UCSC Genome Browser

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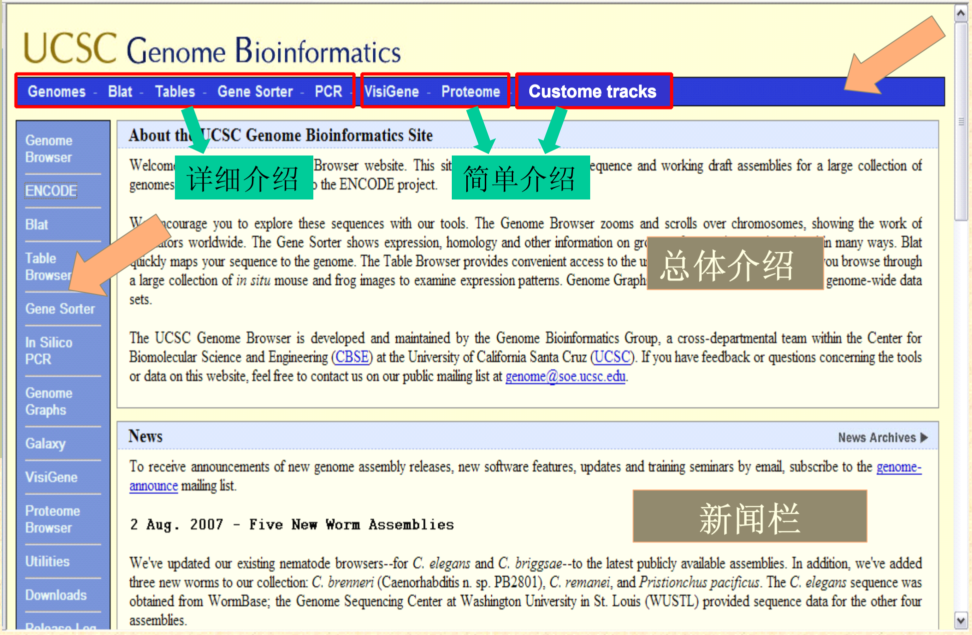
简 介

- 给浏览基因组数据提供了可靠和迅速的方式。
- 数据来源：约有一半的注释信息是UCSC通过来自公开的序列数据计算得出，另外一半来自世界各地的科学工作者。
- 本身并不下任何结论，而只是收集各种相关信息供用户参考。
- 支持数据库检索和序列相似性搜索。

The UCSC Home page: http://genome.ucsc.edu



详细介绍

简单介绍

总体介绍

新闻栏

About the UCSC Genome Bioinformatics Site

Welcom Browser website. This sit equence and working draft assemblies for a large collection of genomes the ENCODE project.

We courage you to explore these sequences with our tools. The Genome Browser zooms and scrolls over chromosomes, showing the work of tors worldwide. The Gene Sorter shows expression, homology and other information on gr in many ways. Blat quickly maps your sequence to the genome. The Table Browser provides convenient access to the u ou browse through a large collection of *in situ* mouse and frog images to examine expression patterns. Genome Graph genome-wide data sets.

The UCSC Genome Browser is developed and maintained by the Genome Bioinformatics Group, a cross-departmental team within the Center for Biomolecular Science and Engineering (CBSE) at the University of California Santa Cruz (UCSC). If you have feedback or questions concerning the tools or data on this website, feel free to contact us on our public mailing list at genome@soe.ucsc.edu.

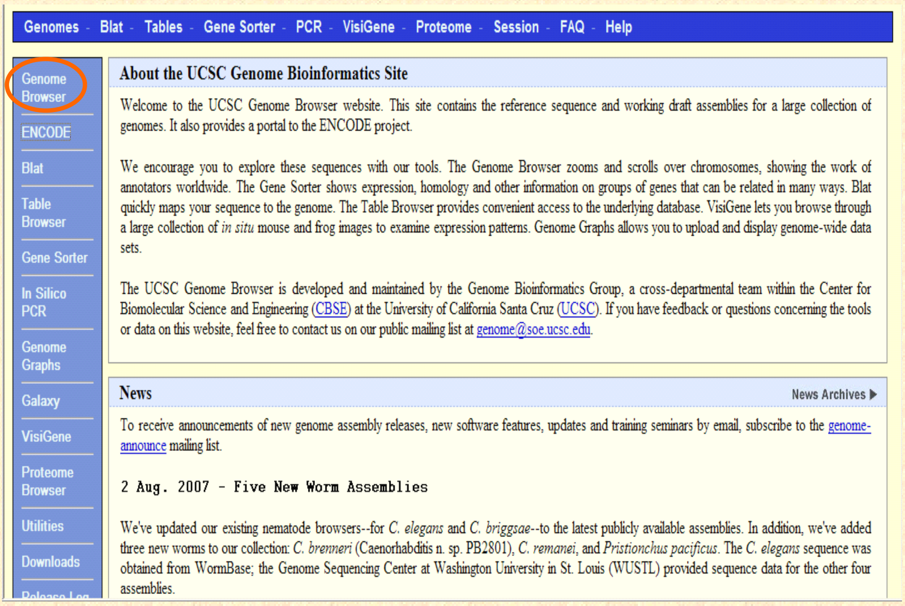
News

To receive announcements of new genome assembly releases, new software features, updates and training seminars by email, subscribe to the genome-announce mailing list.

`2 Aug. 2007 - Five New Worm Assemblies`

We've updated our existing nematode browsers--for *C. elegans* and *C. briggsae*--to the latest publicly available assemblies. In addition, we've added three new worms to our collection: *C. brenneri* (Caenorhabditis n. sp. PB2801), *C. remanei*, and *Pristionchus pacificus*. The *C. elegans* sequence was obtained from WormBase; the Genome Sequencing Center at Washington University in St. Louis (WUSTL) provided sequence data for the other four assemblies.

Genome Browser



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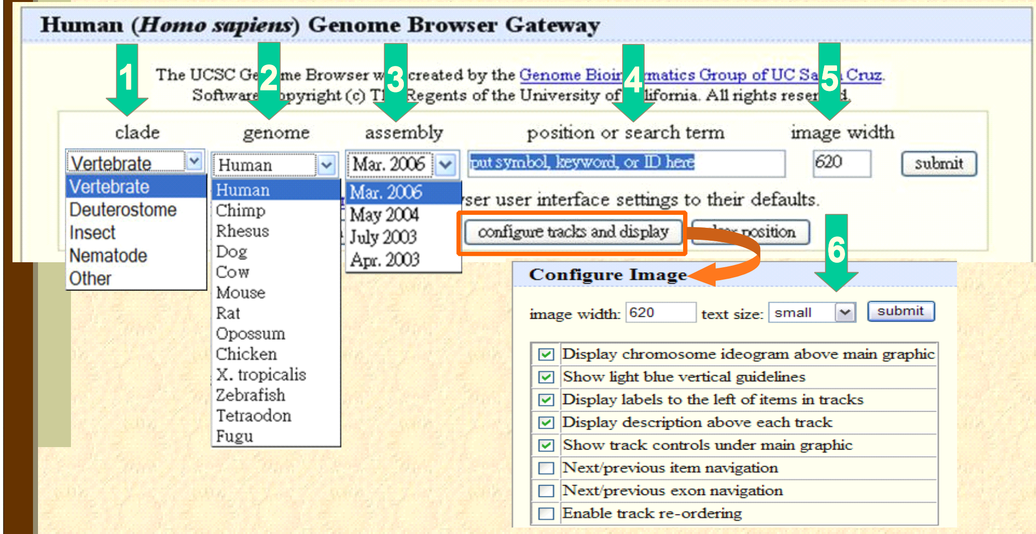
The Genome Browser 输入界面



Human (*Homo sapiens*) Genome Browser Gateway

The UCSC Ge me Browser w created by the Genome Bioin matics Group of UC Sa Cruz.
Software pyright (c) T Regents of the University of lifornia. All rights reser d.

clade: Vertebrate
genome: Human
assembly: Mar. 2006
position or search term: put symbol, keyword, or ID here
image width: 620

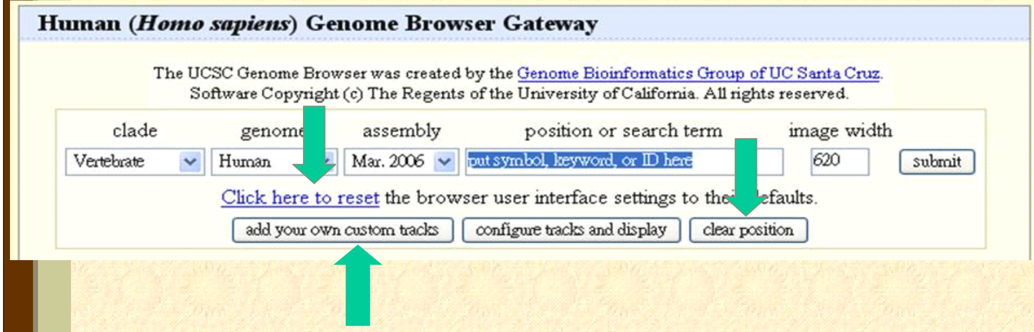
ser user interface settings to their defaults.

