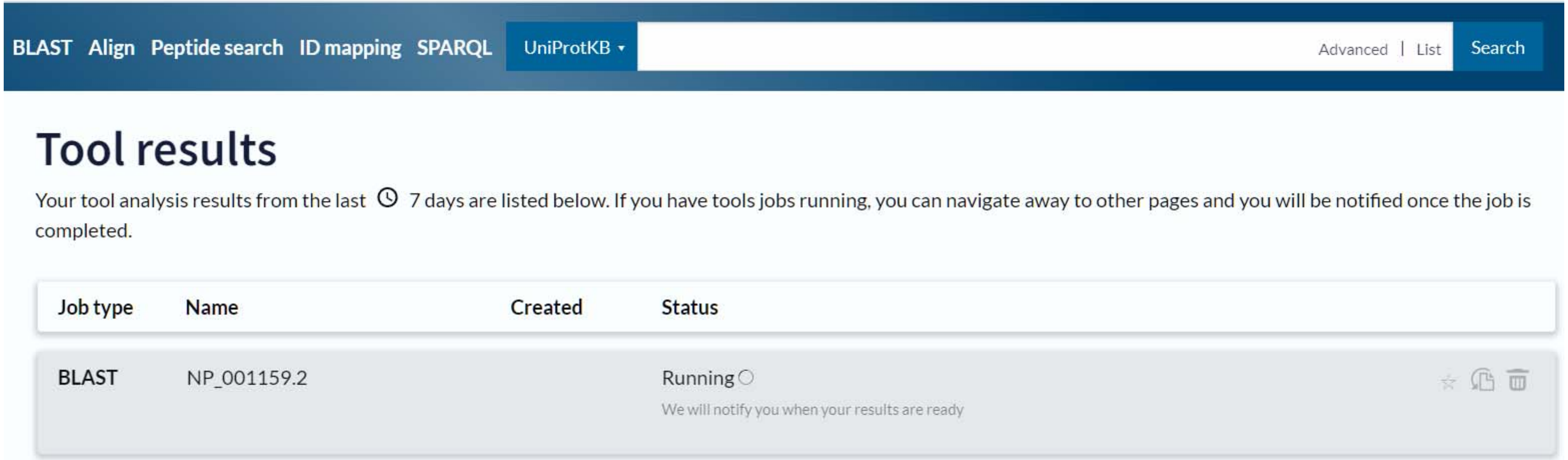
```
>NP_001159.2 baculoviral IAP repeat-containing protein 5 isoform 1 [Homo sapiens]
MGAPTLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEPD
DDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNKKKEFEETAEKVRRAIEQLAA
MD
```

Your input contains 1 sequence

Target database: UniProtKB reference proteomes + Swiss-Prot

Restrict by taxonomy: Homo sapiens [9606] ×

提交序列

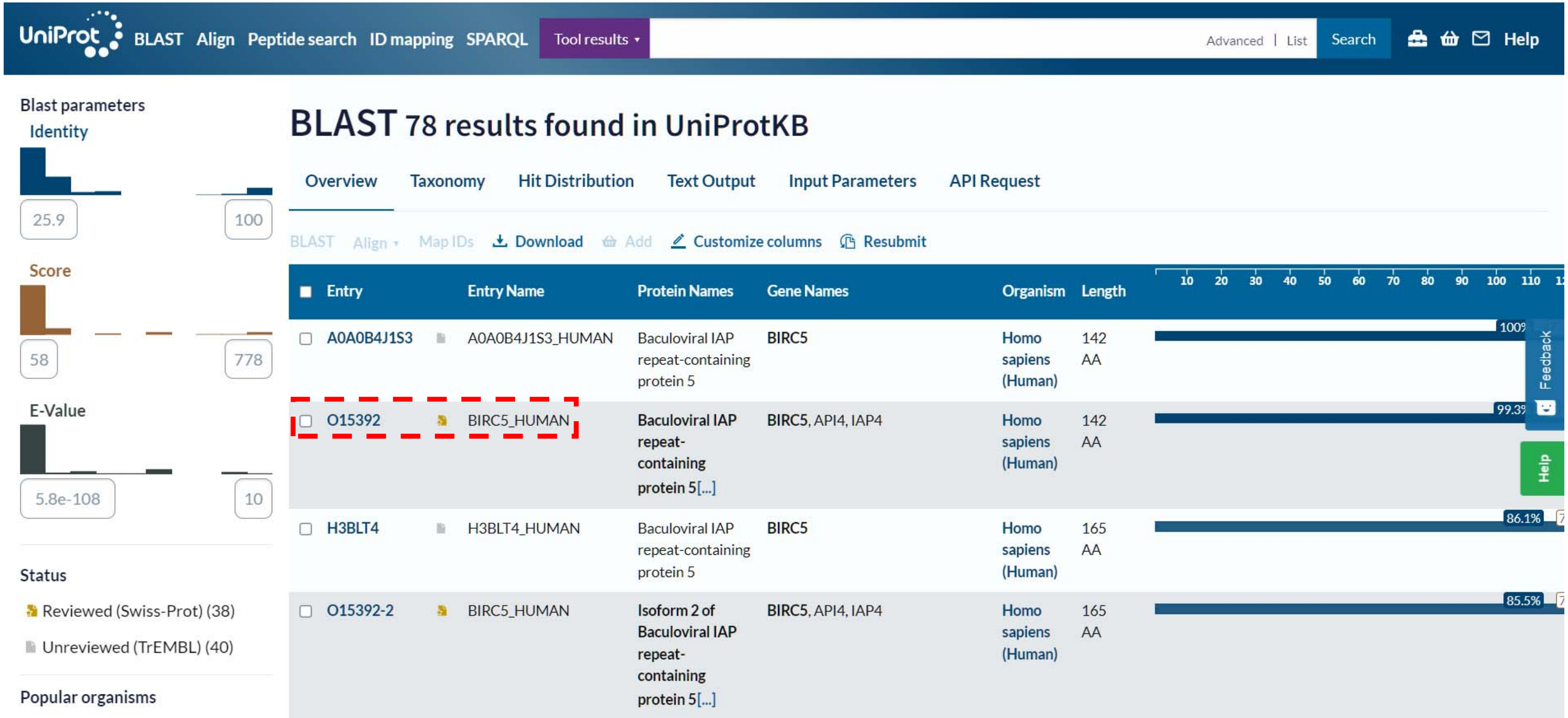


Tool results

Your tool analysis results from the last 7 days are listed below. If you have tools jobs running, you can navigate away to other pages and you will be notified once the job is completed.

Job type	Name	Created	Status
BLAST	NP_001159.2		Running ○ We will notify you when your results are ready

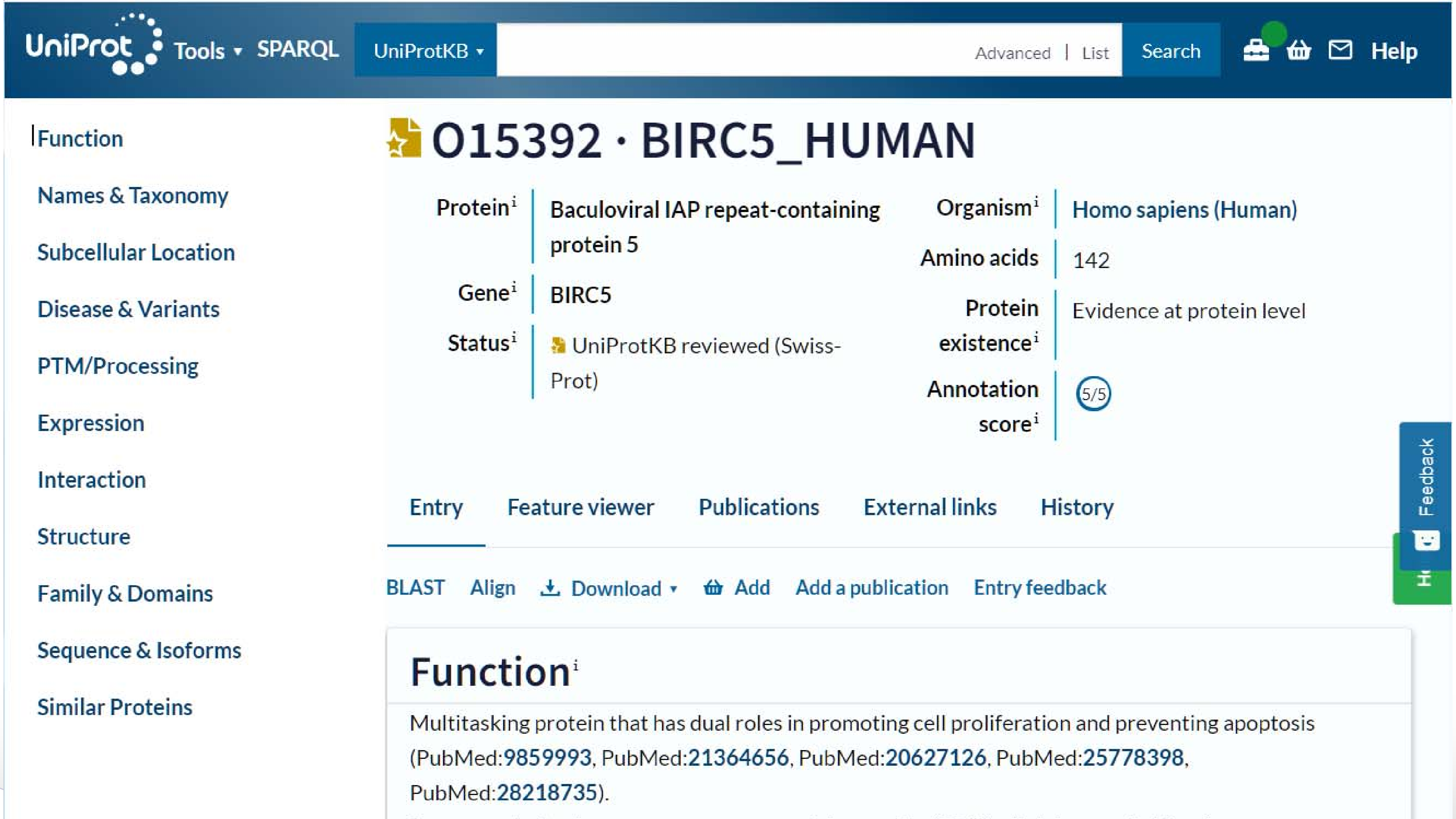
BIRC5：O15392



BLAST 78 results found in UniProtKB

☐	Entry	Entry Name	Protein Names	Gene Names	Organism	Length
☐	A0A0B4J1S3	A0A0B4J1S3_HUMAN	Baculoviral IAP repeat-containing protein 5	BIRC5	Homo sapiens (Human)	142 AA
☐	O15392	BIRC5_HUMAN	Baculoviral IAP repeat-containing protein 5[...]	BIRC5, API4, IAP4	Homo sapiens (Human)	142 AA
☐	H3BLT4	H3BLT4_HUMAN	Baculoviral IAP repeat-containing protein 5	BIRC5	Homo sapiens (Human)	165 AA
☐	O15392-2	BIRC5_HUMAN	Isoform 2 of Baculoviral IAP repeat-containing protein 5[...]	BIRC5, API4, IAP4	Homo sapiens (Human)	165 AA

BIRC5的蛋白质信息



O15392 · BIRC5_HUMAN

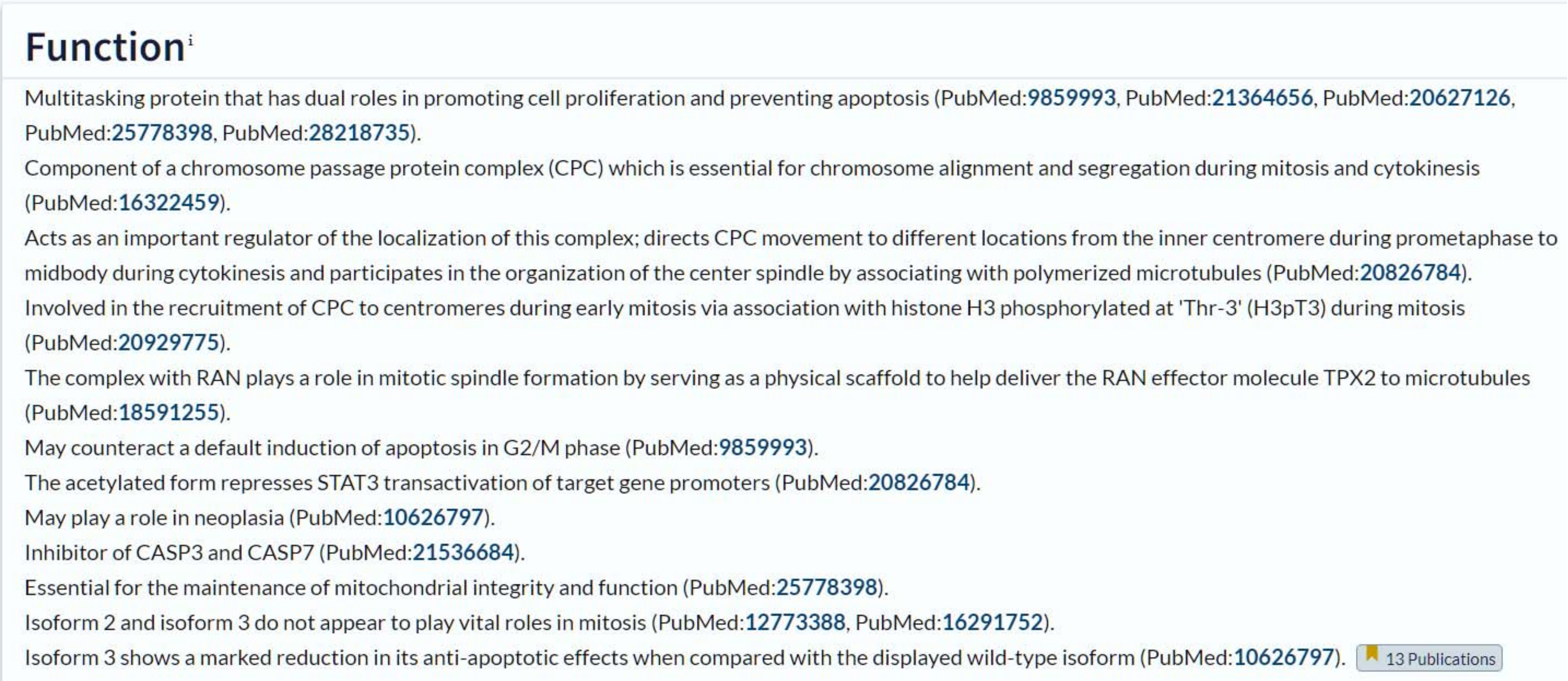
Protein	Baculoviral IAP repeat-containing protein 5	Organism	Homo sapiens (Human)
Gene	BIRC5	Amino acids	142
Status	UniProtKB reviewed (Swiss-Prot)	Protein existence	Evidence at protein level
		Annotation score	5/5

Function

Multitasking protein that has dual roles in promoting cell proliferation and preventing apoptosis (PubMed:9859993, PubMed:21364656, PubMed:20627126, PubMed:25778398, PubMed:28218735).

Component of a chromosome passage protein complex (CPC) which is essential for chromosome alignment and segregation during mitosis and cytokinesis (PubMed:16322459)

BIRC5的功能



Function

Multitasking protein that has dual roles in promoting cell proliferation and preventing apoptosis (PubMed:9859993, PubMed:21364656, PubMed:20627126, PubMed:25778398, PubMed:28218735).

Component of a chromosome passage protein complex (CPC) which is essential for chromosome alignment and segregation during mitosis and cytokinesis (PubMed:16322459).

Acts as an important regulator of the localization of this complex; directs CPC movement to different locations from the inner centromere during prometaphase to midbody during cytokinesis and participates in the organization of the center spindle by associating with polymerized microtubules (PubMed:20826784).

Involved in the recruitment of CPC to centromeres during early mitosis via association with histone H3 phosphorylated at 'Thr-3' (H3pT3) during mitosis (PubMed:20929775).

The complex with RAN plays a role in mitotic spindle formation by serving as a physical scaffold to help deliver the RAN effector molecule TPX2 to microtubules (PubMed:18591255).

May counteract a default induction of apoptosis in G2/M phase (PubMed:9859993).

The acetylated form represses STAT3 transactivation of target gene promoters (PubMed:20826784).

May play a role in neoplasia (PubMed:10626797).

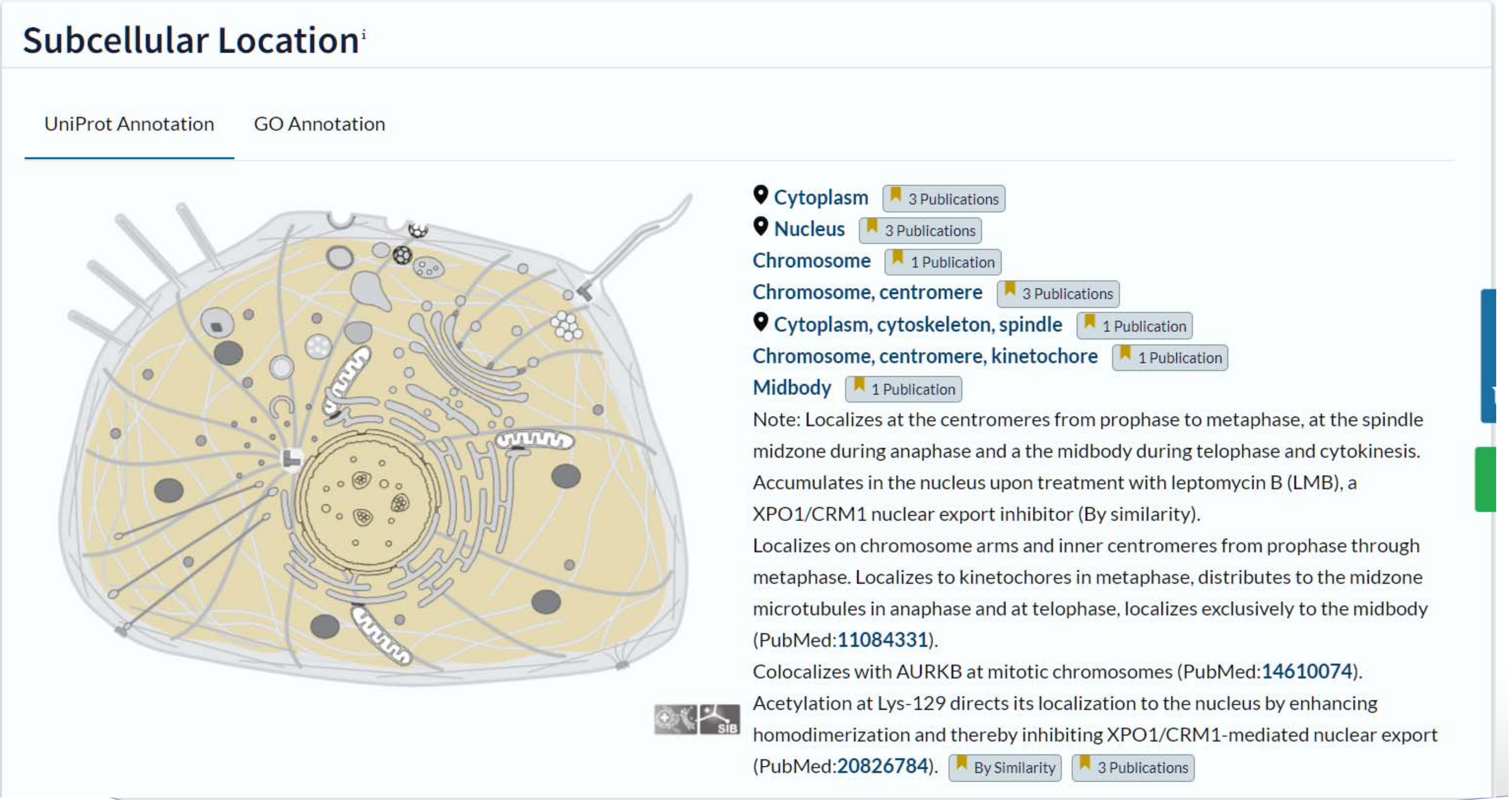
Inhibitor of CASP3 and CASP7 (PubMed:21536684).