Configure Image

image width: 620 text size: small

- ☑ Display chromosome ideogram above main graphic
- ☑ Show light blue vertical guidelines
- ☑ Display labels to the left of items in tracks
- ☑ Display description above each track
- ☑ Show track controls under main graphic
- ☐ Next/previous item navigation
- ☐ Next/previous exon navigation
- ☐ Enable track re-ordering

The Genome Browser 输入界面



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Software Copyright (c) The Regents of the University of California. All rights reserved.

clade: Vertebrate
genome: Human
assembly: Mar. 2006
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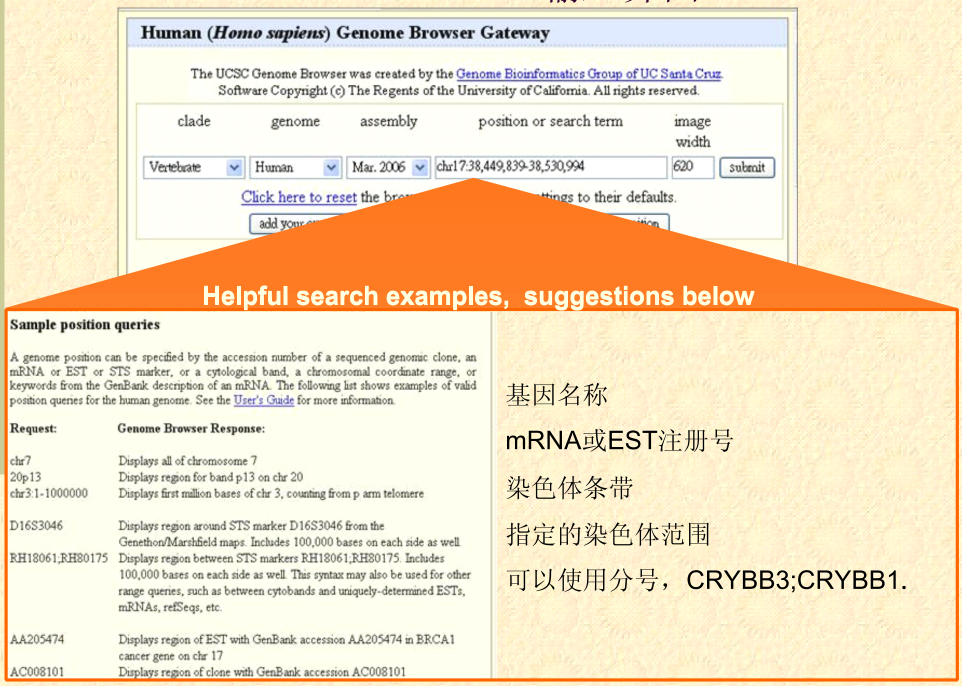
image width: 620

Click here to reset the browser user interface settings to their defaults.

The Genome Browser输入界面



Human (*Homo sapiens*) Genome Browser Gateway

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Software Copyright (c) The Regents of the University of California. All rights reserved.

clade	genome	assembly	position or search term	image width
Vertebrate	Human	Mar. 2006	chr17:38,449,839-38,530,994	620

Helpful search examples, suggestions below

Sample position queries

A genome position can be specified by the accession number of a sequenced genomic clone, an mRNA or EST or STS marker, or a cytological band, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the human genome. See the User's Guide for more information.

Request:	Genome Browser Response:
chr7	Displays all of chromosome 7
20p13	Displays region for band p13 on chr 20
chr3:1-1000000	Displays first million bases of chr 3, counting from p arm telomere
D16S3046	Displays region around STS marker D16S3046 from the Genethon/Marshfield maps. Includes 100,000 bases on each side as well.
RH18061;RH80175	Displays region between STS markers RH18061;RH80175. Includes 100,000 bases on each side as well. This syntax may also be used for other range queries, such as between cytobands and uniquely-determined ESTs, mRNAs, refSeqs, etc.
AA205474	Displays region of EST with GenBank accession AA205474 in BRCA1 cancer gene on chr 17
AC008101	Displays region of clone with GenBank accession AC008101

基因名称

mRNA或EST注册号

染色体条带

指定的染色体范围

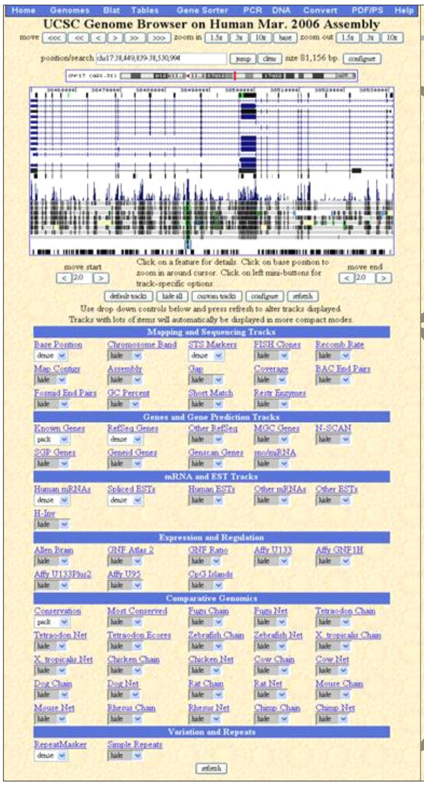
可以使用分号，CRYBB3;CRYBB1.

The Genome Browser

- 搜索实例: human, Mar 2006 assembly, BRCA1

UCSC Genes

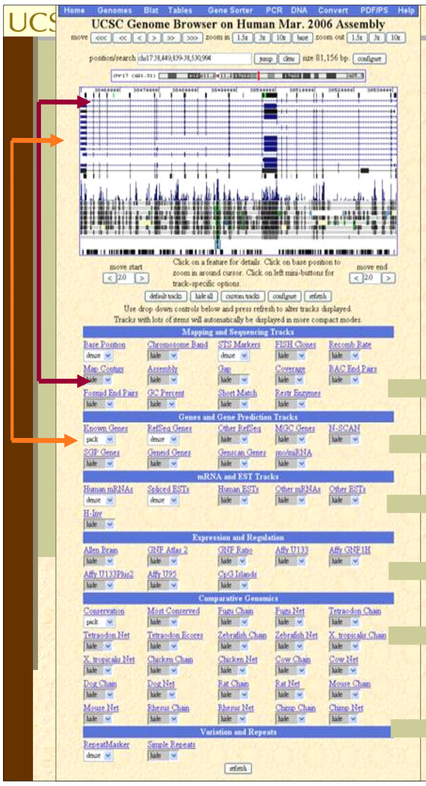
```
BRCA1 (uc002ide.1) at chr17:38496978-38510499 - breast cancer 1, early onset isoform
BRCA1 (uc002idd.1) at chr17:38496644-38529658 - breast cancer 1, early onset isoform
BRCA1 (uc002idc.1) at chr17:38468876-38530994 - breast cancer 1, early onset isoform
BRCA1 (uc002idb.1) at chr17:38449840-38530994 - breast cancer 1, early onset isoform
BRCA1 (uc002ida.1) at chr17:38449840-38530994 - breast cancer 1, early onset isoform
BRCA1 (uc002icz.1) at chr17:38449840-38530994 - breast cancer 1, early onset isoform
BRCA1 (uc002icy.1) at chr17:38449840-38530994 - breast cancer 1, early onset isoform
BRCA1 (uc002icx.1) at chr17:38449840-38530994 - breast cancer 1, early onset isoform
BRCA1 (uc002icw.1) at chr17:38449840-38530994 - breast cancer 1, early onset isoform 1
BRCA1 (uc002icv.1) at chr17:38449840-38530994 - breast cancer 1, early onset isoform
BRCA1 (uc002icu.1) at chr17:38449840-38530994 - BRCA1 protein.
BRCA1 (uc002ict.1) at chr17:38449840-38530994 - breast cancer 1, early onset isoform 1
BRCA1 (uc002ics.1) at chr17:38449840-38530994 - breast cancer 1, early onset isoform
BRCA1 (uc002icr.1) at chr17:38449840-38530994 - breast cancer 1, early onset isoform
BRCA1 (uc002icq.1) at chr17:38449840-38530994 - breast cancer 1, early onset isoform 1
BRCA1 (uc002icp.1) at chr17:38449840-38530831 - Breast and ovarian cancer susceptibility protein splice variant.
BRCA1 (uc002ico.1) at chr17:38449840-38530657 - breast cancer 1, early onset isoform 1
BRCC3 (uc004fnb.1) at chrX:153952904-154004543 - BRCA1/BRCA2-containing complex, subunit 3
BRCC3 (uc004fna.1) at chrX:153952904-154004543 - BRCA1/BRCA2-containing complex, subunit 3
BAP1 (uc003ddx.1) at chr3:52410065-52419049 - BRCA1 associated protein-1
BARD1 (uc002veu.1) at chr2:215301522-215382611 - BRCA1 associated RING domain 1
BRIP1 (uc002izl.1) at chr17:57116915-57213148 - BRCA1 interacting protein C-terminal helicase 1
BRIP1 (uc002izk.1) at chr17:57114767-57295537 - BRCA1 interacting protein C-terminal helicase 1
BRAP (uc001tsn.1) at chr12:110566279-110608122 - BRCA1 associated protein
COBRA1 (uc004cmm.1) at chr9:139269768-139287814 - cofactor of BRCA1
NBR1 (uc002kgz.1) at chr17_random:469329-480810 - neighbor of BRCA1 gene 1
NBR1 (uc002idl.1) at chr17:38576772-38719233 - neighbor of BRCA1 gene 1
NBR1 (uc002idk.1) at chr17:38576037-38719233 - neighbor of BRCA1 gene 1
NBR1 (uc002idj.1) at chr17:38576024-38719233 - neighbor of BRCA1 gene 1
NBR2 (uc002idf.1) at chr17:38531126-38545868 - Homo sapiens neighbor of BRCA1 gene 2, mRNA (cDNA clone IMAGE:4826858), with apparent reta
NBR2 (uc002idh.1) at chr17:38531126-38559214 - Homo sapiens chromosome 17 neighbor of BRCA1 gene 2 (NBR2) mRNA, complete cds, alternative
NBR2 (uc002idg.1) at chr17:38531126-38550651 - Homo sapiens chromosome 17 neighbor of BRCA1 gene 2 (NBR2) mRNA, complete cds, alternative
```