Essential for the maintenance of mitochondrial integrity and function (PubMed:25778398).

Isoform 2 and isoform 3 do not appear to play vital roles in mitosis (PubMed:12773388, PubMed:16291752).

Isoform 3 shows a marked reduction in its anti-apoptotic effects when compared with the displayed wild-type isoform (PubMed:10626797).

BIRC5的亚细胞定位



Subcellular Location

Cytoplasm 3 Publications

Nucleus 3 Publications

Chromosome 1 Publication

Chromosome, centromere 3 Publications

Cytoplasm, cytoskeleton, spindle 1 Publication

Chromosome, centromere, kinetochore 1 Publication

Midbody 1 Publication

Note: Localizes at the centromeres from prophase to metaphase, at the spindle midzone during anaphase and a the midbody during telophase and cytokinesis. Accumulates in the nucleus upon treatment with leptomycin B (LMB), a XPO1/CRM1 nuclear export inhibitor (By similarity).

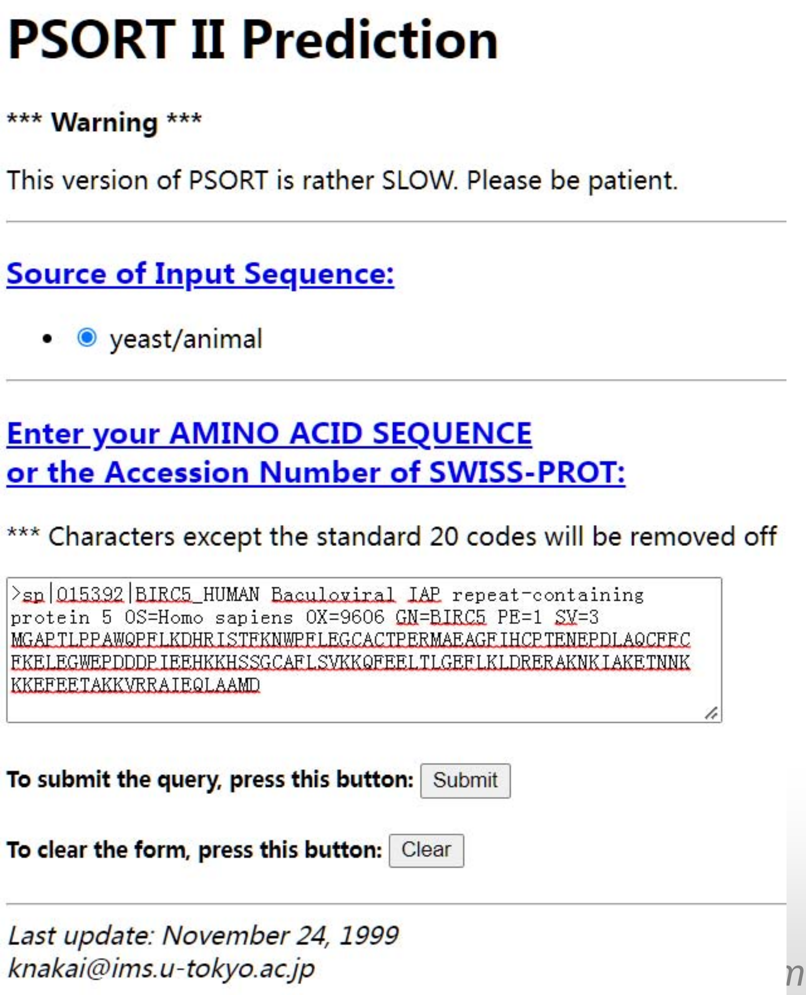
Localizes on chromosome arms and inner centromeres from prophase through metaphase. Localizes to kinetochores in metaphase, distributes to the midzone microtubules in anaphase and at telophase, localizes exclusively to the midbody (PubMed:11084331).

Colocalizes with AURKB at mitotic chromosomes (PubMed:14610074).

Acetylation at Lys-129 directs its localization to the nucleus by enhancing homodimerization and thereby inhibiting XPO1/CRM1-mediated nuclear export (PubMed:20826784). By Similarity 3 Publications

PSORT II

- https://psort.hgc.jp/form2.html



PSORT II Prediction

***** Warning *****

This version of PSORT is rather SLOW. Please be patient.

Source of Input Sequence:

- ● yeast/animal

Enter your AMINO ACID SEQUENCE
or the Accession Number of SWISS-PROT:

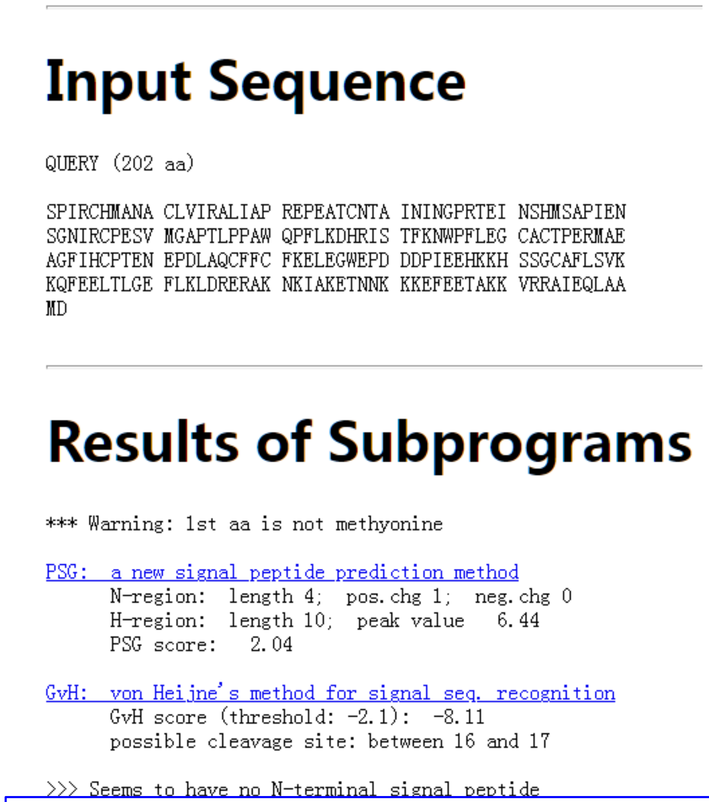
*** Characters except the standard 20 codes will be removed off

```
>sp|O15392|BIRC5_HUMAN Baculoviral IAP repeat-containing
protein 5 OS=Homo sapiens OX=9606 GN=BIRC5 PE=1 SV=3
MGAPTLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFFC
FKELEGWEPDDDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNK
KKEFEETAKKVRRAIEQLAAMD
```

To submit the query, press this button: Submit

To clear the form, press this button: Clear

Last update: November 24, 1999
knakai@ims.u-tokyo.ac.jp



Input Sequence

```
QUERY (202 aa)

SPIRCHMANA CLVIRALIAP REPEATCNTA ININGPRTEI NSHMSAPIEN
SGNIRCPESV MGAPTLPPAW QPFLKDHRIS TFKNWPFLEG CACTPERMAE
AGFIHCPTEN EPDLAQCFFC FKELEGWEPD DDPIEEHKKH SSGCAFLSVK
KQFEELTLGE FLKLDRERAK NKIAKETNNK KKEFEETAKK VRRAIEQLAA
MD
```

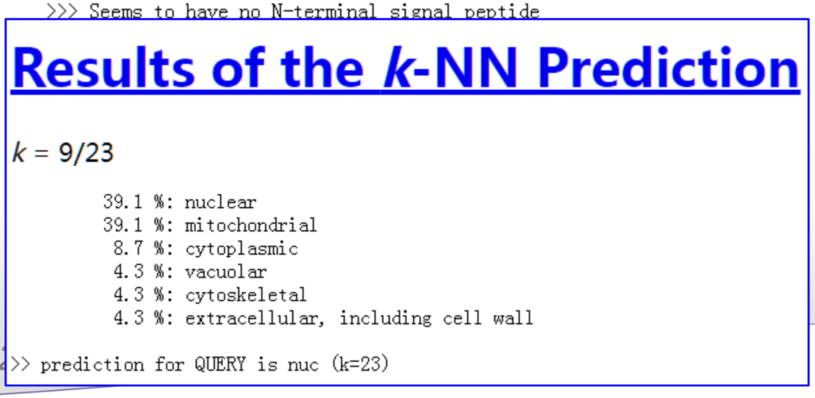
Results of Subprograms

```
*** Warning: 1st aa is not methyonine

PSG:  a new signal peptide prediction method
      N-region:  length 4;  pos.chg 1;  neg.chg 0
      H-region:  length 10;  peak value   6.44
      PSG score:   2.04

GvH:  von Heijne's method for signal seq. recognition
      GvH score (threshold: -2.1):  -8.11
      possible cleavage site: between 16 and 17

>>> Seems to have no N-terminal signal peptide
```



Results of the *k*-NN Prediction

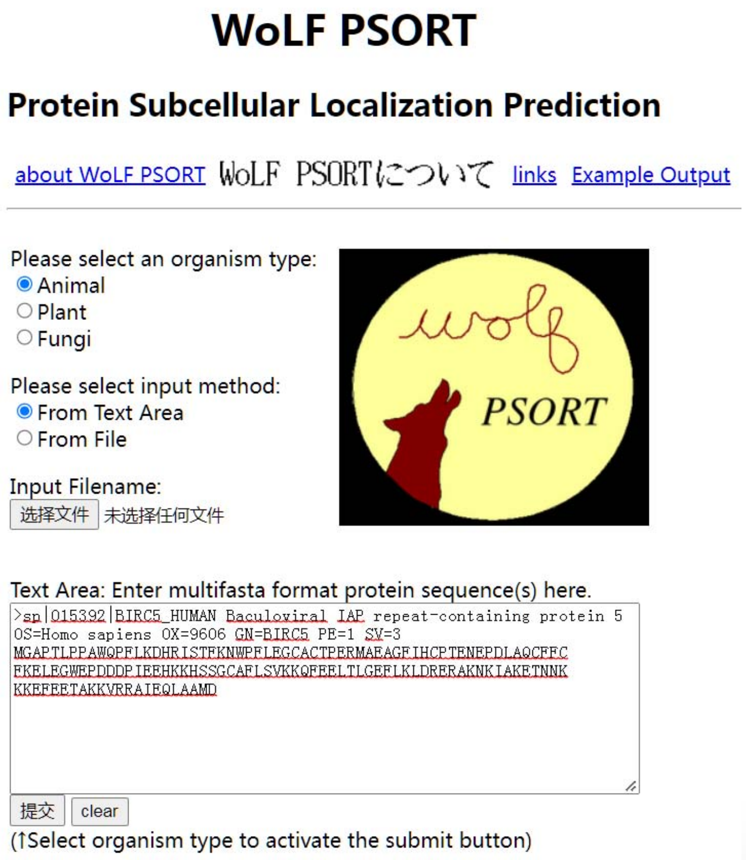
k = 9/23

```
        39.1 %: nuclear
        39.1 %: mitochondrial
         8.7 %: cytoplasmic
         4.3 %: vacuolar
         4.3 %: cytoskeletal
         4.3 %: extracellular, including cell wall

>> prediction for QUERY is nuc (k=23)
```

WoLF PSORT

- https://wolfpsort.hgc.jp/



WoLF PSORT

Protein Subcellular Localization Prediction

Please select an organism type:
● Animal
○ Plant
○ Fungi

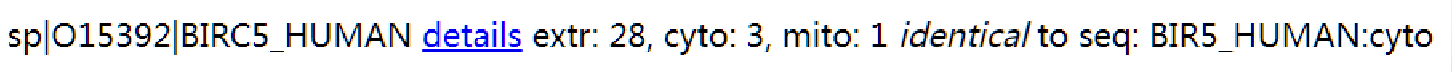
Please select input method:
● From Text Area
○ From File

Input Filename:

Text Area: Enter multifasta format protein sequence(s) here.

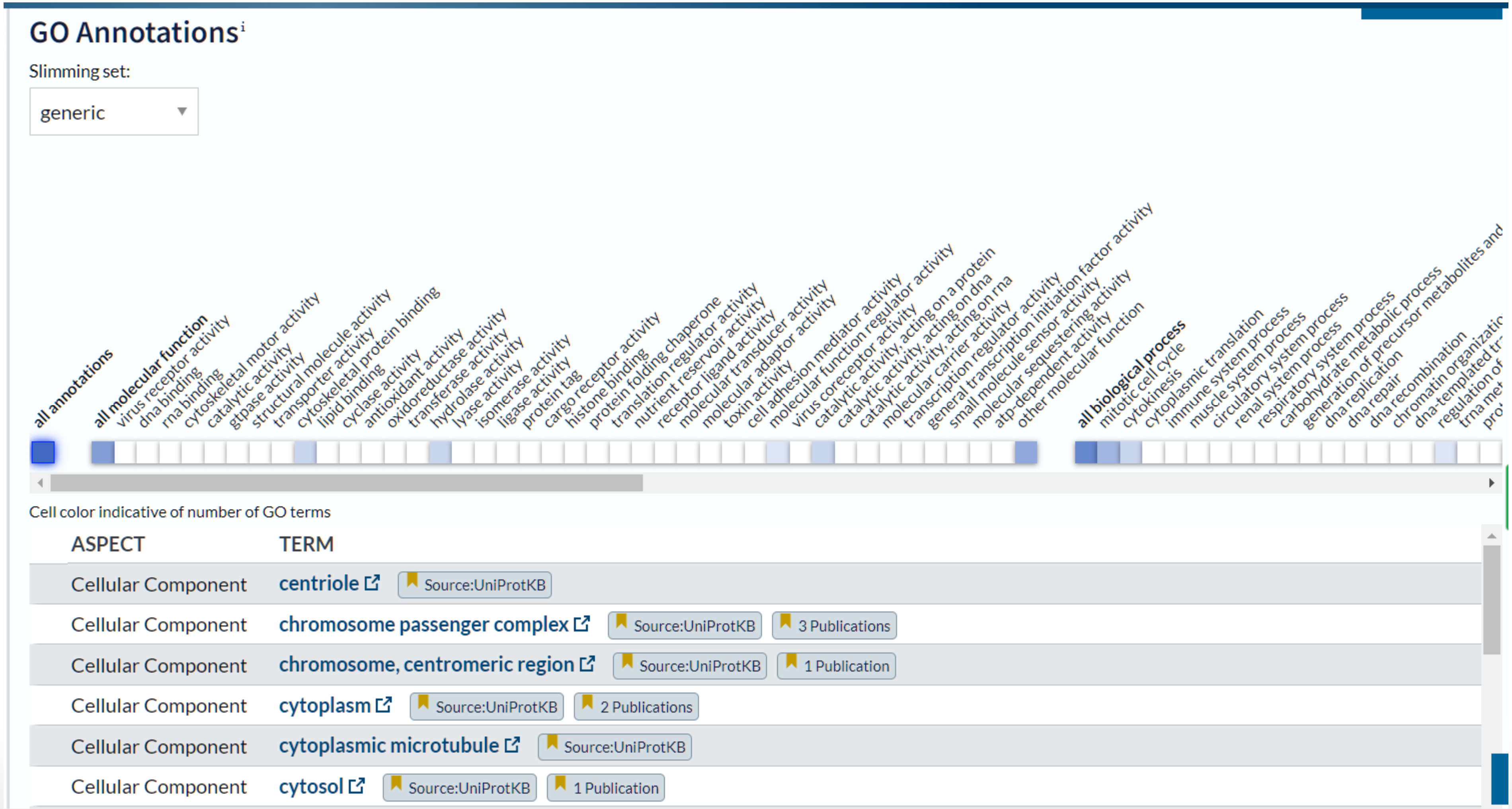
```
>sp|O15392|BIRC5_HUMAN Baculoviral IAP repeat-containing protein 5
OS=Homo sapiens OX=9606 GN=BIRC5 PE=1 SV=3
MGAPTLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFFC
FKELEGWEPDDDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNK
KKEFEETAKKVRRAIEQLAAMD
```

(↑Select organism type to activate the submit button)



sp|O15392|BIRC5_HUMAN details extr: 28, cyto: 3, mito: 1 *identical* to seq: BIR5_HUMAN:cyto