Genome Browser
结果显示页面

基因组注释信息显示窗口

显示结果的调节部分
(112条路径)

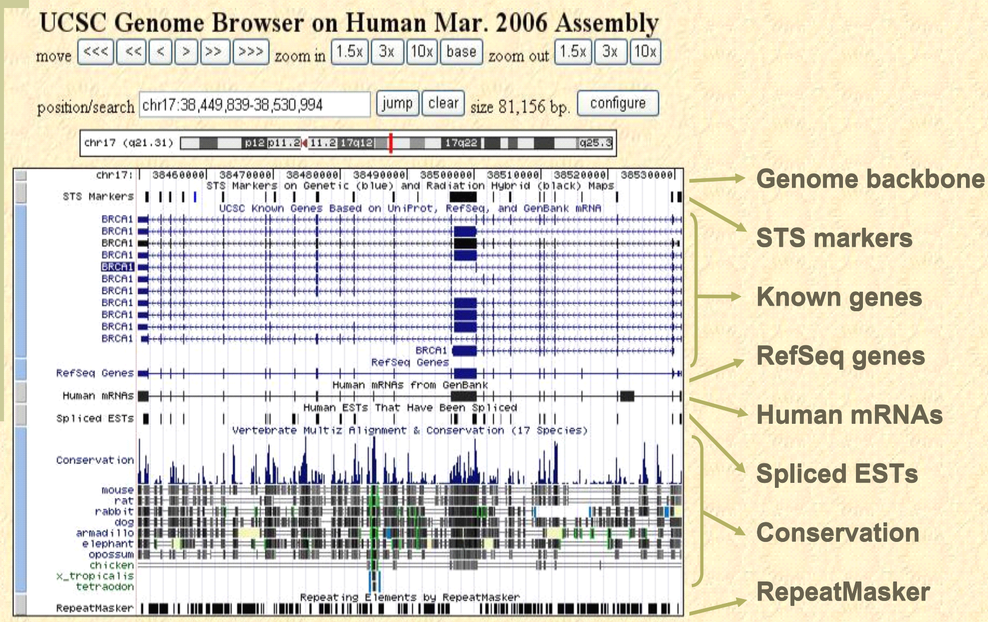


Genome Browser
结果显示页面

六组数据

- Mapping and Sequencing Tracks
- Genes and Gene Prediction Tracks
- mRNA and EST Tracks
- Expression and Regulation
- Comparative Genomics
- Variation and Repeats

Genome Browser示例：BRCA1



UCSC Genome Browser on Human Mar. 2006 Assembly

position/search chr17:38,449,839-38,530,994 size 81,156 bp.

Genome backbone

STS markers

Known genes

RefSeq genes

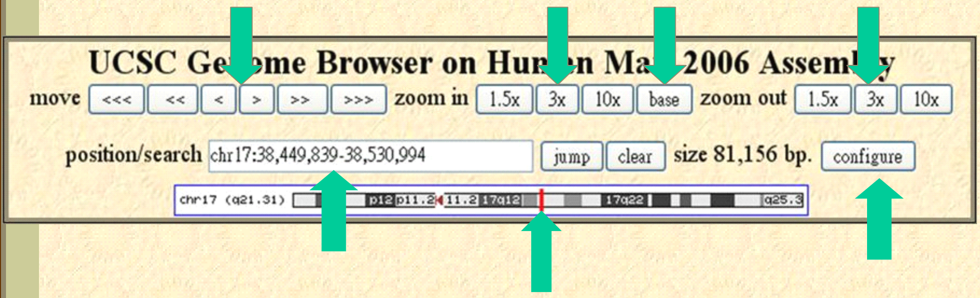
Human mRNAs

Spliced ESTs

Conservation

RepeatMasker

Genome Browser示例：BRCA1



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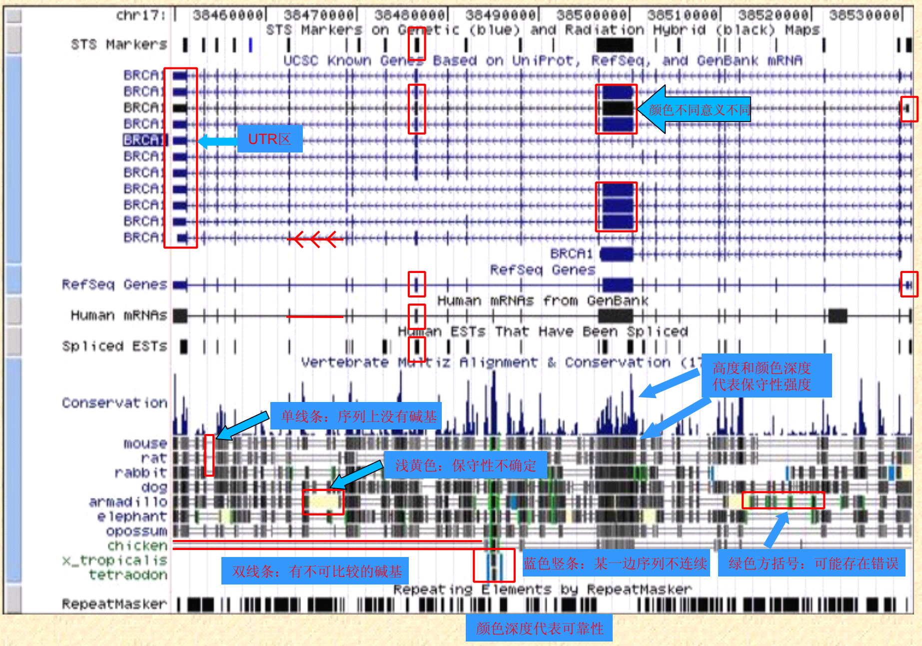


颜色不同意义不同

UTR区

高度和颜色深度代表保守性强度

单线条：序列上没有碱基

浅黄色：保守性不确定

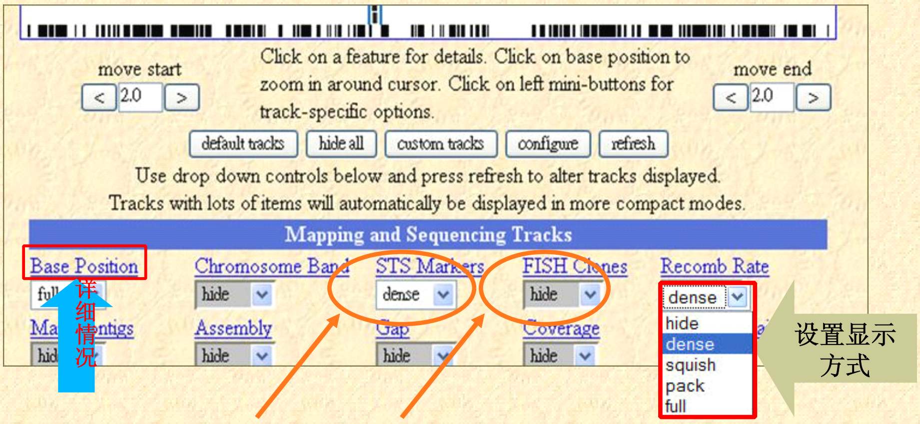
双线条：有不可比较的碱基

蓝色竖条：某一边序列不连续

绿色方括号：可能存在错误

颜色深度代表可靠性

Genome Browser示例：BRCA1



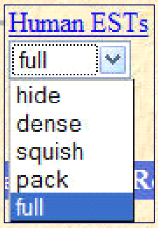
Click on a feature for details. Click on base position to zoom in around cursor. Click on left mini-buttons for track-specific options.

Use drop down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes.

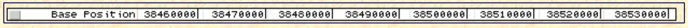
Base Position: full
Chromosome Band: hide
STS Markers: dense
FISH Clones: hide
Recomb Rate: dense
Map Contigs: hide
Assembly: hide
Gap: hide
Coverage: hide