基因本体注释



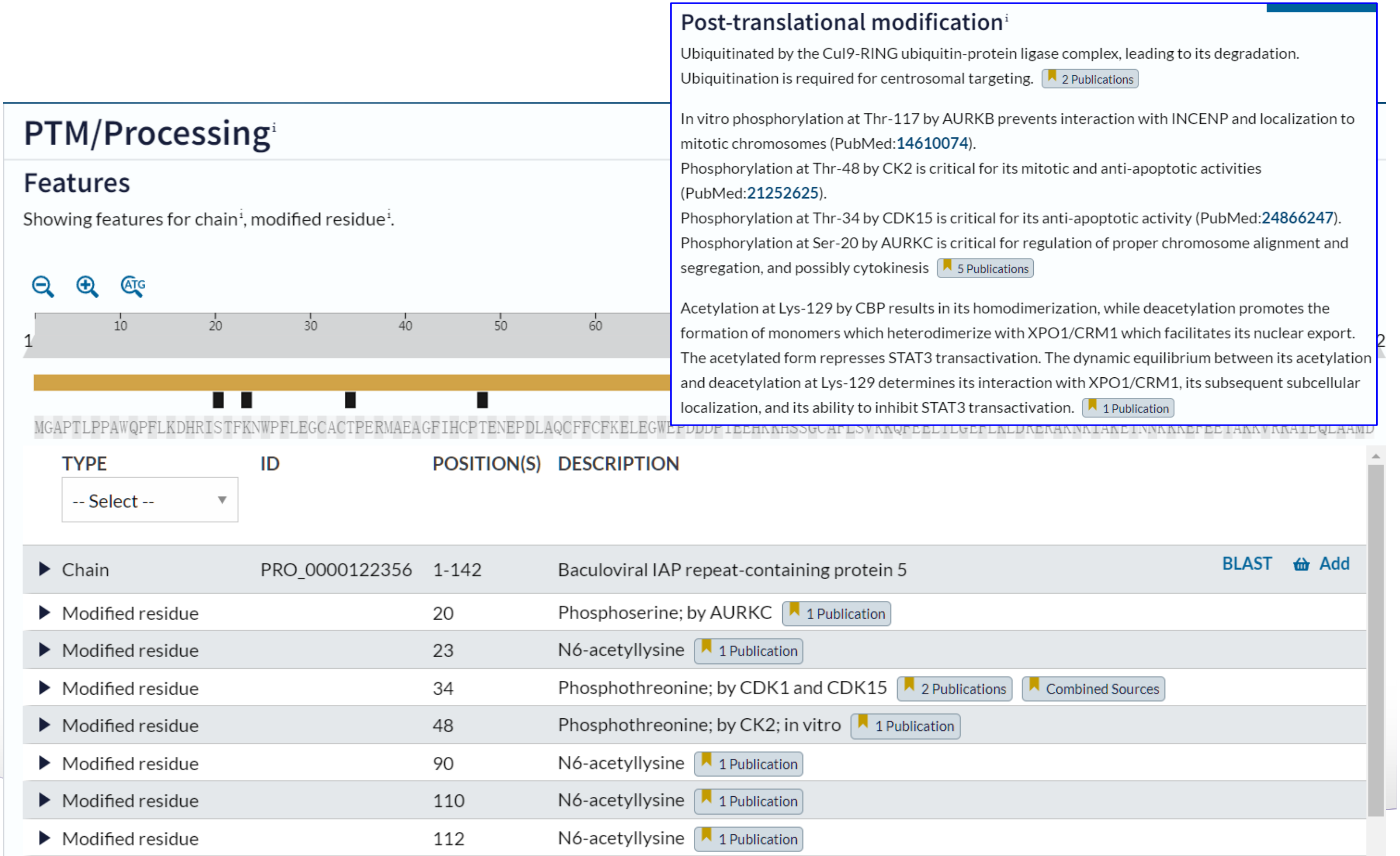
GO Annotations

Slimming set: generic

Cell color indicative of number of GO terms

ASPECT	TERM
Cellular Component	**centriole** Source:UniProtKB
Cellular Component	**chromosome passenger complex** Source:UniProtKB 3 Publications
Cellular Component	**chromosome, centromeric region** Source:UniProtKB 1 Publication
Cellular Component	**cytoplasm** Source:UniProtKB 2 Publications
Cellular Component	**cytoplasmic microtubule** Source:UniProtKB
Cellular Component	**cytosol** Source:UniProtKB 1 Publication

翻译后修饰



Post-translational modification

Ubiquitinated by the Cul9-RING ubiquitin-protein ligase complex, leading to its degradation. Ubiquitination is required for centrosomal targeting. 2 Publications

In vitro phosphorylation at Thr-117 by AURKB prevents interaction with INCENP and localization to mitotic chromosomes (PubMed:14610074).
Phosphorylation at Thr-48 by CK2 is critical for its mitotic and anti-apoptotic activities (PubMed:21252625).
Phosphorylation at Thr-34 by CDK15 is critical for its anti-apoptotic activity (PubMed:24866247).
Phosphorylation at Ser-20 by AURKC is critical for regulation of proper chromosome alignment and segregation, and possibly cytokinesis 5 Publications

Acetylation at Lys-129 by CBP results in its homodimerization, while deacetylation promotes the formation of monomers which heterodimerize with XPO1/CRM1 which facilitates its nuclear export. The acetylated form represses STAT3 transactivation. The dynamic equilibrium between its acetylation and deacetylation at Lys-129 determines its interaction with XPO1/CRM1, its subsequent subcellular localization, and its ability to inhibit STAT3 transactivation. 1 Publication

PTM/Processing

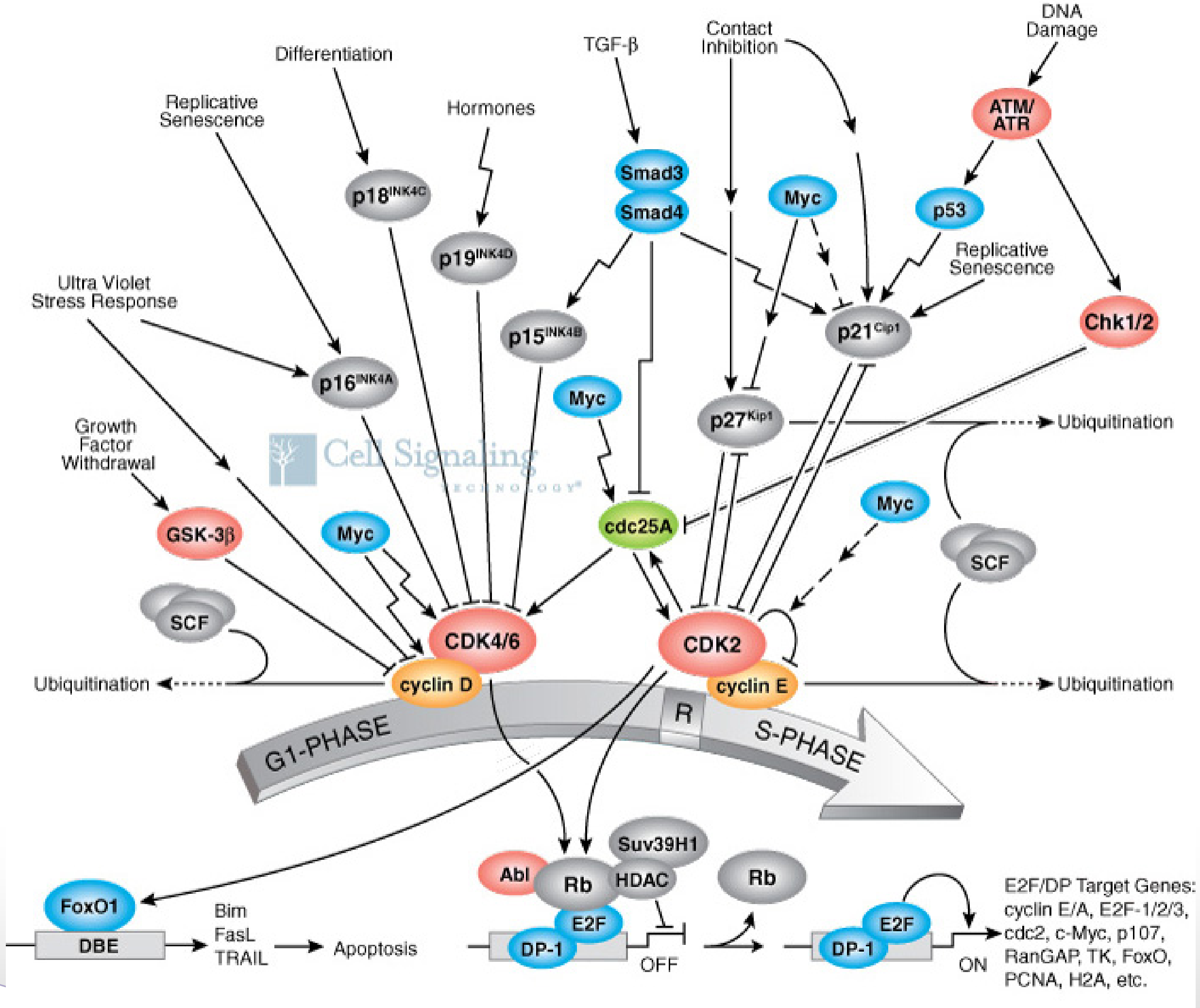
Features

Showing features for chain, modified residue.

MGAPTLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEPDDDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQLAAMD

TYPE -- Select --	ID	POSITION(S)	DESCRIPTION
▶ Chain	PRO_0000122356	1-142	Baculoviral IAP repeat-containing protein 5 BLAST Add
▶ Modified residue		20	Phosphoserine; by AURKC 1 Publication
▶ Modified residue		23	N6-acetyllysine 1 Publication
▶ Modified residue		34	Phosphothreonine; by CDK1 and CDK15 2 Publications Combined Sources
▶ Modified residue		48	Phosphothreonine; by CK2; in vitro 1 Publication
▶ Modified residue		90	N6-acetyllysine 1 Publication
▶ Modified residue		110	N6-acetyllysine 1 Publication
▶ Modified residue		112	N6-acetyllysine 1 Publication

细胞信号通路

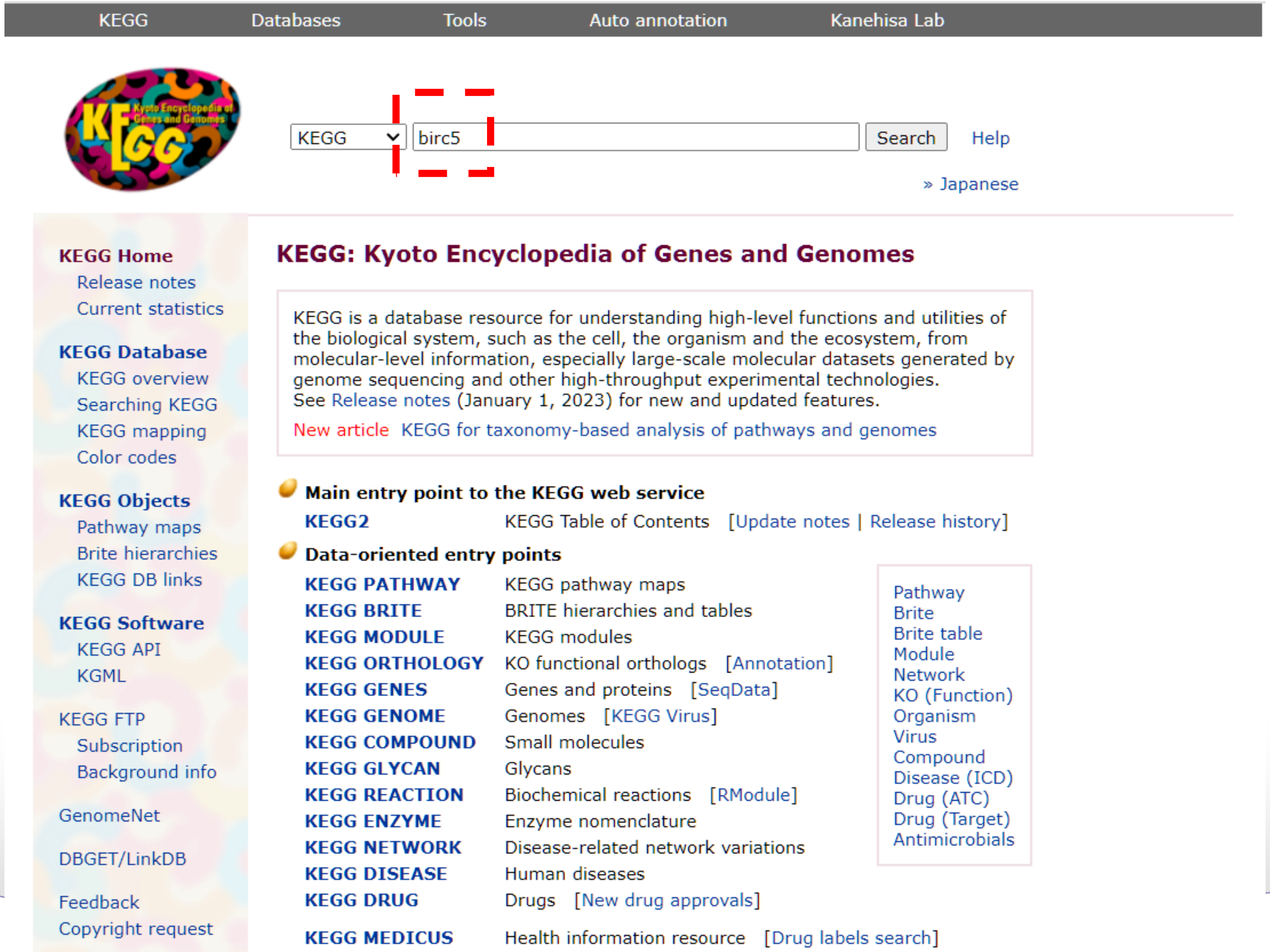


G1/S检验点：

有调控方向

KEGG PATHWAY Database

- ❐ https://www.genome.jp/kegg/kegg2.html



KEGG Home
- Release notes
- Current statistics

KEGG Database
- KEGG overview
- Searching KEGG
- KEGG mapping
- Color codes

KEGG Objects
- Pathway maps
- Brite hierarchies
- KEGG DB links

KEGG Software
- KEGG API
- KGML

KEGG FTP
- Subscription
- Background info

GenomeNet

DBGET/LinkDB

Feedback
Copyright request

KEGG: Kyoto Encyclopedia of Genes and Genomes

KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies.
See Release notes (January 1, 2023) for new and updated features.

New article KEGG for taxonomy-based analysis of pathways and genomes

Main entry point to the KEGG web service

KEGG2	KEGG Table of Contents [Update notes | Release history]

Data-oriented entry points

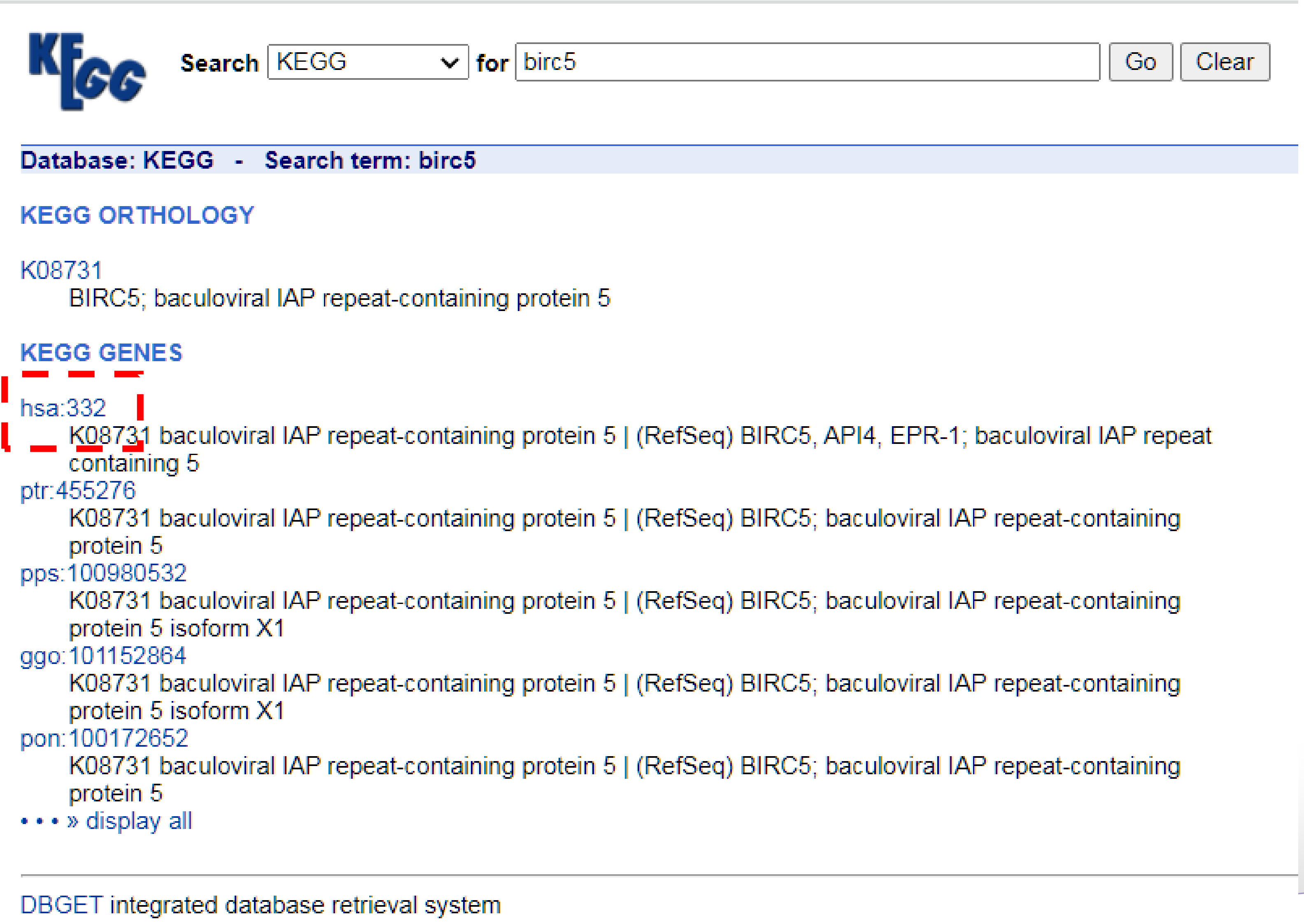
KEGG PATHWAY	KEGG pathway maps
KEGG BRITE	BRITE hierarchies and tables
KEGG MODULE	KEGG modules
KEGG ORTHOLOGY	KO functional orthologs [Annotation]
KEGG GENES	Genes and proteins [SeqData]
KEGG GENOME	Genomes [KEGG Virus]
KEGG COMPOUND	Small molecules
KEGG GLYCAN	Glycans
KEGG REACTION	Biochemical reactions [RModule]
KEGG ENZYME	Enzyme nomenclature
KEGG NETWORK	Disease-related network variations
KEGG DISEASE	Human diseases
KEGG DRUG	Drugs [New drug approvals]
KEGG MEDICUS	Health information resource [Drug labels search]

Pathway
Brite
Brite table
Module
Network
KO (Function)
Organism
Virus
Compound
Disease (ICD)
Drug (ATC)
Drug (Target)
Antimicrobials

KEGG

- 生物分子的相互作用和反应网络
- 手工收集和绘制
- KEGG PATHWAY
  - 代谢通路
  - 遗传信息的处理
  - 环境信息的处理
  - 细胞过程
  - 人类疾病
  - 与药物开发的关系

KEGG搜索结果



Database: KEGG - Search term: birc5

KEGG ORTHOLOGY

K08731
BIRC5; baculoviral IAP repeat-containing protein 5

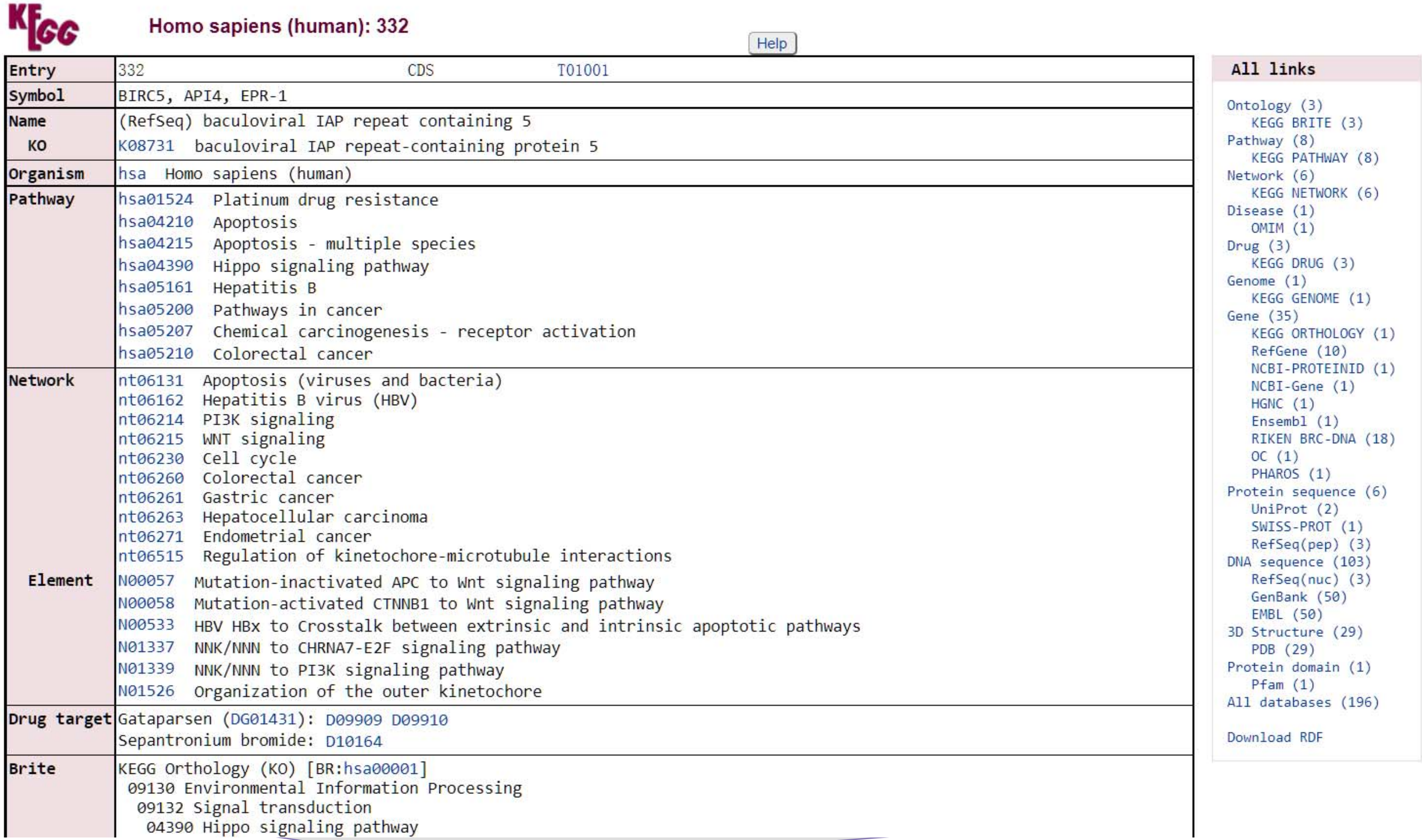
KEGG GENES

hsa:332
K08731 baculoviral IAP repeat-containing protein 5 | (RefSeq) BIRC5, API4, EPR-1; baculoviral IAP repeat containing 5
ptr:455276
K08731 baculoviral IAP repeat-containing protein 5 | (RefSeq) BIRC5; baculoviral IAP repeat-containing protein 5
pps:100980532
K08731 baculoviral IAP repeat-containing protein 5 | (RefSeq) BIRC5; baculoviral IAP repeat-containing protein 5 isoform X1
ggo:101152864
K08731 baculoviral IAP repeat-containing protein 5 | (RefSeq) BIRC5; baculoviral IAP repeat-containing protein 5 isoform X1
pon:100172652
K08731 baculoviral IAP repeat-containing protein 5 | (RefSeq) BIRC5; baculoviral IAP repeat-containing protein 5
• • • » display all

DBGET integrated database retrieval system

Human BIRC5

- 参与通路：癌症、结肠癌、乙肝感染



Homo sapiens (human): 332

Help

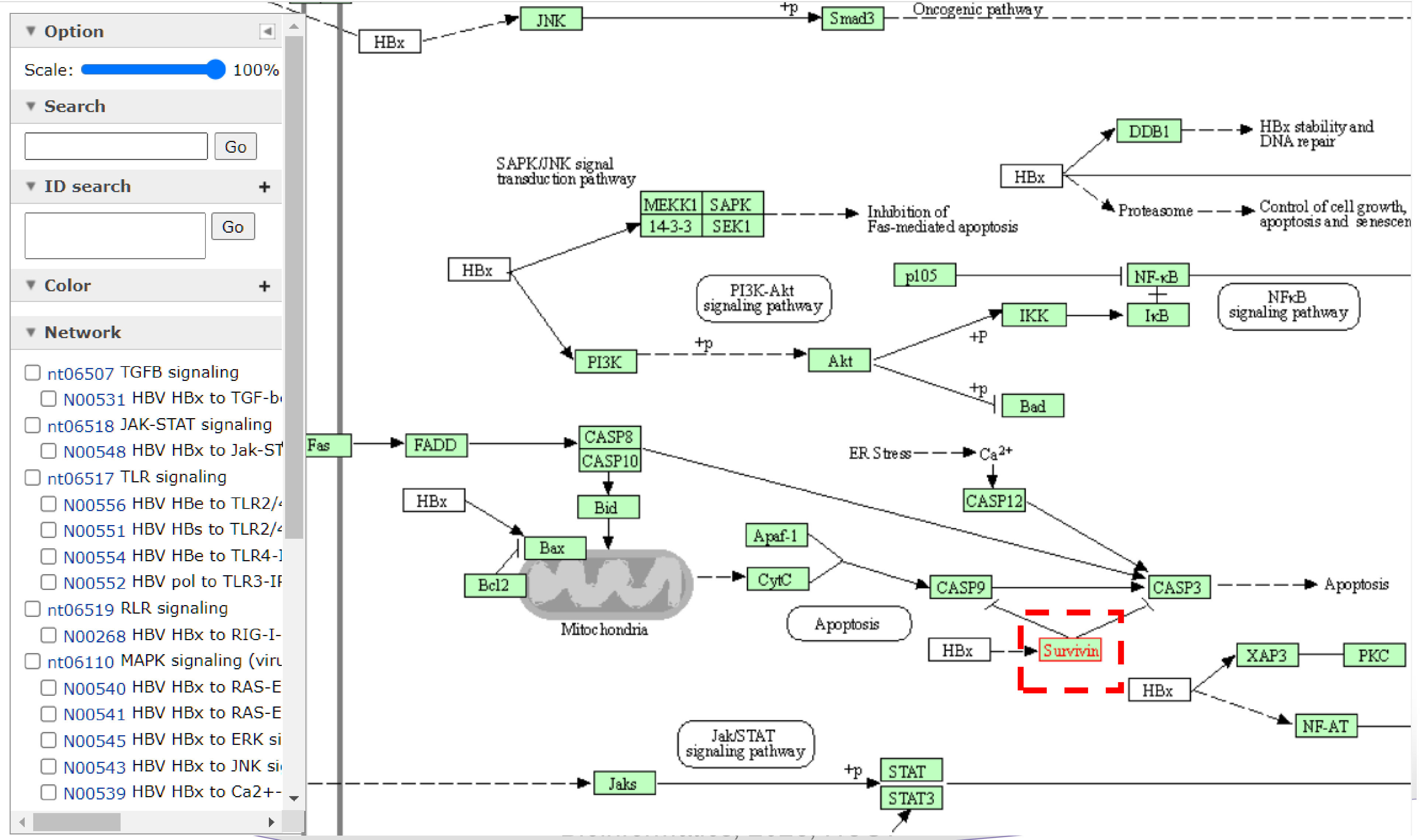
Entry	332 CDS T01001
Symbol	BIRC5, API4, EPR-1
Name	(RefSeq) baculoviral IAP repeat containing 5
KO	K08731 baculoviral IAP repeat-containing protein 5
Organism	hsa Homo sapiens (human)
Pathway	hsa01524 Platinum drug resistance hsa04210 Apoptosis hsa04215 Apoptosis - multiple species hsa04390 Hippo signaling pathway hsa05161 Hepatitis B hsa05200 Pathways in cancer hsa05207 Chemical carcinogenesis - receptor activation hsa05210 Colorectal cancer
Network	nt06131 Apoptosis (viruses and bacteria) nt06162 Hepatitis B virus (HBV) nt06214 PI3K signaling nt06215 WNT signaling nt06230 Cell cycle nt06260 Colorectal cancer nt06261 Gastric cancer nt06263 Hepatocellular carcinoma nt06271 Endometrial cancer nt06515 Regulation of kinetochore-microtubule interactions
Element	N00057 Mutation-inactivated APC to Wnt signaling pathway N00058 Mutation-activated CTNNB1 to Wnt signaling pathway N00533 HBV HBx to Crosstalk between extrinsic and intrinsic apoptotic pathways N01337 NNK/NNN to CHRNA7-E2F signaling pathway N01339 NNK/NNN to PI3K signaling pathway N01526 Organization of the outer kinetochore
Drug target	Gataparsen (DG01431): D09909 D09910 Sepantronium bromide: D10164
Brite	KEGG Orthology (KO) [BR:hsa00001] 09130 Environmental Information Processing 09132 Signal transduction 04390 Hippo signaling pathway

All links

- Ontology (3)
  - KEGG BRITE (3)
- Pathway (8)
  - KEGG PATHWAY (8)
- Network (6)
  - KEGG NETWORK (6)
- Disease (1)
  - OMIM (1)
- Drug (3)
  - KEGG DRUG (3)
- Genome (1)
  - KEGG GENOME (1)
- Gene (35)
  - KEGG ORTHOLOGY (1)
  - RefGene (10)
  - NCBI-PROTEINID (1)
  - NCBI-Gene (1)
  - HGNC (1)
  - Ensembl (1)
  - RIKEN BRC-DNA (18)
  - OC (1)
  - PHAROS (1)
- Protein sequence (6)
  - UniProt (2)
  - SWISS-PROT (1)
  - RefSeq(pep) (3)
- DNA sequence (103)
  - RefSeq(nuc) (3)
  - GenBank (50)
  - EMBL (50)
- 3D Structure (29)
  - PDB (29)
- Protein domain (1)
  - Pfam (1)
- All databases (196)

Download RDF

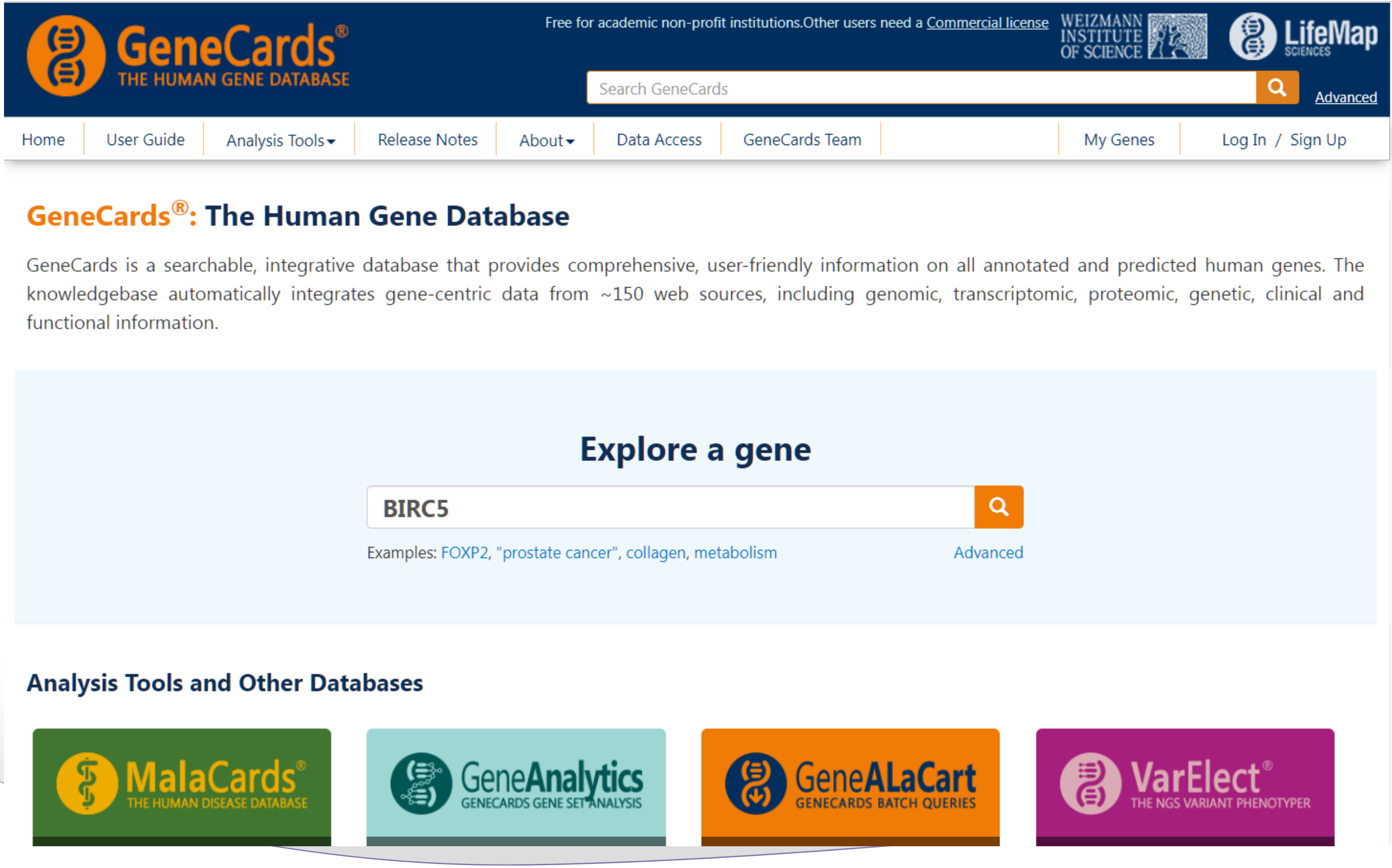
Hepatitis B (hsa05161)



- ☐ nt06507 TGFB signaling
  - ☐ N00531 HBV HBx to TGF-b
- ☐ nt06518 JAK-STAT signaling
  - ☐ N00548 HBV HBx to Jak-ST
- ☐ nt06517 TLR signaling
  - ☐ N00556 HBV HBe to TLR2/
  - ☐ N00551 HBV HBs to TLR2/
  - ☐ N00554 HBV HBe to TLR4-
  - ☐ N00552 HBV pol to TLR3-I
- ☐ nt06519 RLR signaling
  - ☐ N00268 HBV HBx to RIG-I-
- ☐ nt06110 MAPK signaling (viru
  - ☐ N00540 HBV HBx to RAS-E
  - ☐ N00541 HBV HBx to RAS-E
  - ☐ N00545 HBV HBx to ERK si
  - ☐ N00543 HBV HBx to JNK si
  - ☐ N00539 HBV HBx to Ca2+-

GeneCards

- https://www.genecards.org/



GeneCards®: The Human Gene Database

GeneCards is a searchable, integrative database that provides comprehensive, user-friendly information on all annotated and predicted human genes. The knowledgebase automatically integrates gene-centric data from ~150 web sources, including genomic, transcriptomic, proteomic, genetic, clinical and functional information.