详细情况

设置显示方式

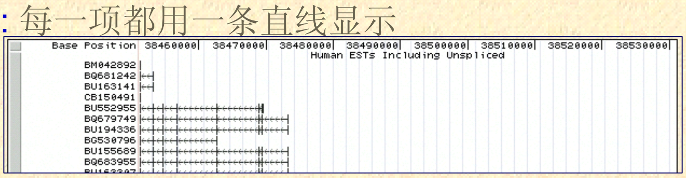


- Hide: 不显示

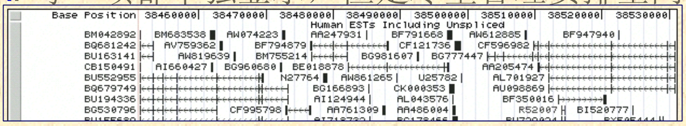


- Dense: 所有信息在一条直线里显示出来

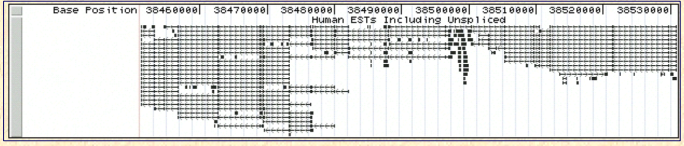
- Full: 每一项都用一条直线显示

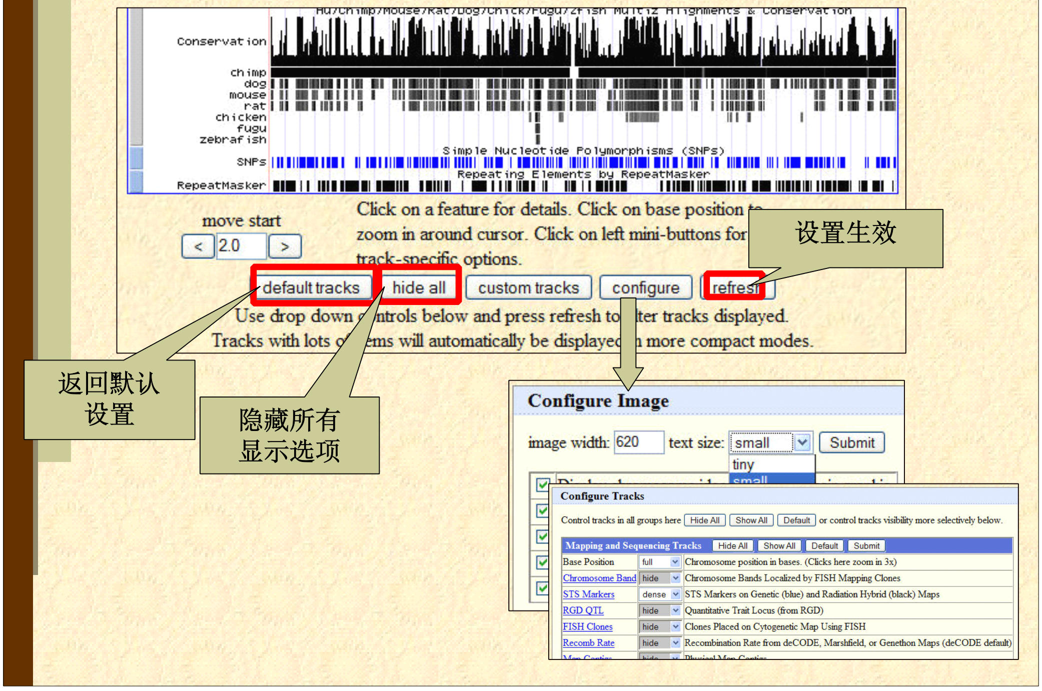


- Pack: 每一项都单独显示，但是尽量合理安排空间



- Squish: 和pack类似，但是高度只有一半





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设置生效

返回默认设置

隐藏所有显示选项

Configure Image

image width: 620 text size: small Submit

tiny
small

Configure Tracks

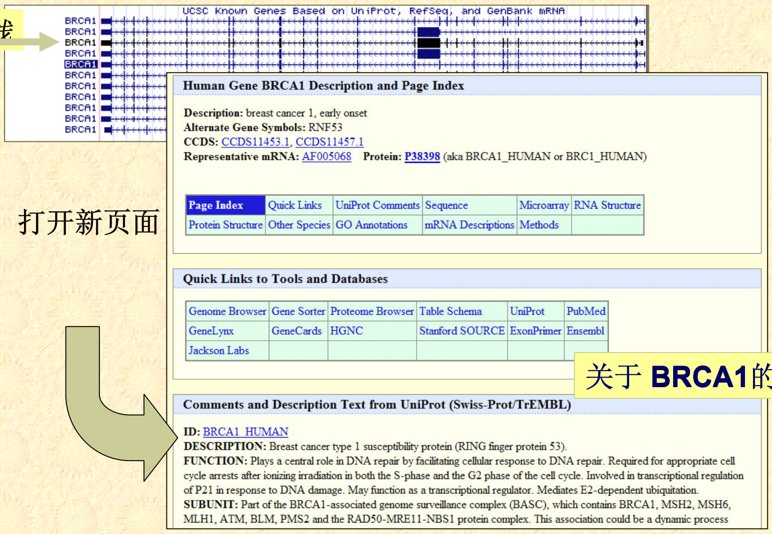
Control tracks in all groups here Hide All Show All Default or control tracks visibility more selectively below.

Mapping and Sequencing Tracks Hide All Show All Default Submit

Base Position	full	Chromosome position in bases. (Clicks here zoom in 3x)
Chromosome Band	hide	Chromosome Bands Localized by FISH Mapping Clones
STS Markers	dense	STS Markers on Genetic (blue) and Radiation Hybrid (black) Maps
RGD QTL	hide	Quantitative Trait Locus (from RGD)
FISH Clones	hide	Clones Placed on Cytogenetic Map Using FISH
Recomb Rate	hide	Recombination Rate from deCODE, Marshfield, or Genethon Maps (deCODE default)
Map Contigs	hide	Physical Map Contigs

Genome Browser示例：BRCA1

将返回关于该项的详细描述



点击某条直线

打开新页面

Human Gene BRCA1 Description and Page Index

Description: breast cancer 1, early onset
Alternate Gene Symbols: RNF53
CCDS: CCDS11453.1, CCDS11457.1
Representative mRNA: AF005068 **Protein:** P38398 (aka BRCA1_HUMAN or BRC1_HUMAN)

Page Index	Quick Links	UniProt Comments	Sequence	Microarray	RNA Structure
Protein Structure	Other Species	GO Annotations	mRNA Descriptions	Methods	

Quick Links to Tools and Databases

Genome Browser	Gene Sorter	Proteome Browser	Table Schema	UniProt	PubMed
GeneLynx	GeneCards	HGNC	Stanford SOURCE	ExonPrimer	Ensembl
Jackson Labs					

关于 **BRCA1**的详细情况

Comments and Description Text from UniProt (Swiss-Prot/TrEMBL)

ID: BRCA1_HUMAN
DESCRIPTION: Breast cancer type 1 susceptibility protein (RING finger protein 53).
FUNCTION: Plays a central role in DNA repair by facilitating cellular response to DNA repair. Required for appropriate cell cycle arrests after ionizing irradiation in both the S-phase and the G2 phase of the cell cycle. Involved in transcriptional regulation of P21 in response to DNA damage. May function as a transcriptional regulator. Mediates E2-dependent ubiquitation.
SUBUNIT: Part of the BRCA1-associated genome surveillance complex (BASC), which contains BRCA1, MSH2, MSH6, MLH1, ATM, BLM, PMS2 and the RAD50-MRE11-NBS1 protein complex. This association could be a dynamic process

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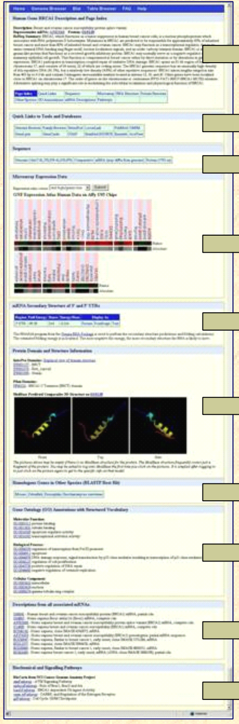


informative description

other resource links

links to sequences

microarray data

mRNA secondary structure

protein domains/structure

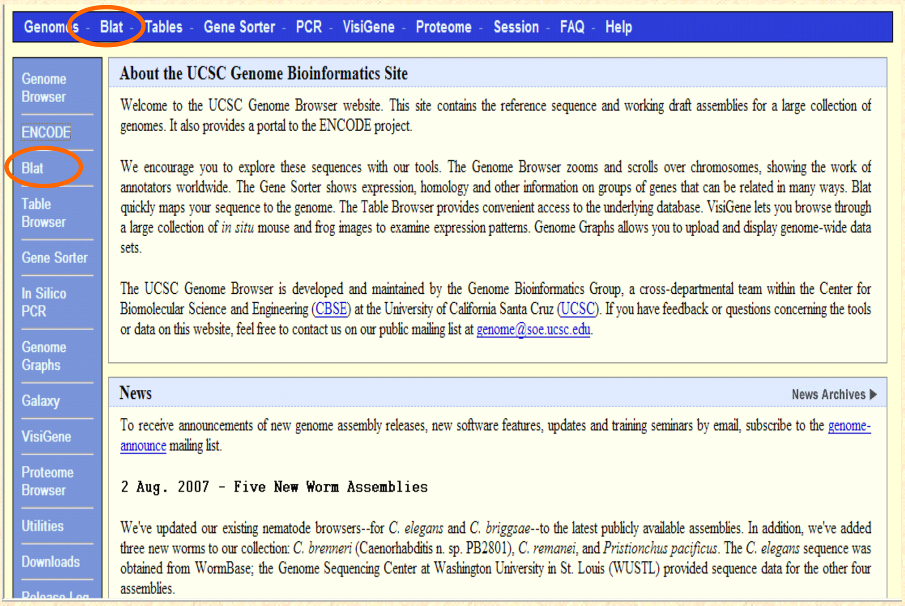
homologs in other species

Gene Ontology™ descriptions

mRNA descriptions

pathways

Blat



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Blat

- 对于DNA序列，BLAT是用来设计寻找95%及以上相似至少40个碱基的序列。
- 对于蛋白序列，BLAT是用来设计寻找80%及以上相似至少20个氨基酸的序列。
- 用法：--查找mRNA或蛋白在基因组中的位置

  --决定基因外显子的结构

  --显示全长基因的编码区域

  --分离一个物种他自己的EST

  --查找基因家族

  --从其他物种中查找人类基因的同源物

Blat

Human BLAT Search

BLAT Search Genome

Genome: Human
Assembly: Mar. 2006
Query type: protein
Sort output: query,score
Output type: hyperlink