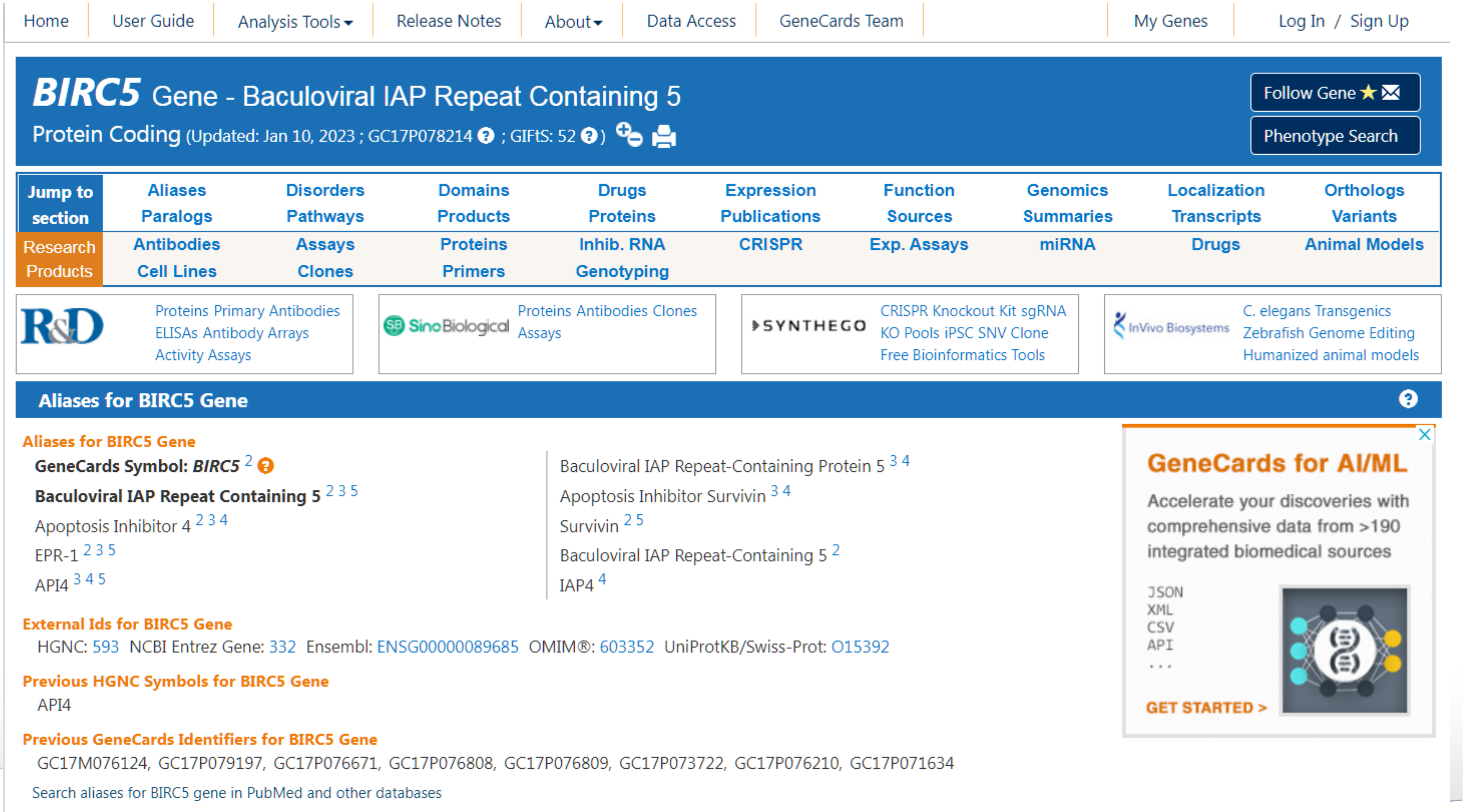
Explore a gene

BIRC5

Examples: FOXP2, "prostate cancer", collagen, metabolism

Analysis Tools and Other Databases

BIRC5的标识符和别名



***BIRC5* Gene - Baculoviral IAP Repeat Containing 5**

Protein Coding (Updated: Jan 10, 2023 ; GC17P078214 ; GIFtS: 52)

Aliases for BIRC5 Gene

Aliases for BIRC5 Gene

GeneCards Symbol: *BIRC5* [2]	Baculoviral IAP Repeat-Containing Protein 5 [3,4]
Baculoviral IAP Repeat Containing 5 [2,3,5]	Apoptosis Inhibitor Survivin [3,4]
Apoptosis Inhibitor 4 [2,3,4]	Survivin [2,5]
EPR-1 [2,3,5]	Baculoviral IAP Repeat-Containing 5 [2]
API4 [3,4,5]	IAP4 [4]

External Ids for BIRC5 Gene

HGNC: 593 NCBI Entrez Gene: 332 Ensembl: ENSG00000089685 OMIM®: 603352 UniProtKB/Swiss-Prot: O15392

Previous HGNC Symbols for BIRC5 Gene

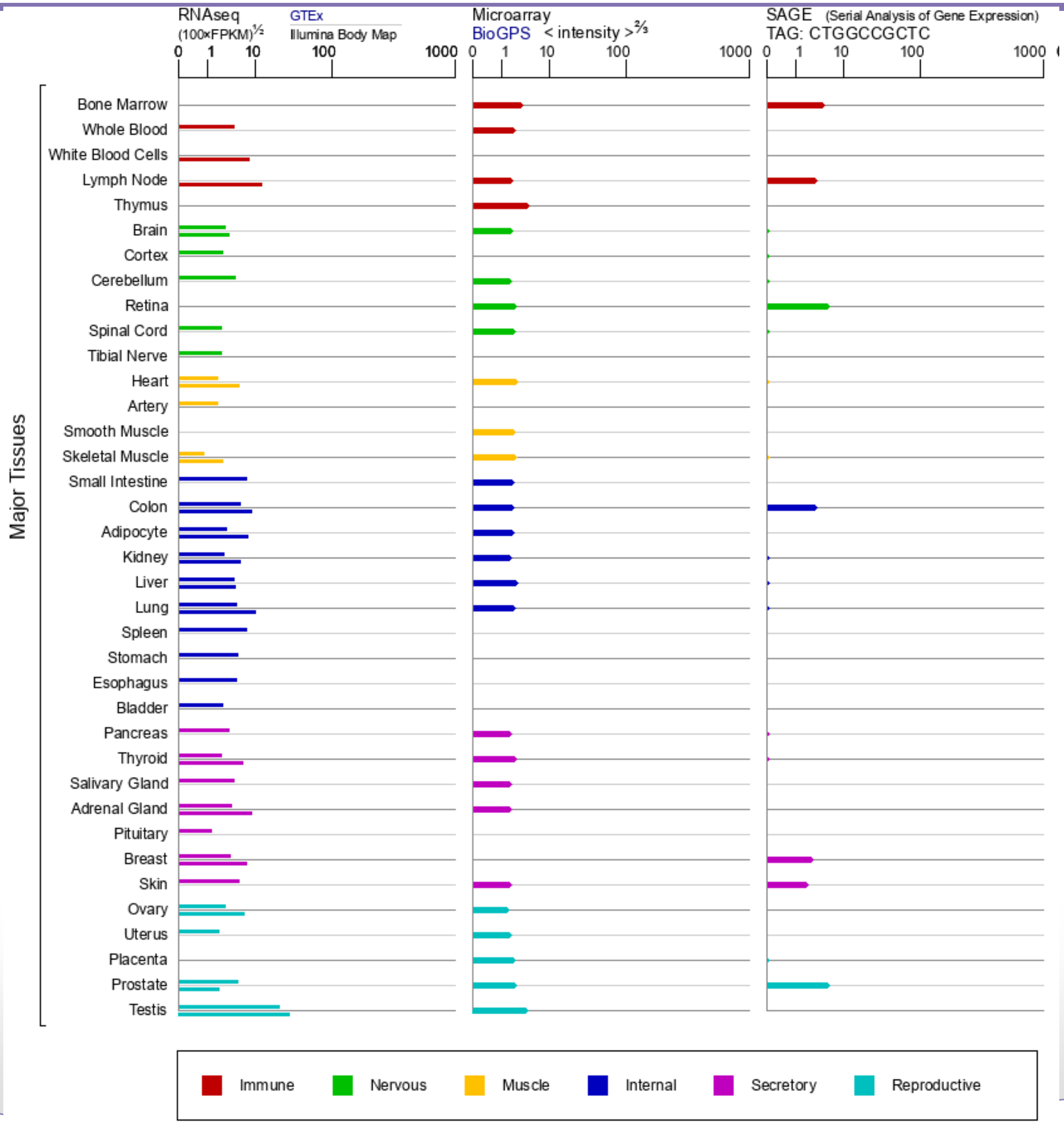
API4

Previous GeneCards Identifiers for BIRC5 Gene

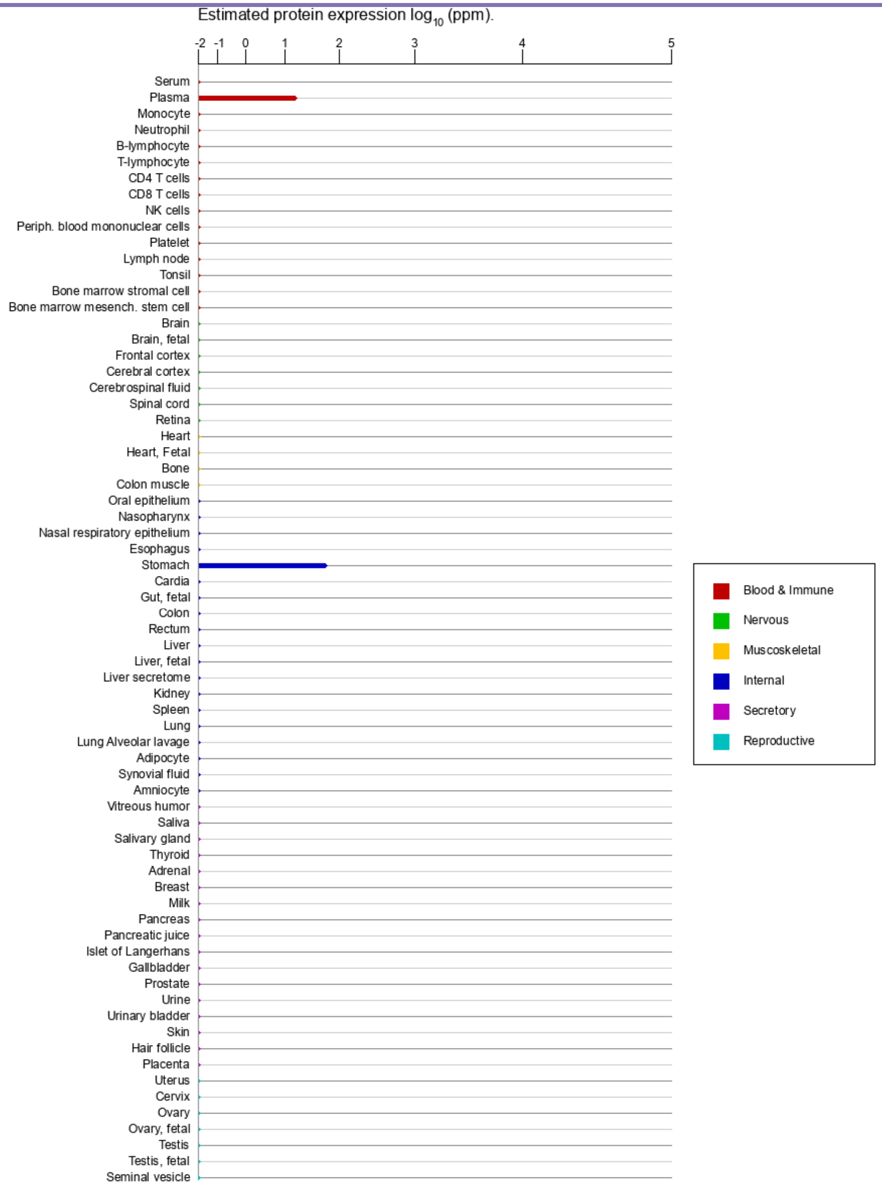
GC17M076124, GC17P079197, GC17P076671, GC17P076808, GC17P076809, GC17P073722, GC17P076210, GC17P071634

Search aliases for BIRC5 gene in PubMed and other databases

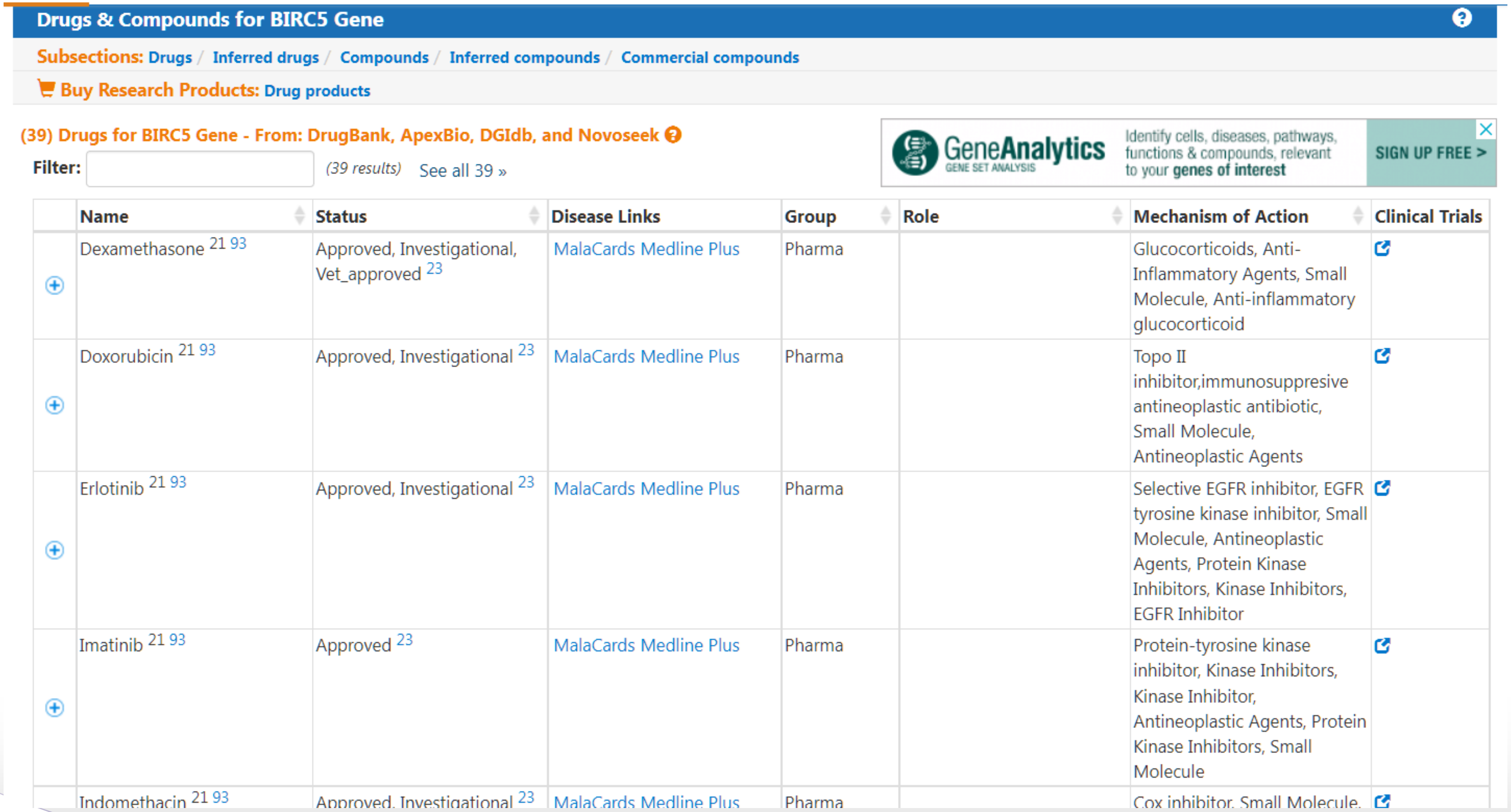
BIRC5基因的组织特异性表达信息



BIRC5蛋白的组织特异性表达信息



药物 & 化合物信息



Drugs & Compounds for BIRC5 Gene

Subsections: Drugs / Inferred drugs / Compounds / Inferred compounds / Commercial compounds

Buy Research Products: Drug products

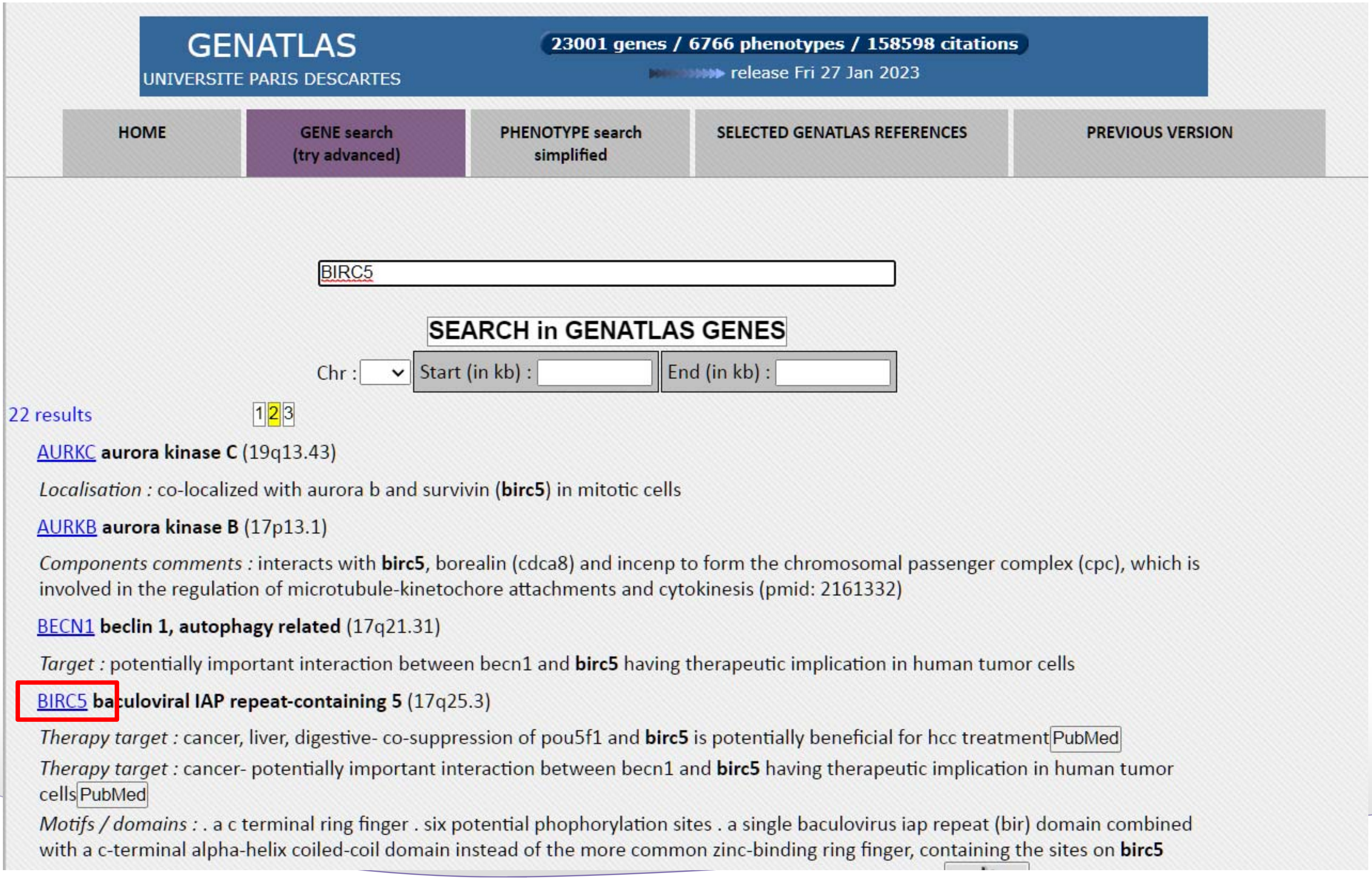
(39) Drugs for BIRC5 Gene - From: DrugBank, ApexBio, DGIdb, and Novoseek