MAAAWTVVLVTLVLGLAVAGPVPTS

用于搜索的序列

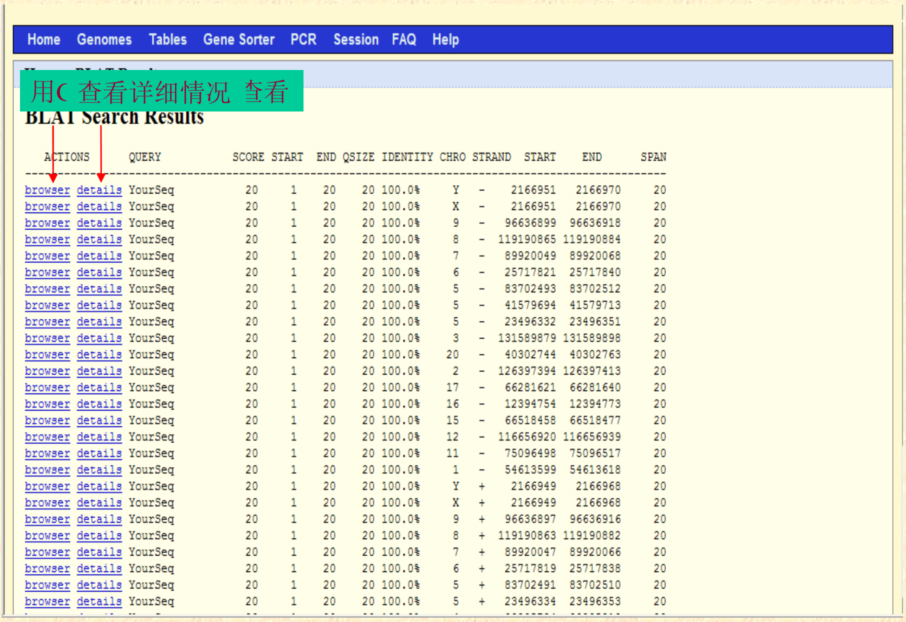
Paste in a query sequence to find its location in the the genome. Multiple sequences may be searched if separated by lines starting with '>' followed by the sequence name.

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

Upload sequence:

上传序列文件

Blat 结果

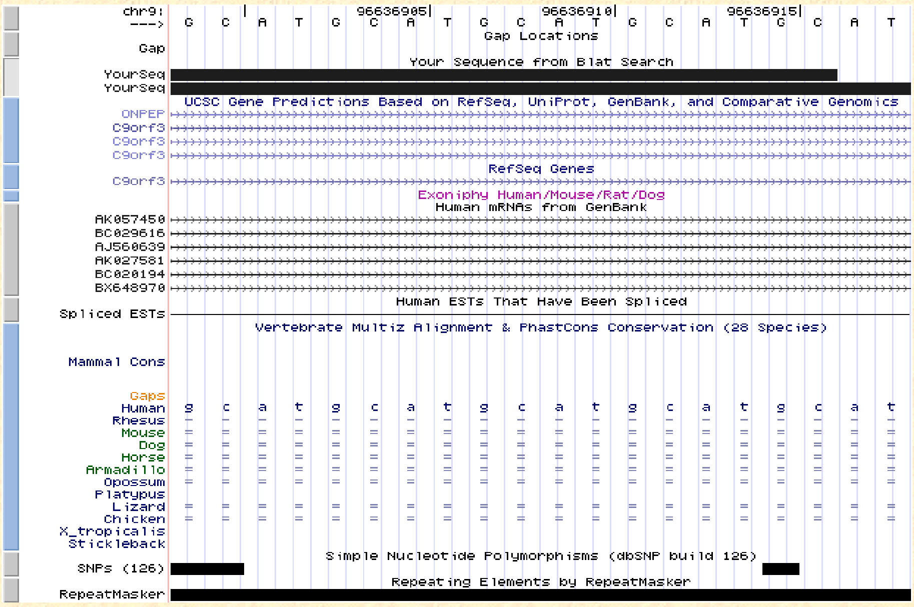


用C 查看详细情况 查看

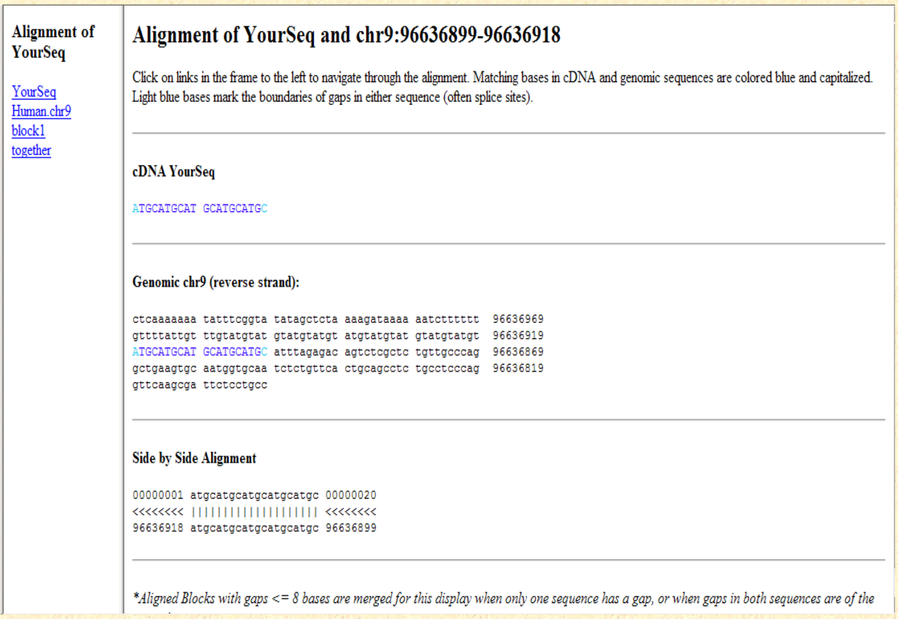
BLAT Search Results

```
   ACTIONS      QUERY           SCORE START  END QSIZE IDENTITY CHRO STRAND  START    END       SPAN
---------------------------------------------------------------------------------------------------
browser details YourSeq           20     1    20    20 100.0%     Y   -     2166951   2166970    20
browser details YourSeq           20     1    20    20 100.0%     X   -     2166951   2166970    20
browser details YourSeq           20     1    20    20 100.0%     9   -    96636899  96636918    20
browser details YourSeq           20     1    20    20 100.0%     8   -   119190865 119190884    20
browser details YourSeq           20     1    20    20 100.0%     7   -    89920049  89920068    20
browser details YourSeq           20     1    20    20 100.0%     6   -    25717821  25717840    20
browser details YourSeq           20     1    20    20 100.0%     5   -    83702493  83702512    20
browser details YourSeq           20     1    20    20 100.0%     5   -    41579694  41579713    20
browser details YourSeq           20     1    20    20 100.0%     5   -    23496332  23496351    20
browser details YourSeq           20     1    20    20 100.0%     3   -   131589879 131589898    20
browser details YourSeq           20     1    20    20 100.0%    20   -    40302744  40302763    20
browser details YourSeq           20     1    20    20 100.0%     2   -   126397394 126397413    20
browser details YourSeq           20     1    20    20 100.0%    17   -    66281621  66281640    20
browser details YourSeq           20     1    20    20 100.0%    16   -    12394754  12394773    20
browser details YourSeq           20     1    20    20 100.0%    15   -    66518458  66518477    20
browser details YourSeq           20     1    20    20 100.0%    12   -   116656920 116656939    20
browser details YourSeq           20     1    20    20 100.0%    11   -    75096498  75096517    20
browser details YourSeq           20     1    20    20 100.0%     1   -    54613599  54613618    20
browser details YourSeq           20     1    20    20 100.0%     Y   +     2166949   2166968    20
browser details YourSeq           20     1    20    20 100.0%     X   +     2166949   2166968    20
browser details YourSeq           20     1    20    20 100.0%     9   +    96636897  96636916    20
browser details YourSeq           20     1    20    20 100.0%     8   +   119190863 119190882    20
browser details YourSeq           20     1    20    20 100.0%     7   +    89920047  89920066    20
browser details YourSeq           20     1    20    20 100.0%     6   +    25717819  25717838    20
browser details YourSeq           20     1    20    20 100.0%     5   +    83702491  83702510    20
browser details YourSeq           20     1    20    20 100.0%     5   +    23496334  23496353    20
```

用Genome Browser查看Blat结果



Blat结果的详细情况



Alignment of YourSeq

YourSeq
Human.chr9
block1
together

Alignment of YourSeq and chr9:96636899-96636918

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

cDNA YourSeq

```
ATGCATGCAT GCATGCATGC
```

Genomic chr9 (reverse strand):

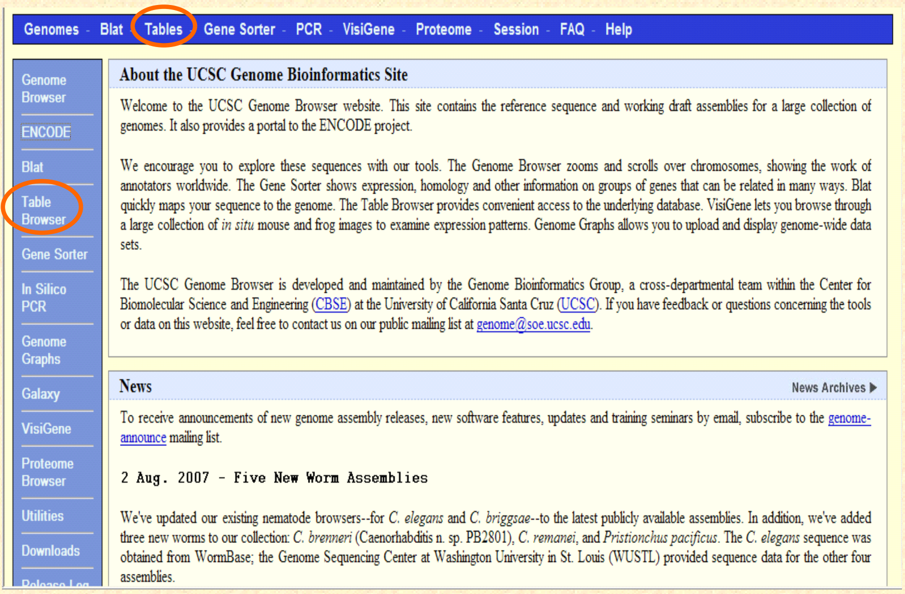
```
ctcaaaaaaa tatttcggta tatagctcta aaagataaaa aatctttttt  96636969
gttttattgt ttgtatgtat gtatgtatgt atgtatgtat gtatgtatgt  96636919
ATGCATGCAT GCATGCATGC atttagagac agtctcgctc tgttgcccag  96636869
gctgaagtgc aatggtgcaa tctctgttca ctgcagcctc tgcctcccag  96636819
gttcaagcga ttctcctgcc
```