Filter: *(39 results)* See all 39 »

	Name	Status	Disease Links	Group	Role	Mechanism of Action	Clinical Trials
⊕	Dexamethasone [21] [93]	Approved, Investigational, Vet_approved [23]	MalaCards Medline Plus	Pharma		Glucocorticoids, Anti-Inflammatory Agents, Small Molecule, Anti-inflammatory glucocorticoid	↗
⊕	Doxorubicin [21] [93]	Approved, Investigational [23]	MalaCards Medline Plus	Pharma		Topo II inhibitor,immunosuppresive antineoplastic antibiotic, Small Molecule, Antineoplastic Agents	↗
⊕	Erlotinib [21] [93]	Approved, Investigational [23]	MalaCards Medline Plus	Pharma		Selective EGFR inhibitor, EGFR tyrosine kinase inhibitor, Small Molecule, Antineoplastic Agents, Protein Kinase Inhibitors, Kinase Inhibitors, EGFR Inhibitor	↗
⊕	Imatinib [21] [93]	Approved [23]	MalaCards Medline Plus	Pharma		Protein-tyrosine kinase inhibitor, Kinase Inhibitors, Kinase Inhibitor, Antineoplastic Agents, Protein Kinase Inhibitors, Small Molecule	↗
	Indomethacin [21] [93]	Approved, Investigational [23]	MalaCards Medline Plus	Pharma		Cox inhibitor, Small Molecule,	↗

GENATLAS

- http://genatlas.medecine.univ-paris5.fr/



BIRC5

22 results

AURKC **aurora kinase C** (19q13.43)

Localisation : co-localized with aurora b and survivin (**birc5**) in mitotic cells

AURKB **aurora kinase B** (17p13.1)

Components comments : interacts with **birc5**, borealin (cdca8) and incenp to form the chromosomal passenger complex (cpc), which is involved in the regulation of microtubule-kinetochore attachments and cytokinesis (pmid: 2161332)

BECN1 **beclin 1, autophagy related** (17q21.31)

Target : potentially important interaction between becn1 and **birc5** having therapeutic implication in human tumor cells

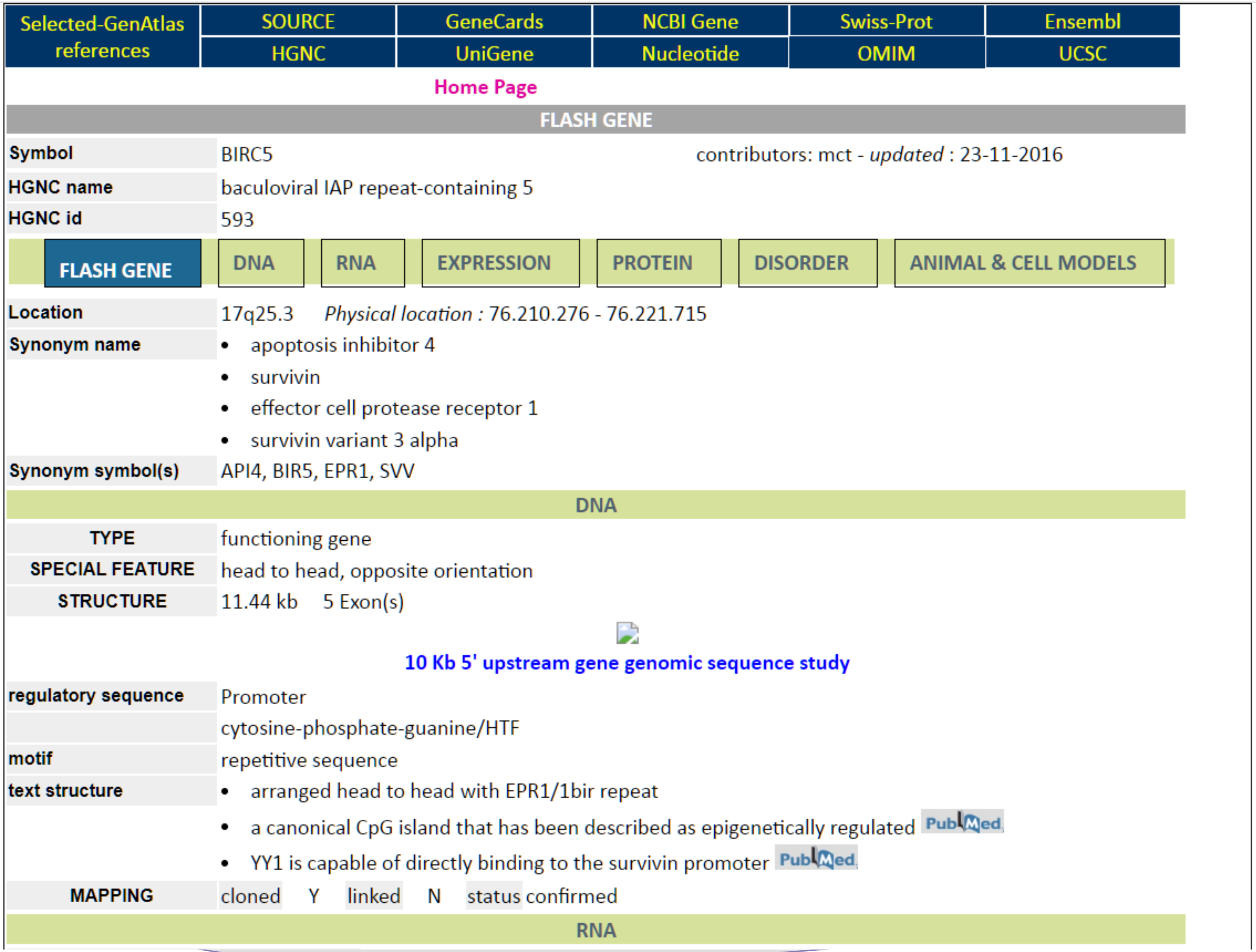
BIRC5 **baculoviral IAP repeat-containing 5** (17q25.3)

Therapy target : cancer, liver, digestive- co-suppression of pou5f1 and **birc5** is potentially beneficial for hcc treatment PubMed

Therapy target : cancer- potentially important interaction between becn1 and **birc5** having therapeutic implication in human tumor cells PubMed

Motifs / domains : . a c terminal ring finger . six potential phophorylation sites . a single baculovirus iap repeat (bir) domain combined with a c-terminal alpha-helix coiled-coil domain instead of the more common zinc-binding ring finger, containing the sites on **birc5**

基本信息



Selected-GenAtlas references	SOURCE	GeneCards	NCBI Gene	Swiss-Prot	Ensembl
	HGNC	UniGene	Nucleotide	OMIM	UCSC

Home Page

FLASH GENE

Symbol	BIRC5	contributors: mct - *updated* : 23-11-2016
HGNC name	baculoviral IAP repeat-containing 5	
HGNC id	593	

FLASH GENE | DNA | RNA | EXPRESSION | PROTEIN | DISORDER | ANIMAL & CELL MODELS

Location	17q25.3 *Physical location :* 76.210.276 - 76.221.715
Synonym name	• apoptosis inhibitor 4 • survivin • effector cell protease receptor 1 • survivin variant 3 alpha
Synonym symbol(s)	API4, BIR5, EPR1, SVV

DNA

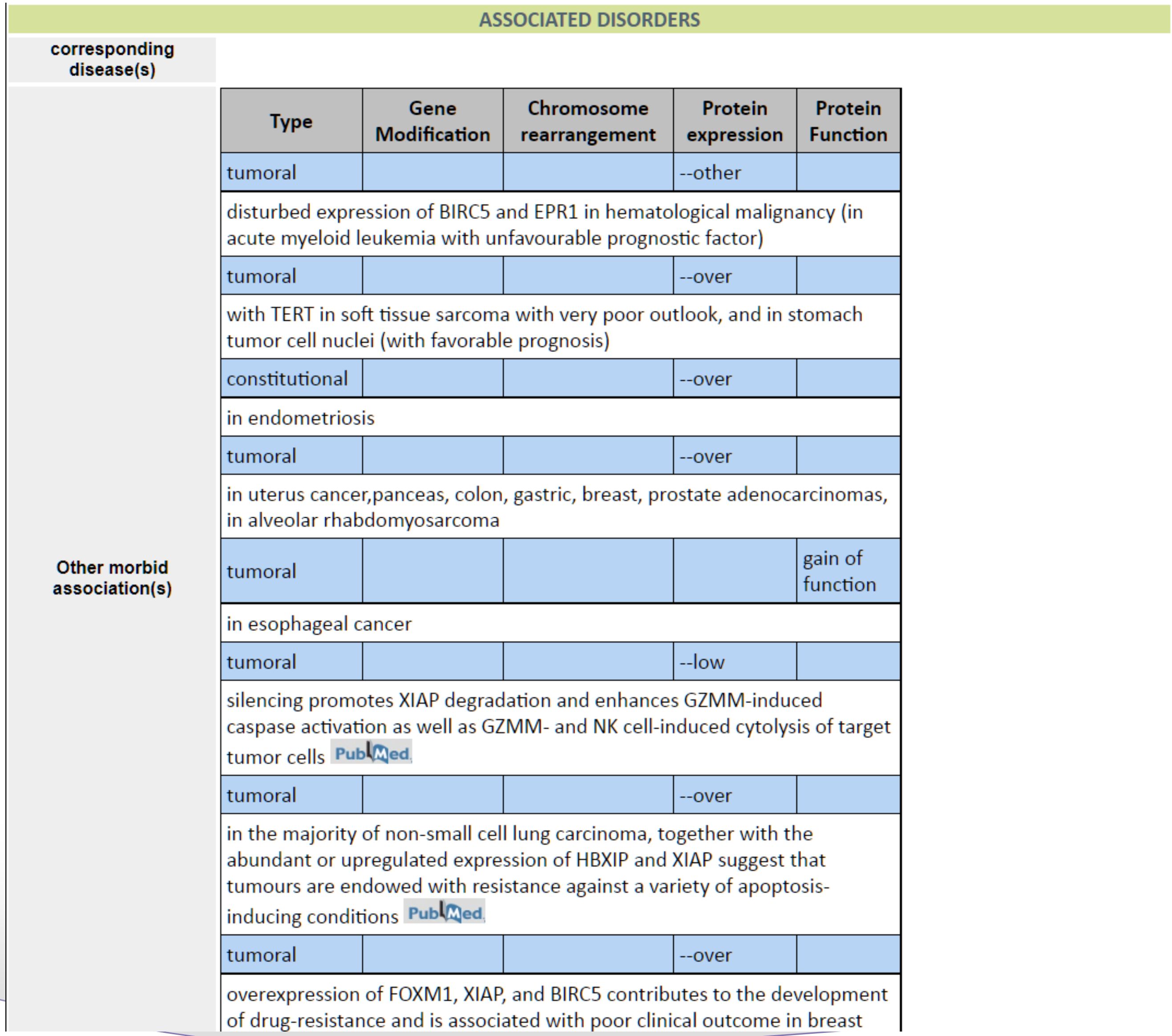
TYPE	functioning gene
SPECIAL FEATURE	head to head, opposite orientation
STRUCTURE	11.44 kb 5 Exon(s)

10 Kb 5' upstream gene genomic sequence study

regulatory sequence	Promoter
	cytosine-phosphate-guanine/HTF
motif	repetitive sequence
text structure	• arranged head to head with EPR1/1bir repeat • a canonical CpG island that has been described as epigenetically regulated PubMed • YY1 is capable of directly binding to the survivin promoter PubMed
MAPPING	cloned Y linked N status confirmed

RNA

BIRC5疾病相关信息



ASSOCIATED DISORDERS

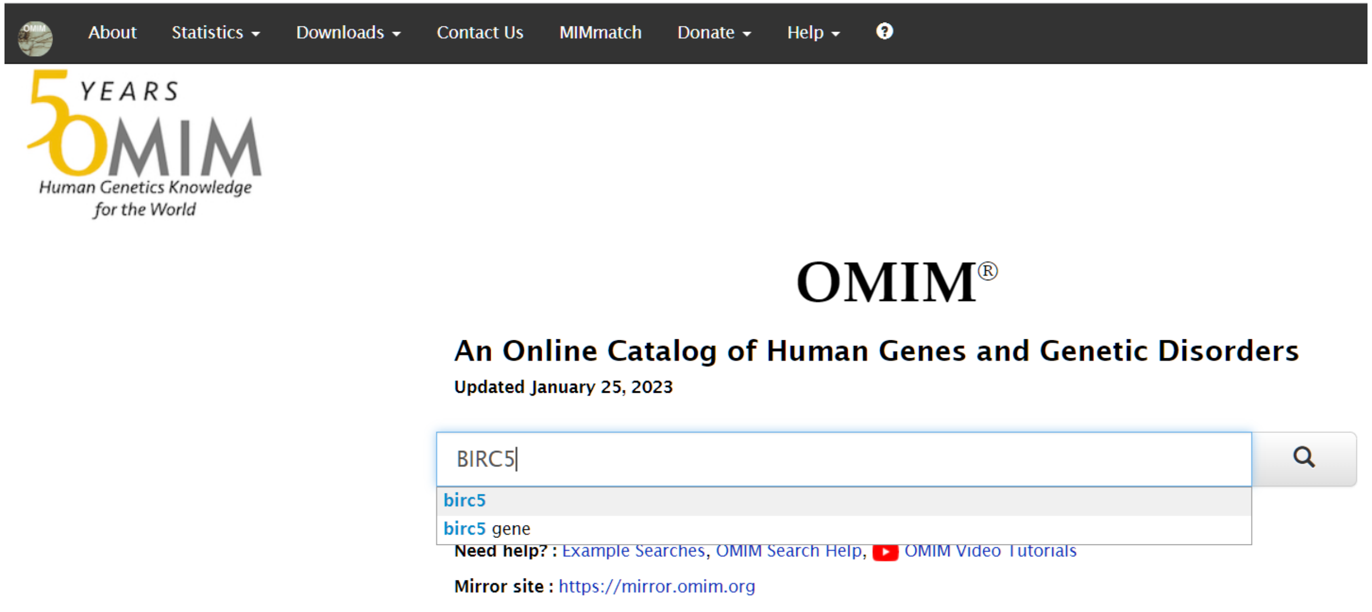
corresponding disease(s)

Other morbid association(s)

Type	Gene Modification	Chromosome rearrangement	Protein expression	Protein Function
tumoral			--other	
disturbed expression of BIRC5 and EPR1 in hematological malignancy (in acute myeloid leukemia with unfavourable prognostic factor)				
tumoral			--over	
with TERT in soft tissue sarcoma with very poor outlook, and in stomach tumor cell nuclei (with favorable prognosis)				
constitutional			--over	
in endometriosis				
tumoral			--over	
in uterus cancer,panceas, colon, gastric, breast, prostate adenocarcinomas, in alveolar rhabdomyosarcoma				
tumoral				gain of function
in esophageal cancer				
tumoral			--low	
silencing promotes XIAP degradation and enhances GZMM-induced caspase activation as well as GZMM- and NK cell-induced cytolysis of target tumor cells PubMed				
tumoral			--over	
in the majority of non-small cell lung carcinoma, together with the abundant or upregulated expression of HBXIP and XIAP suggest that tumours are endowed with resistance against a variety of apoptosis-inducing conditions PubMed				
tumoral			--over	
overexpression of FOXM1, XIAP, and BIRC5 contributes to the development of drug-resistance and is associated with poor clinical outcome in breast				

OMIM

- ❐ https://omim.org/



OMIM®

An Online Catalog of Human Genes and Genetic Disorders

Updated January 25, 2023

BIRC5

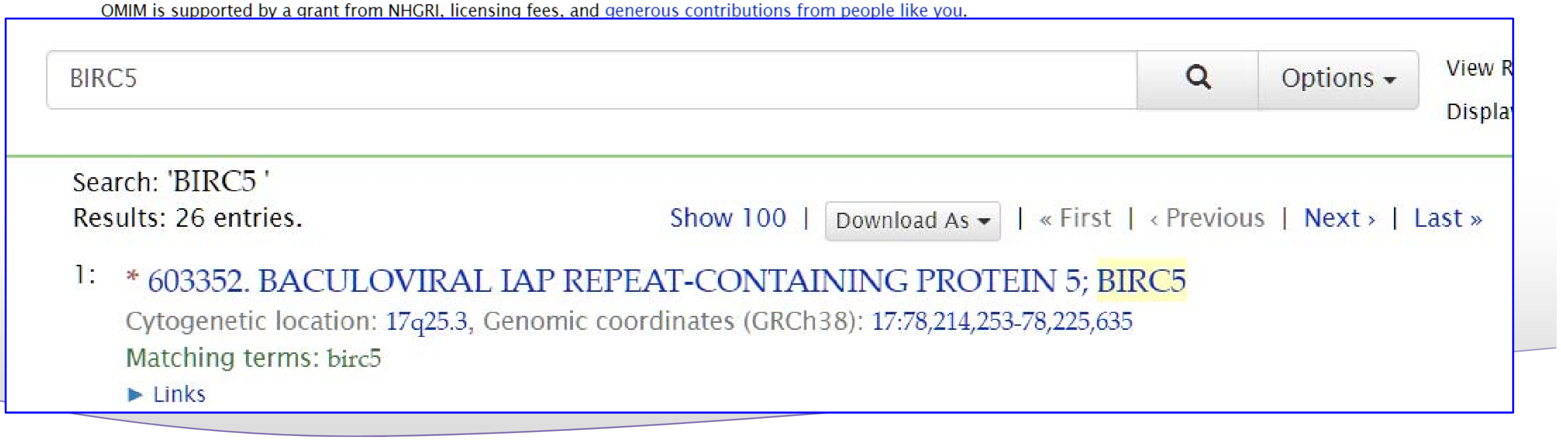
birc5

birc5 gene

Need help? : Example Searches, OMIM Search Help, OMIM Video Tutorials

Mirror site : https://mirror.omim.org

OMIM is supported by a grant from NHGRI, licensing fees, and generous contributions from people like you.