Side by Side Alignment

```
00000001 atgcatgcatgcatgcatgc 00000020
<<<<<<<< |||||||||||||||||||| <<<<<<<<
96636918 atgcatgcatgcatgcatgc 96636899
```

**Aligned Blocks with gaps <= 8 bases are merged for this display when only one sequence has a gap, or when gaps in both sequences are of the*

Table Browser



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The UCSC Genome Browser is developed and maintained by the Genome Bioinformatics Group, a cross-departmental team within the Center for Biomolecular Science and Engineering (CBSE) at the University of California Santa Cruz (UCSC). If you have feedback or questions concerning the tools or data on this website, feel free to contact us on our public mailing list at genome@soe.ucsc.edu.

News

To receive announcements of new genome assembly releases, new software features, updates and training seminars by email, subscribe to the genome-announce mailing list.

`2 Aug. 2007 - Five New Worm Assemblies`

We've updated our existing nematode browsers--for *C. elegans* and *C. briggsae*--to the latest publicly available assemblies. In addition, we've added three new worms to our collection: *C. brenneri* (Caenorhabditis n. sp. PB2801), *C. remanei*, and *Pristionchus pacificus*. The *C. elegans* sequence was obtained from WormBase; the Genome Sequencing Center at Washington University in St. Louis (WUSTL) provided sequence data for the other four assemblies.

- From the Genome Browser home page, select Table Browser

Table Browser

- 提供了访问数据库的便利入口.
- 用文本形式来获取存储在Genome Browser数据库中的基因组汇编和注释数据。

功能

- 为整个染色体或者一些特定的序列获取DNA序列信息或者注释信息。
- 用特定的条件对输出结果进行筛选。
- 创建自己的路径，并且在Genome Browser里可视化地显示出来。
- 整合多重查询，并为其产生相关的输出。
- 为选定的数据集提供基本的统计结果。
- 显示一个数据表格的详细情况，并且列出在数据库中与其相关的所有表格。
- 根据其它应用程序和数据库的要求，对输出结果进行格式化。

Table Browser

实例:

下载从第四条染色体开始简单重复10次以上 的人类序列。

Table Browser 实例

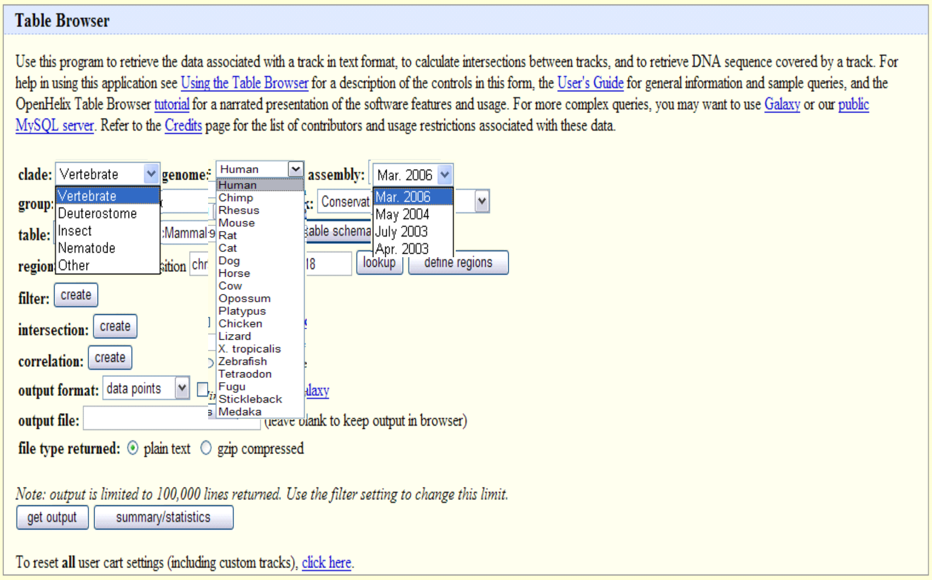


Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see Using the Table Browser for a description of the controls in this form, the User's Guide for general information and sample queries, and the OpenHelix Table Browser tutorial for a narrated presentation of the software features and usage. For more complex queries, you may want to use Galaxy or our public MySQL server. Refer to the Credits page for the list of contributors and usage restrictions associated with these data.

clade: Vertebrate **genome:** Human **assembly:** Mar. 2006

output format: data points

output file: (leave blank to keep output in browser)

file type returned: ● plain text ○ gzip compressed

Note: output is limited to 100,000 lines returned. Use the filter setting to change this limit.

To reset **all** user cart settings (including custom tracks), click here.

Table Browser 实例

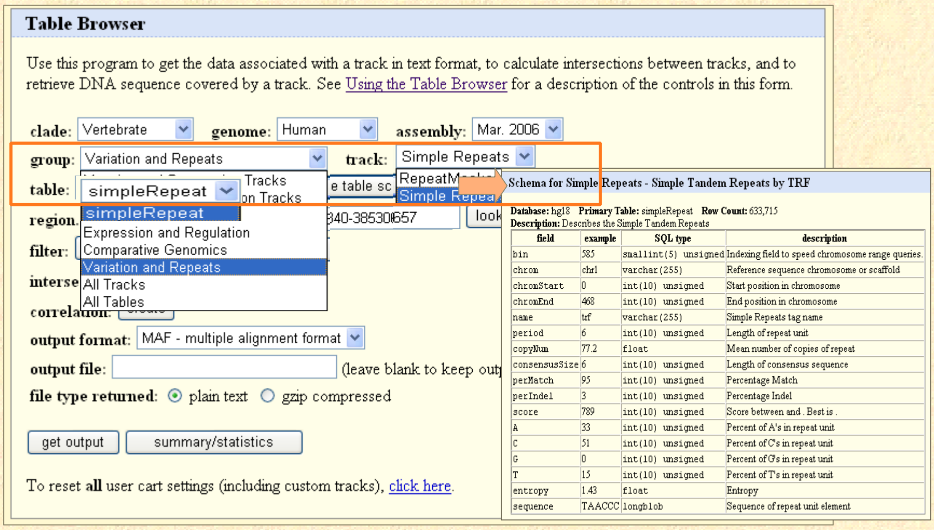


Table Browser

Use this program to get the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. See Using the Table Browser for a description of the controls in this form.

clade: Vertebrate **genome:** Human **assembly:** Mar. 2006

group: Variation and Repeats **track:** Simple Repeats

table: simpleRepeat

output format: MAF - multiple alignment format

output file: (leave blank to keep out

file type returned: ● plain text ○ gzip compressed

To reset **all** user cart settings (including custom tracks), click here.

Schema for Simple Repeats - Simple Tandem Repeats by TRF

Database: hg18 **Primary Table:** simpleRepeat **Row Count:** 633,715
Description: Describes the Simple Tandem Repeats

field	example	SQL type	description
bin	585	smallint(5) unsigned	Indexing field to speed chromosome range queries.
chrom	chr1	varchar(255)	Reference sequence chromosome or scaffold
chromStart	0	int(10) unsigned	Start position in chromosome
chromEnd	468	int(10) unsigned	End position in chromosome
name	trf	varchar(255)	Simple Repeats tag name
period	6	int(10) unsigned	Length of repeat unit
copyNum	77.2	float	Mean number of copies of repeat
consensusSize	6	int(10) unsigned	Length of consensus sequence
perMatch	95	int(10) unsigned	Percentage Match
perIndel	3	int(10) unsigned	Percentage Indel
score	789	int(10) unsigned	Score between and . Best is .
A	33	int(10) unsigned	Percent of A's in repeat unit
C	51	int(10) unsigned	Percent of C's in repeat unit
G	0	int(10) unsigned	Percent of G's in repeat unit
T	15	int(10) unsigned	Percent of T's in repeat unit
entropy	1.43	float	Entropy
sequence	TAACCC	longblob	Sequence of repeat unit element

通过哪个表格来查找数据，这个有赖于对Genome Browser路径的了解。

Table Browser 实例

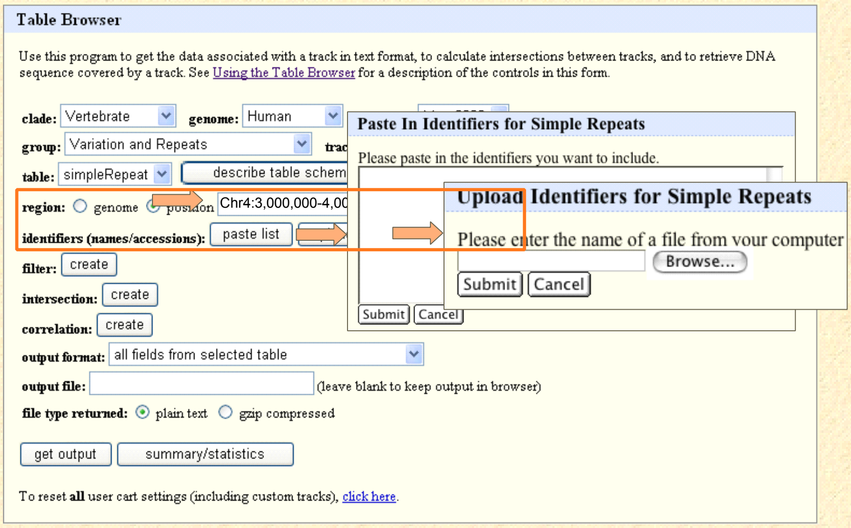


Table Browser

Use this program to get the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. See Using the Table Browser for a description of the controls in this form.

clade: Vertebrate **genome:** Human

group: Variation and Repeats

table: simpleRepeat

region: ○ genome ● position Chr4:3,000,000-4,00

identifiers (names/accessions):

output format: all fields from selected table

output file: (leave blank to keep output in browser)

file type returned: ● plain text ○ gzip compressed

To reset **all** user cart settings (including custom tracks), click here.

Paste In Identifiers for Simple Repeats

Please paste in the identifiers you want to include.

Upload Identifiers for Simple Repeats

Please enter the name of a file from your computer

选择搜索区域，或者上传要搜索的文件

Table Browser实例

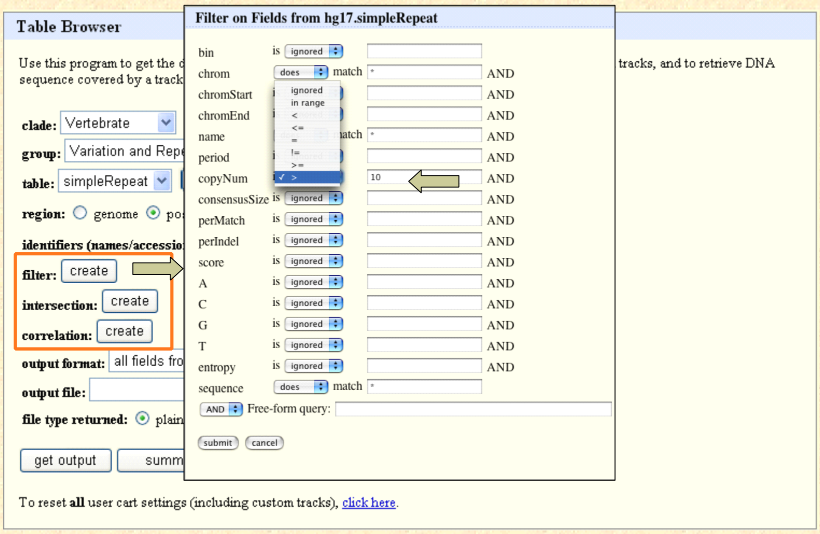


Table Browser

Use this program to get the d… tracks, and to retrieve DNA sequence covered by a track…

clade: Vertebrate

group: Variation and Repe…

table: simpleRepeat

region: ○ genome ● po…

identifiers (names/accessio…

filter: create

intersection: create

correlation: create

output format: all fields fro…

output file:

file type returned: ● plain…

get output | summ…

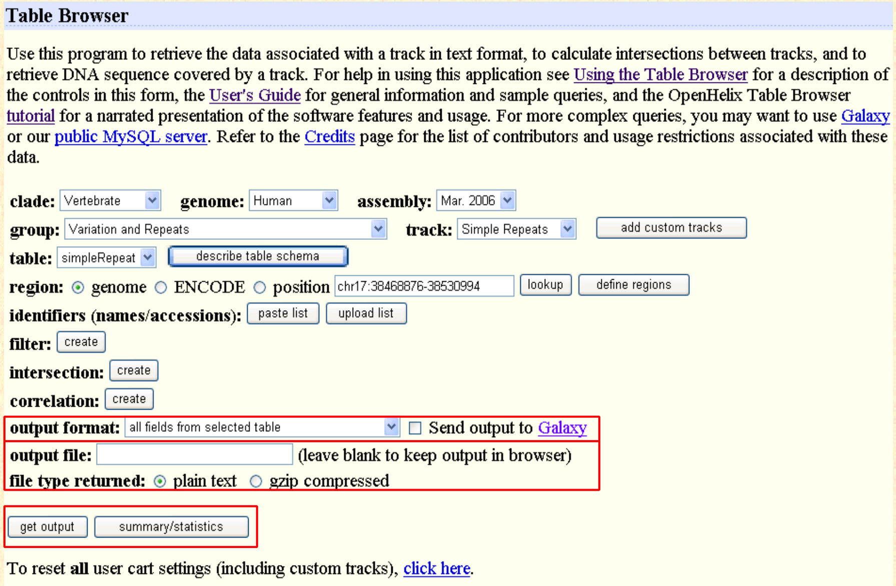
To reset **all** user cart settings (including custom tracks), click here.

Filter on Fields from hg17.simpleRepeat

bin is ignored
chrom does match * AND
chromStart is ignored AND
chromEnd is ignored AND
name does match * AND
period is ignored AND
copyNum is > 10 AND
consensusSize is ignored AND
perMatch is ignored AND
perIndel is ignored AND
score is ignored AND
A is ignored AND
C is ignored AND
G is ignored AND
T is ignored AND
entropy is ignored AND
sequence does match *
AND Free-form query:

对结果进行筛选

Table Browser实例



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clade: Vertebrate **genome:** Human **assembly:** Mar. 2006

group: Variation and Repeats **track:** Simple Repeats

table: simpleRepeat

region: ● genome ○ ENCODE ○ position chr17:38468876-38530994

identifiers (names/accessions):

filter: create

intersection: create

correlation: create

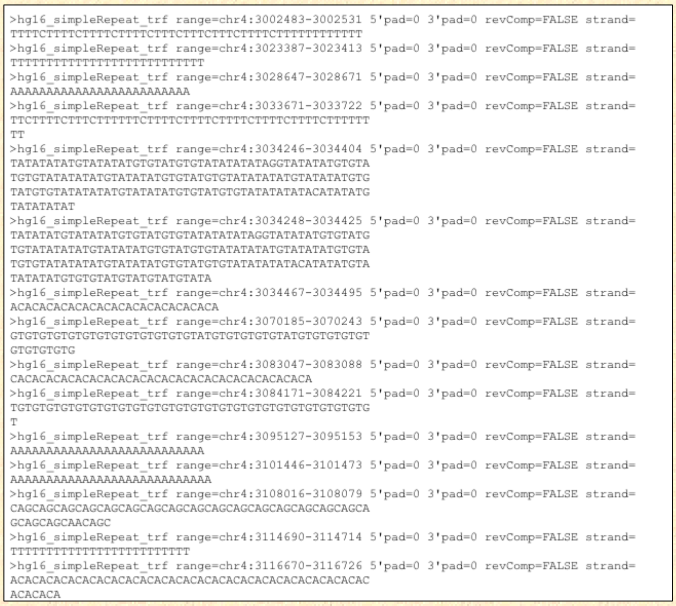
output format: all fields from selected table ☐ Send output to Galaxy

output file: (leave blank to keep output in browser)

file type returned: ● plain text ○ gzip compressed

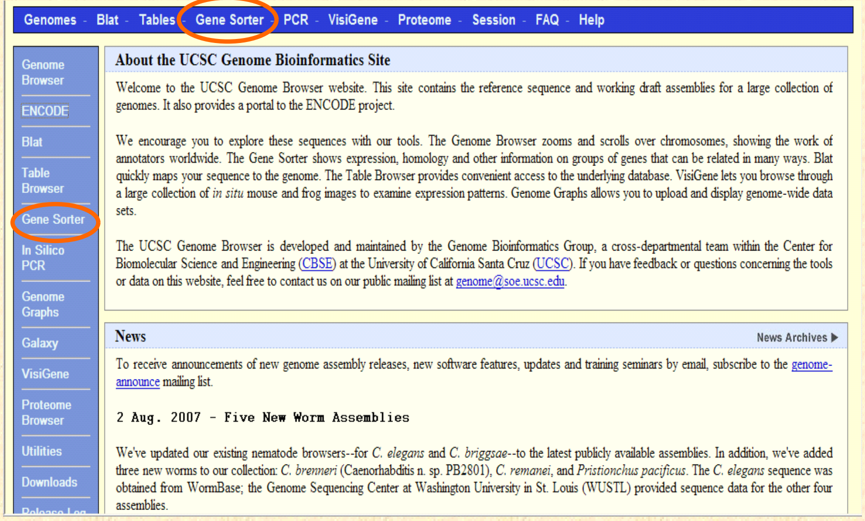
To reset **all** user cart settings (including custom tracks), click here.