Search: 'BIRC5 '

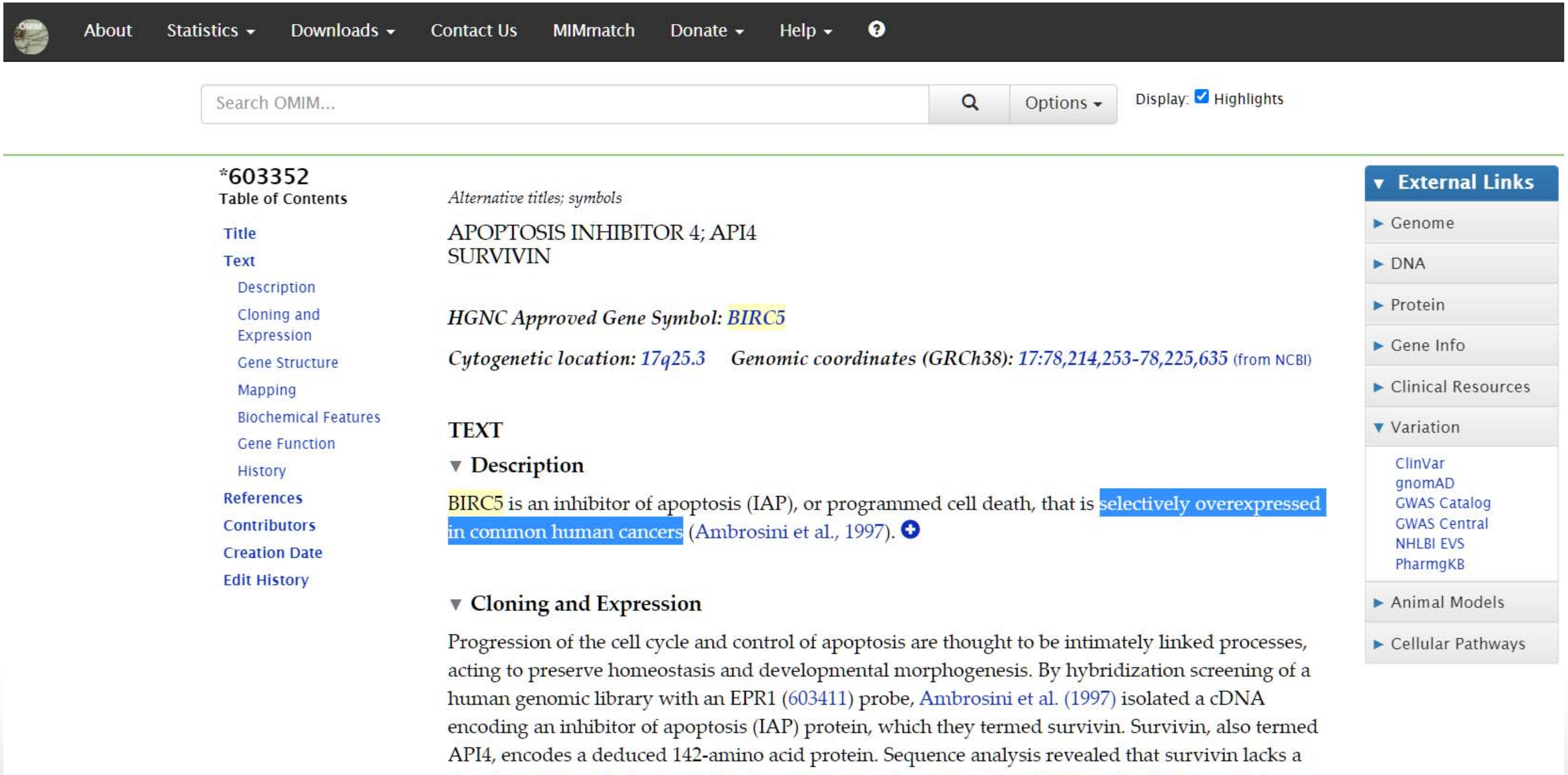
Results: 26 entries.

1: * 603352. BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 5; BIRC5

Cytogenetic location: 17q25.3, Genomic coordinates (GRCh38): 17:78,214,253-78,225,635

Matching terms: birc5

BIRC5 in human cancer



*603352

Alternative titles; symbols

APOPTOSIS INHIBITOR 4; API4
SURVIVIN

HGNC Approved Gene Symbol: BIRC5

Cytogenetic location: 17q25.3 *Genomic coordinates (GRCh38):* 17:78,214,253-78,225,635 (from NCBI)

TEXT

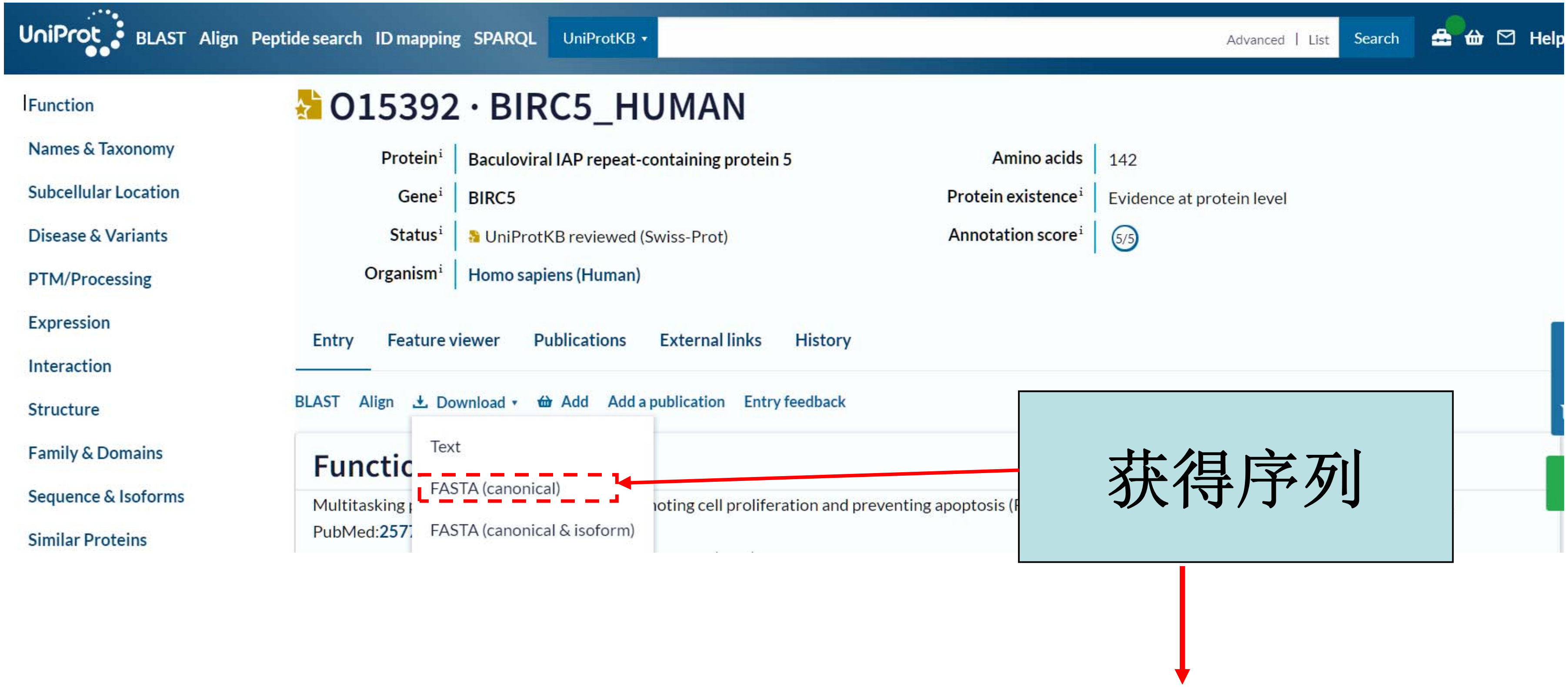
▼ Description

BIRC5 is an inhibitor of apoptosis (IAP), or programmed cell death, that is selectively overexpressed in common human cancers (Ambrosini et al., 1997).

▼ Cloning and Expression

Progression of the cell cycle and control of apoptosis are thought to be intimately linked processes, acting to preserve homeostasis and developmental morphogenesis. By hybridization screening of a human genomic library with an EPR1 (603411) probe, Ambrosini et al. (1997) isolated a cDNA encoding an inhibitor of apoptosis (IAP) protein, which they termed survivin. Survivin, also termed API4, encodes a deduced 142-amino acid protein. Sequence analysis revealed that survivin lacks a

人类BIRC5在酵母中有同源序列吗？



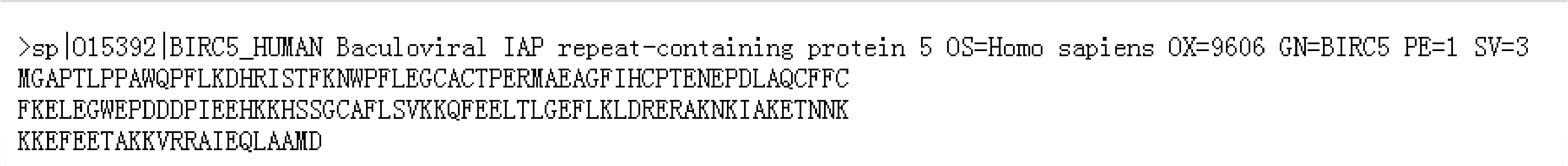
O15392 · BIRC5_HUMAN

Protein: Baculoviral IAP repeat-containing protein 5
Gene: BIRC5
Status: UniProtKB reviewed (Swiss-Prot)
Organism: Homo sapiens (Human)
Amino acids: 142
Protein existence: Evidence at protein level
Annotation score: 5/5

Functic

Multitasking p… noting cell proliferation and preventing apoptosis (F…
PubMed:257…

获得序列



```
>sp|O15392|BIRC5_HUMAN Baculoviral IAP repeat-containing protein 5 OS=Homo sapiens OX=9606 GN=BIRC5 PE=1 SV=3
MGAPTLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFFC
FKELEGWEPDDDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNK
KKEFEETAKKVRRAIEQLAAMD
```

在酵母中进行序列比对

BLAST

Find a protein sequence to run BLAST sequence similarity search by UniProt ID (e.g. P05067 or A4_HUMAN or UPI0000000001).

OR

Enter one or more sequences (20 max). You may also load from a text file.

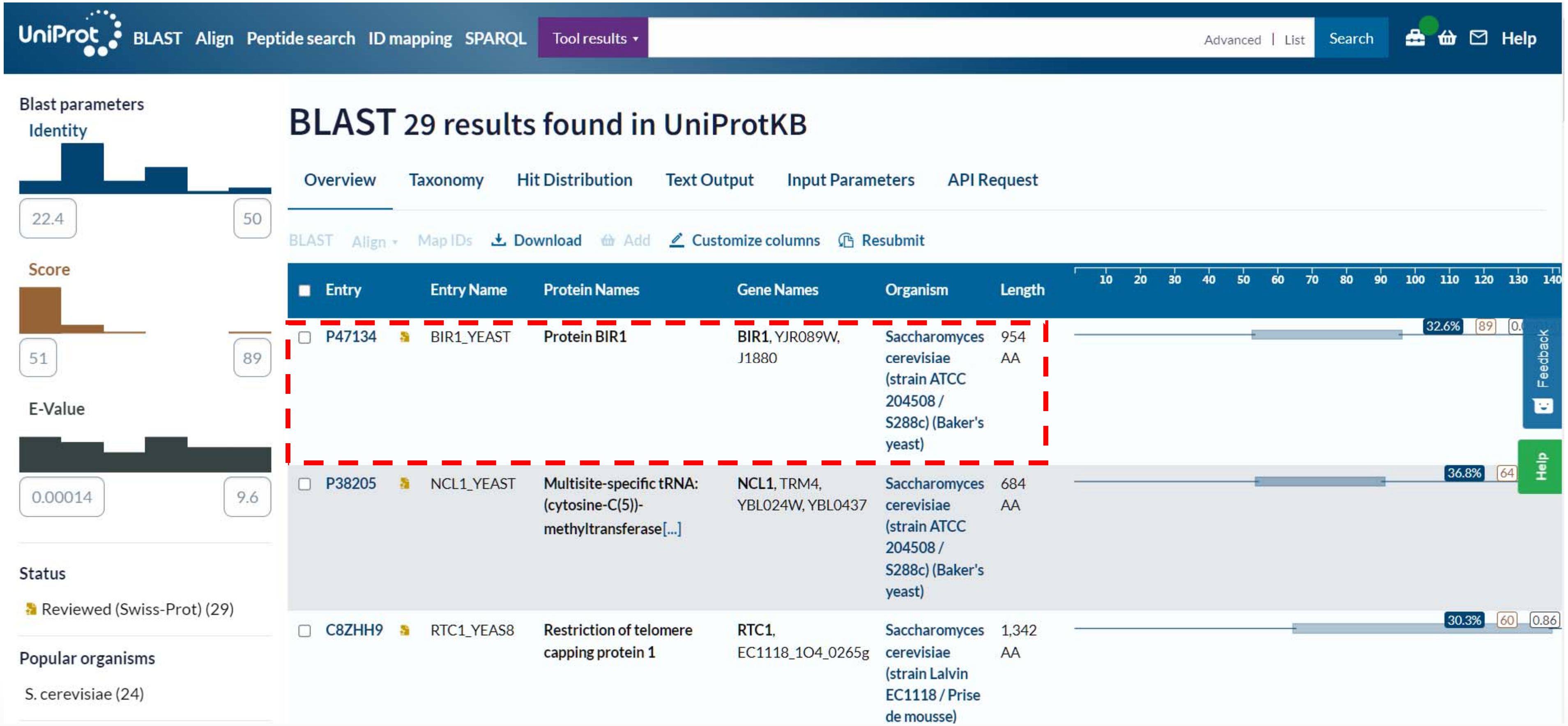
```
>sp|O15392|BIRC5_HUMAN Baculoviral IAP repeat-containing protein 5 OS=Homo sapiens OX=9606 GN=BIRC5 PE=1 SV=3
MGAPTLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFFC
FKELEGWEPDDDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNK
KKEFEETAKKVRRAIEQLAAMD
```

Your input contains 1 sequence

Target database: UniProtKB Swiss-Prot

Restrict by taxonomy: Saccharomyces cerevisiae [4932] ×

酵母BIR1: P47134

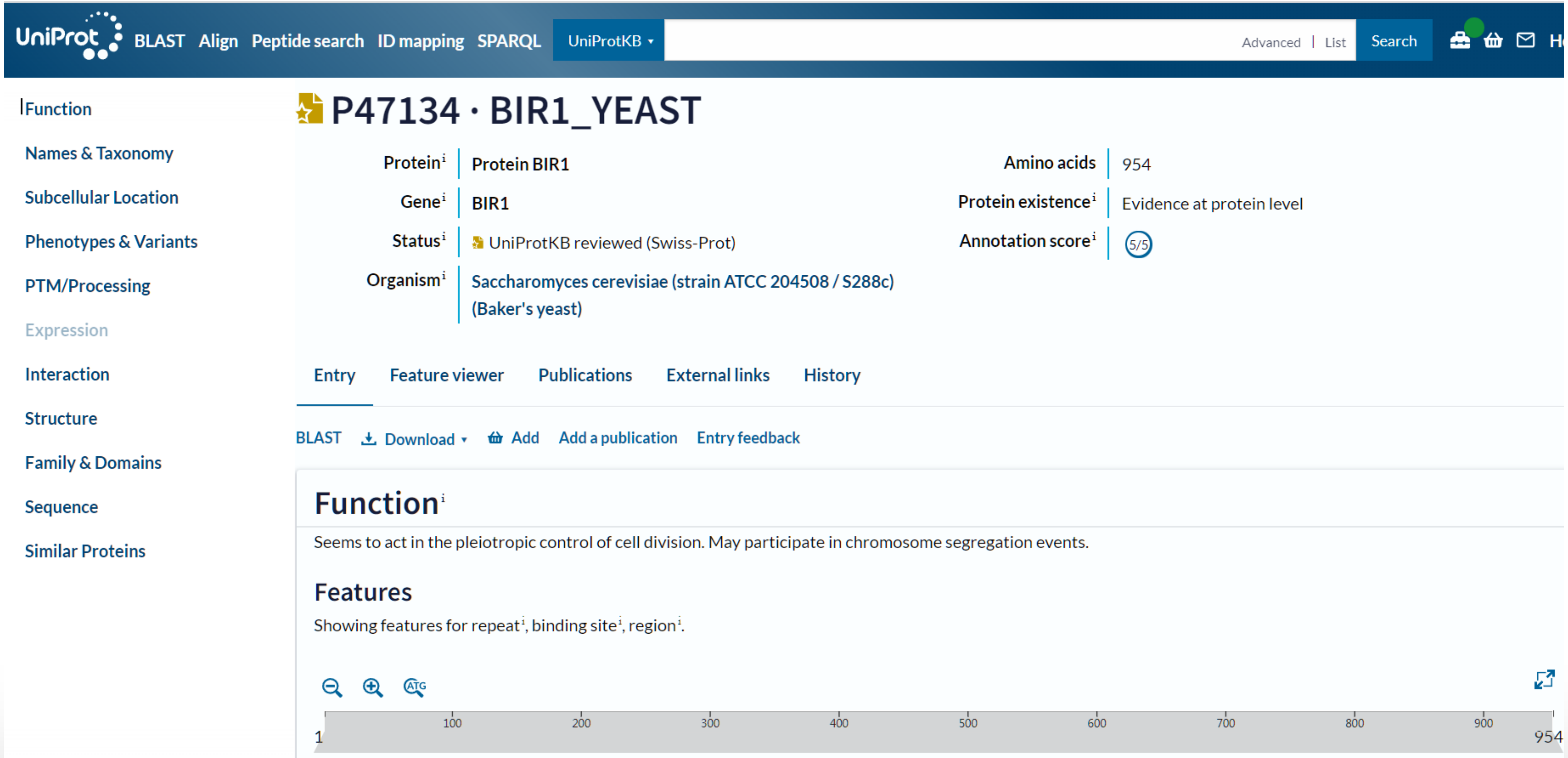


BLAST 29 results found in UniProtKB

☐	Entry	Entry Name	Protein Names	Gene Names	Organism	Length
☐	P47134	BIR1_YEAST	Protein BIR1	**BIR1**, YJR089W, J1880	Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)	954 AA
☐	P38205	NCL1_YEAST	Multisite-specific tRNA:(cytosine-C(5))-methyltransferase[...]	**NCL1**, TRM4, YBL024W, YBL0437	Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)	684 AA
☐	C8ZHH9	RTC1_YEAS8	Restriction of telomere capping protein 1	**RTC1**, EC1118_1O4_0265g	Saccharomyces cerevisiae (strain Lalvin EC1118 / Prise de mousse)	1,342 AA

酵母BIR1的信息

- 人类BIRC5在酵母中的同源序列可能是BIR1



P47134 · BIR1_YEAST

Protein	Protein BIR1
Gene	BIR1
Status	UniProtKB reviewed (Swiss-Prot)
Organism	Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)
Amino acids	954
Protein existence	Evidence at protein level
Annotation score	5/5

Function

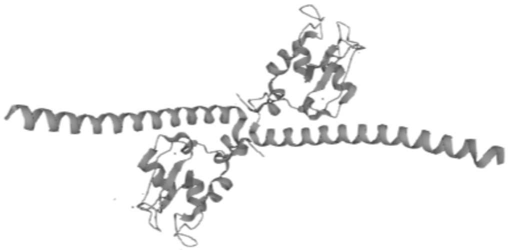
Seems to act in the pleiotropic control of cell division. May participate in chromosome segregation events.

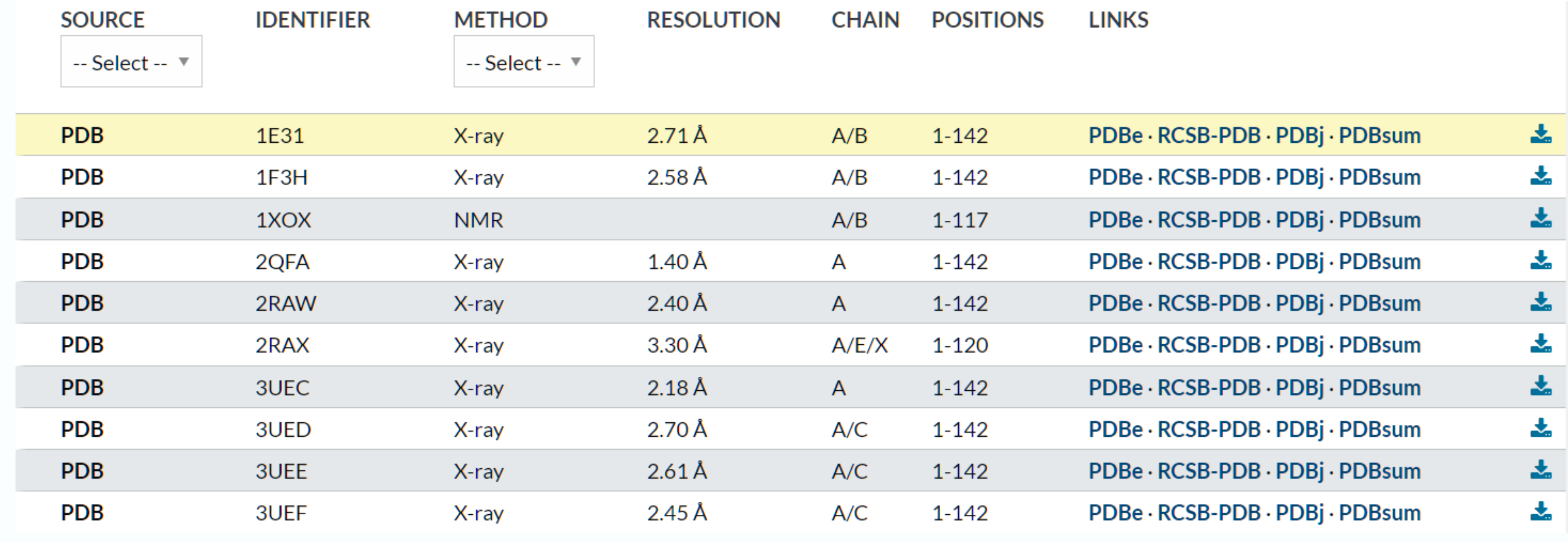
Features

Showing features for repeat, binding site, region.

PDB：三级结构数据库

https://www.uniprot.org/uniprotkb/O15392/entry#structure

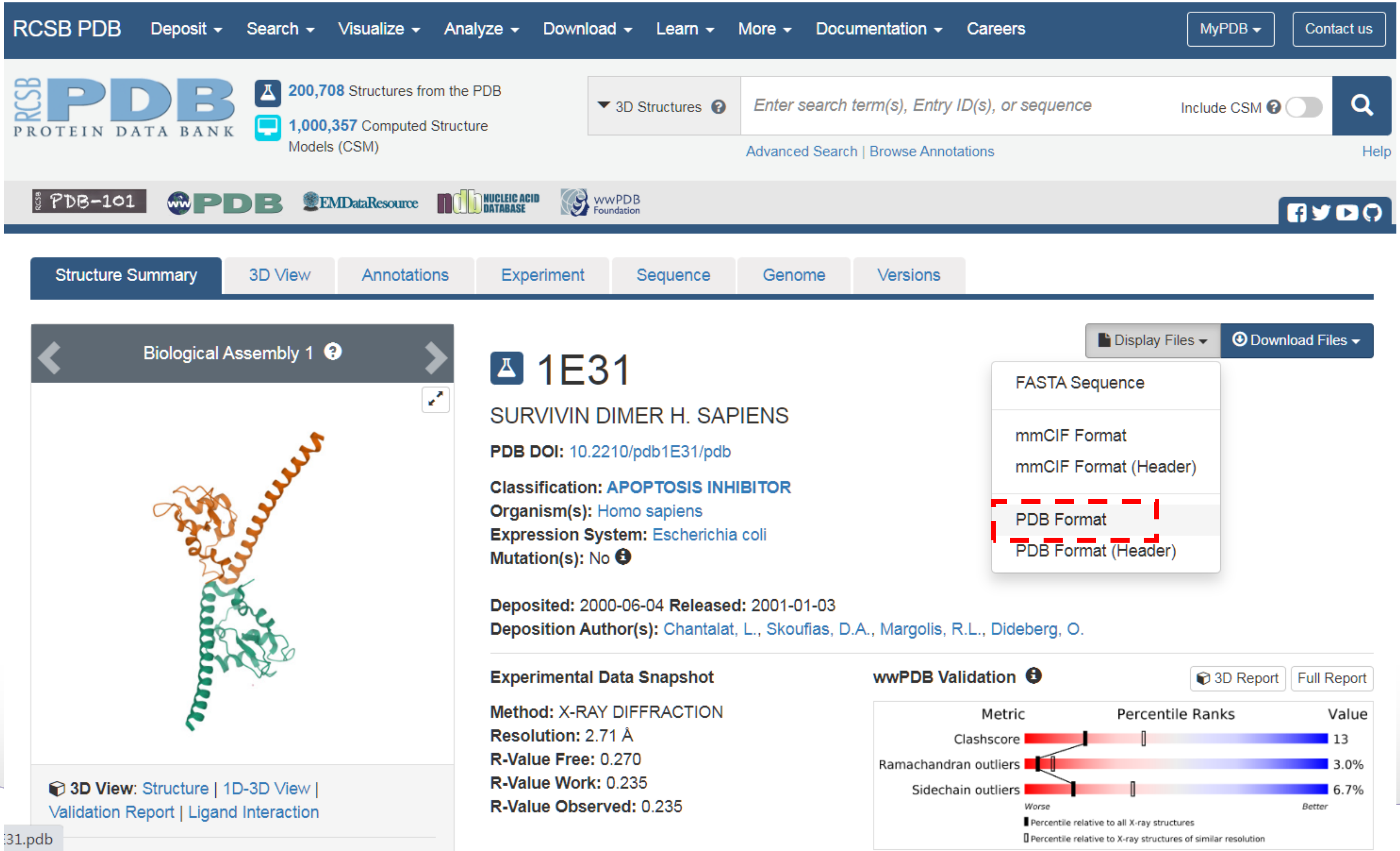




SOURCE	IDENTIFIER	METHOD	RESOLUTION	CHAIN	POSITIONS	LINKS
-- Select --		-- Select --				
PDB	1E31	X-ray	2.71 Å	A/B	1-142	PDBe · RCSB-PDB · PDBj · PDBsum
PDB	1F3H	X-ray	2.58 Å	A/B	1-142	PDBe · RCSB-PDB · PDBj · PDBsum
PDB	1XOX	NMR		A/B	1-117	PDBe · RCSB-PDB · PDBj · PDBsum
PDB	2QFA	X-ray	1.40 Å	A	1-142	PDBe · RCSB-PDB · PDBj · PDBsum
PDB	2RAW	X-ray	2.40 Å	A	1-142	PDBe · RCSB-PDB · PDBj · PDBsum
PDB	2RAX	X-ray	3.30 Å	A/E/X	1-120	PDBe · RCSB-PDB · PDBj · PDBsum
PDB	3UEC	X-ray	2.18 Å	A	1-142	PDBe · RCSB-PDB · PDBj · PDBsum
PDB	3UED	X-ray	2.70 Å	A/C	1-142	PDBe · RCSB-PDB · PDBj · PDBsum
PDB	3UEE	X-ray	2.61 Å	A/C	1-142	PDBe · RCSB-PDB · PDBj · PDBsum
PDB	3UEF	X-ray	2.45 Å	A/C	1-142	PDBe · RCSB-PDB · PDBj · PDBsum

BIRC5的三级结构信息

https://www.rcsb.org/structure/1E31



200,708 Structures from the PDB

1,000,357 Computed Structure Models (CSM)

1E31

SURVIVIN DIMER H. SAPIENS

PDB DOI: 10.2210/pdb1E31/pdb

Classification: APOPTOSIS INHIBITOR

Organism(s): Homo sapiens

Expression System: Escherichia coli

Mutation(s): No

Deposited: 2000-06-04 **Released:** 2001-01-03

Deposition Author(s): Chantalat, L., Skoufias, D.A., Margolis, R.L., Dideberg, O.

Experimental Data Snapshot

Method: X-RAY DIFFRACTION

Resolution: 2.71 Å

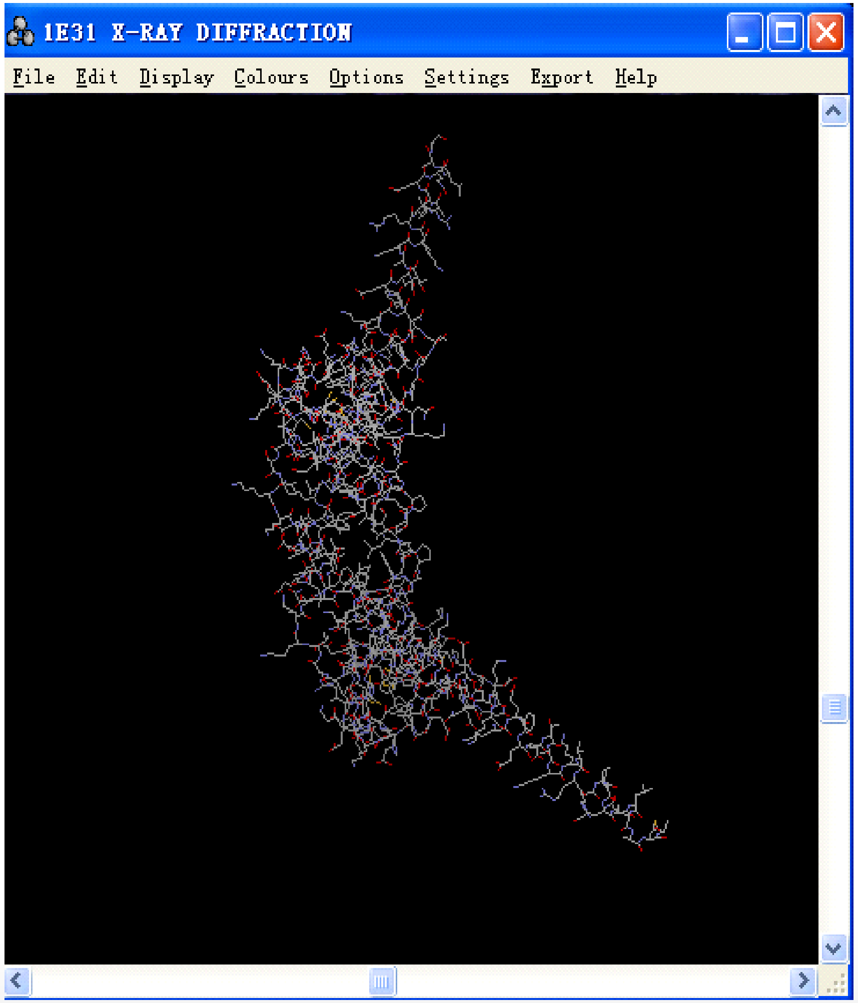
R-Value Free: 0.270

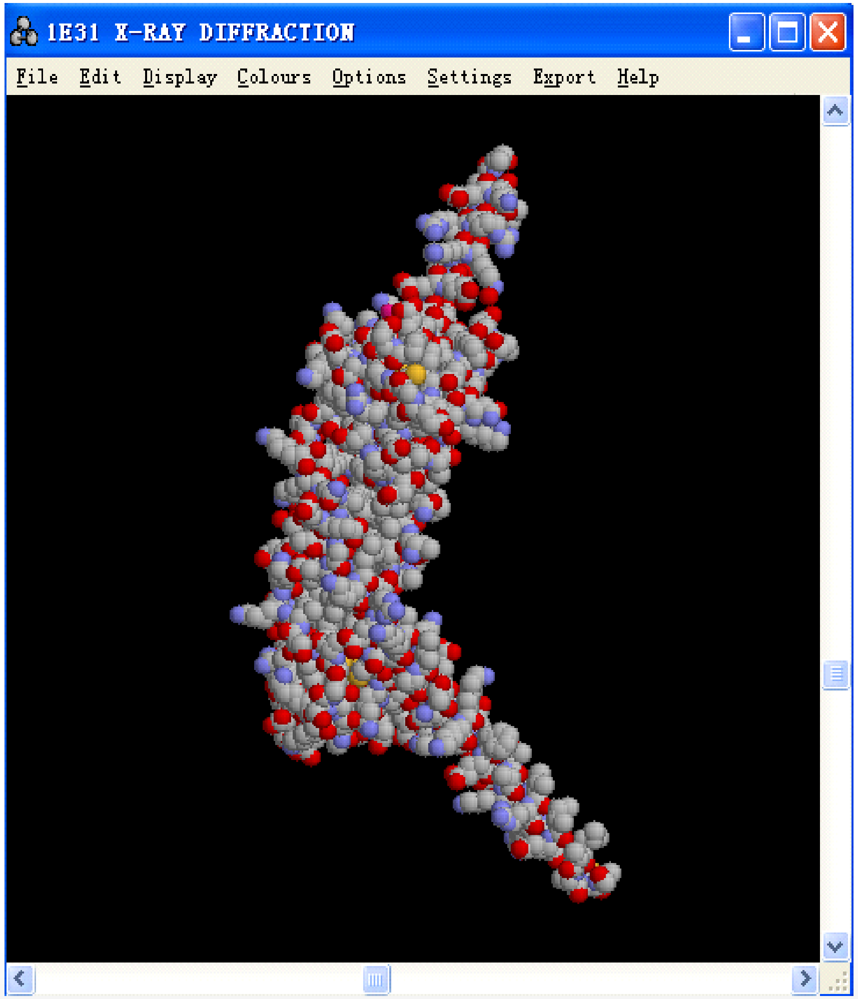
R-Value Work: 0.235

R-Value Observed: 0.235

wwPDB Validation

Raswin: 三级结构显示





结论2

- **BIRC5的细胞亚定位：胞质、细胞核**
- **BIRC5功能有：**
  - 在肿瘤形成过程中可能起一定作用
  - 阻碍G2/M期的细胞编程性凋亡
  - Chromosomal passenger complex (CPC) 的成员之一
  - 参与的生物学通路：癌症、直肠癌、乙肝
  - 蛋白产物在血浆和胃中表达
  - 在人类肿瘤中选择性高表达
- **人的BIRC5在酵母中的同源序列可能是BIR1**
- **BIRC5的三级结构已知，在PDB中的标识符为1E31**

作业 1#

- **通过DNA测序得到小鼠（*Mus musculus*）有丝分裂相关基因*X*，部分序列如下：**

GATGAGCTGCTTATCCTACAACGAGAAGTCGGACATCTGGTCCTTG
GGCTGCCTGCTGTATGAGCTGTGTGCACTAATGCCTCCCTTTACAG
CTTTCAACCAAAAAGAGCTAGCTGGGAAAATCAGGGAAGGGAGGT
TCAGGCGCATCCCCTACCGCTACTCTGATGGCTTGAATGACCTCAT
CACTCGGATGCTGAATTTAAAGGACTACCATCGACCTTCAGTGGAA
GAAATTCTGGAGAGCCCTTTGATAGCAGACTTGGTTGCAGAAGAGC
AAAGGAGAAATCTGGAGAGGAGAGGACGGCGCTCAGGCGAGCCT
TCGAAGCTGCCGGACTCCAGCCCTGTGCTGAGCGAGCTCAAGTTG
AAGGAAAGGCAACTGCAGGATCGAGAGCAAGCACTCAGAGCTCGG
GAGGACATCCT

问题：

- 1. 该小鼠基因*X*的名称是什么？GenBank数据库中的标识符和小鼠基因组的坐标是什么？
- 2. 基因*X*在人类基因组中的同源序列及其标识符是什么？
- 3. 在人类中，该同源基因的蛋白产物及标识符是什么？其功能和细胞亚定位是什么？该基因是酶吗？如果是的话，有没有保守的功能结构域？
- 4. 该基因在酵母（Budding yeast）中是否保守？如果保守，潜在的同原序列及标识符是什么？
- 5. 该基因的人类同源序列是否有三级结构？PDB中的标识符是什么？