Table browser实例: 输出结果



```
>hg16_simpleRepeat_trf range=chr4:3002483-3002531 5'pad=0 3'pad=0 revComp=FALSE strand=
TTTTCTTTTCTTTTCTTTTCTTTCTTTCTTTCTTTTCTTTTTTTTTTTT
>hg16_simpleRepeat_trf range=chr4:3023387-3023413 5'pad=0 3'pad=0 revComp=FALSE strand=
TTTTTTTTTTTTTTTTTTTTTTTTTTT
>hg16_simpleRepeat_trf range=chr4:3028647-3028671 5'pad=0 3'pad=0 revComp=FALSE strand=
AAAAAAAAAAAAAAAAAAAAAAAAA
>hg16_simpleRepeat_trf range=chr4:3033671-3033722 5'pad=0 3'pad=0 revComp=FALSE strand=
TTCTTTTCTTTCTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTTT
TT
>hg16_simpleRepeat_trf range=chr4:3034246-3034404 5'pad=0 3'pad=0 revComp=FALSE strand=
TATATATATGTATATATGTGTATGTGTATATATATAGGTATATATGTGTA
TGTGTATATATATGTATATATGTGTATGTGTATATATATGTATATATGTG
TATGTGTATATATATGTATATATGTGTATGTGTATATATATACATATATG
TATATATAT
>hg16_simpleRepeat_trf range=chr4:3034248-3034425 5'pad=0 3'pad=0 revComp=FALSE strand=
TATATATGTATATATGTGTATGTGTATATATATAGGTATATATGTGTATG
TGTATATATATGTATATATGTGTATGTGTATATATATGTATATATGTGTA
TGTGTATATATATGTATATATGTGTATGTGTATATATATACATATATGTA
TATATATGTGTGTATGTATGTATGTATA
>hg16_simpleRepeat_trf range=chr4:3034467-3034495 5'pad=0 3'pad=0 revComp=FALSE strand=
ACACACACACACACACACACACACACACA
>hg16_simpleRepeat_trf range=chr4:3070185-3070243 5'pad=0 3'pad=0 revComp=FALSE strand=
GTGTGTGTGTGTGTGTGTGTGTGTGTATGTGTGTGTGTATGTGTGTGTGT
GTGTGTGTG
>hg16_simpleRepeat_trf range=chr4:3083047-3083088 5'pad=0 3'pad=0 revComp=FALSE strand=
CACACACACACACACACACACACACACACACACACACACACA
>hg16_simpleRepeat_trf range=chr4:3084171-3084221 5'pad=0 3'pad=0 revComp=FALSE strand=
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
T
>hg16_simpleRepeat_trf range=chr4:3095127-3095153 5'pad=0 3'pad=0 revComp=FALSE strand=
AAAAAAAAAAAAAAAAAAAAAAAAAAA
>hg16_simpleRepeat_trf range=chr4:3101446-3101473 5'pad=0 3'pad=0 revComp=FALSE strand=
AAAAAAAAAAAAAAAAAAAAAAAAAAAA
>hg16_simpleRepeat_trf range=chr4:3108016-3108079 5'pad=0 3'pad=0 revComp=FALSE strand=
CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
GCAGCAGCAACAGC
>hg16_simpleRepeat_trf range=chr4:3114690-3114714 5'pad=0 3'pad=0 revComp=FALSE strand=
TTTTTTTTTTTTTTTTTTTTTTTTT
>hg16_simpleRepeat_trf range=chr4:3116670-3116726 5'pad=0 3'pad=0 revComp=FALSE strand=
ACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACA
```

Gene Sorter



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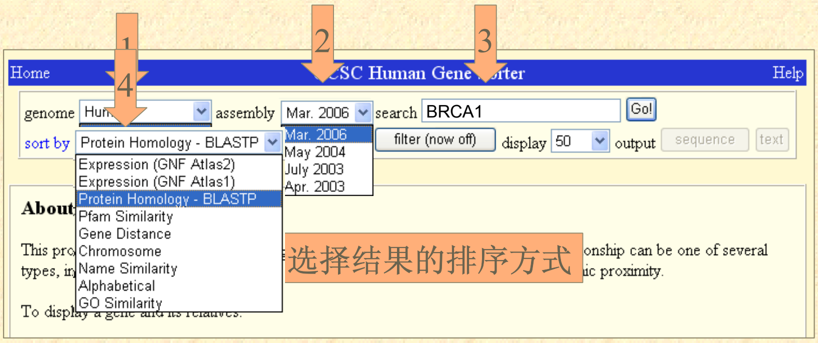
Gene Sorter

- UCSC Gene Sorter是一个用来开发基因家族和基因间关系的一个非常优秀的资源。这个工具显示了与所选基因组相关的其他基因组列表。
- 通过这个工具可以找到：蛋白水平的相似性，基因表达谱的相似性或是基因组的相似性。

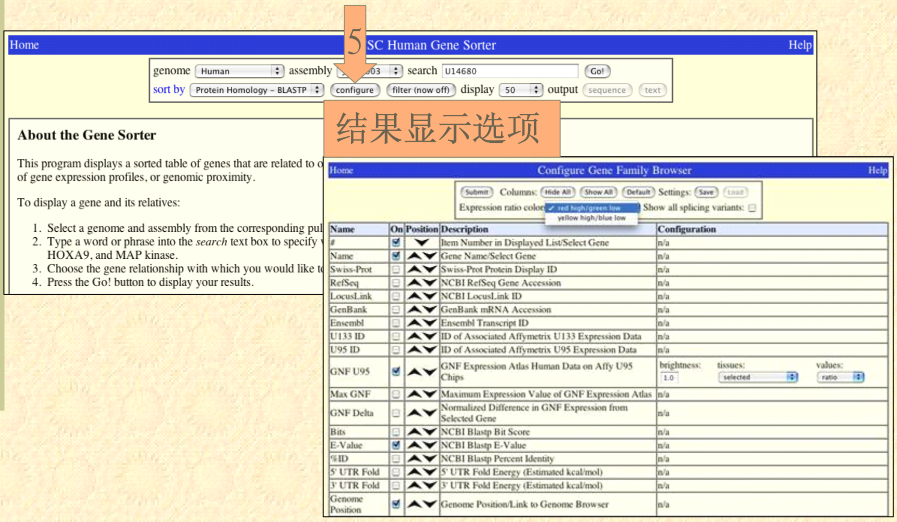
Gene Sorter界面



genome Hu
assembly Mar. 2006
search BRCA1
sort by Protein Homology - BLASTP
display 50
output

选择结果的排序方式

Gene Sorter界面



search: U14680

About the Gene Sorter

This program displays a sorted table of genes that are related to o
of gene expression profiles, or genomic proximity.

To display a gene and its relatives:

1. Select a genome and assembly from the corresponding pul
2. Type a word or phrase into the *search* text box to specify
   HOXA9, and MAP kinase.
3. Choose the gene relationship with which you would like t
4. Press the Go! button to display your results.

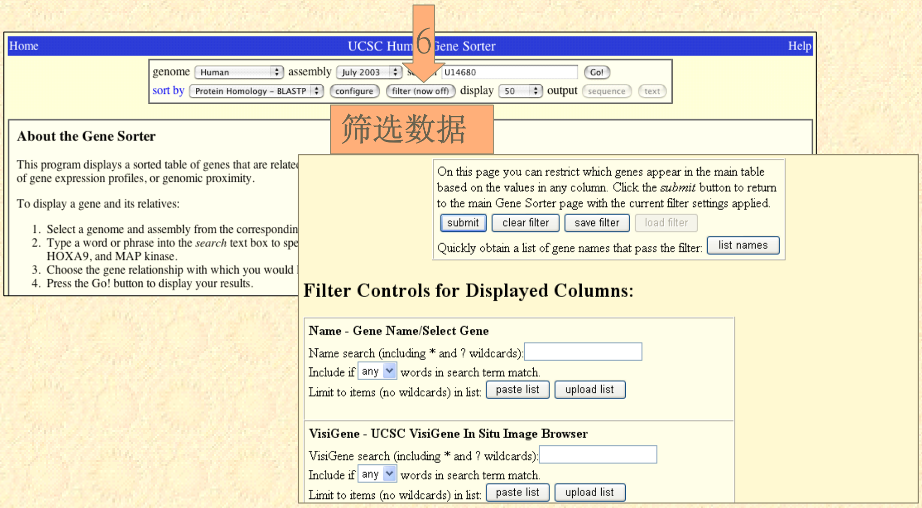
Expression ratio colors: ✓ red high/green low, yellow high/blue low

Show all splicing variants: ☐

Name	On	Position	Description	Configuration
#	☑	▼	Item Number in Displayed List/Select Gene	n/a
Name	☑	▲▼	Gene Name/Select Gene	n/a
Swiss-Prot	☐	▲▼	Swiss-Prot Protein Display ID	n/a
RefSeq	☐	▲▼	NCBI RefSeq Gene Accession	n/a
LocusLink	☐	▲▼	NCBI LocusLink ID	n/a
GenBank	☐	▲▼	GenBank mRNA Accession	n/a
Ensembl	☐	▲▼	Ensembl Transcript ID	n/a
U133 ID	☐	▲▼	ID of Associated Affymetrix U133 Expression Data	n/a
U95 ID	☐	▲▼	ID of Associated Affymetrix U95 Expression Data	n/a
GNF U95	☑	▲▼	GNF Expression Atlas Human Data on Affy U95 Chips	brightness: 1.0 tissues: selected values: ratio
Max GNF	☐	▲▼	Maximum Expression Value of GNF Expression Atlas	n/a
GNF Delta	☐	▲▼	Normalized Difference in GNF Expression from Selected Gene	n/a
Bits	☐	▲▼	NCBI Blastp Bit Score	n/a
E-Value	☑	▲▼	NCBI Blastp E-Value	n/a
%ID	☐	▲▼	NCBI Blastp Percent Identity	n/a
5' UTR Fold	☐	▲▼	5' UTR Fold Energy (Estimated kcal/mol)	n/a
3' UTR Fold	☐	▲▼	3' UTR Fold Energy (Estimated kcal/mol)	n/a
Genome Position	☑	▲▼	Genome Position/Link to Genome Browser	n/a

---

Gene Sorter 界面



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2. Type a word or phrase into the *search* text box to spe
   HOXA9, and MAP kinase.
3. Choose the gene relationship with which you would
4. Press the Go! button to display your results.

On this page you can restrict which genes appear in the main table based on the values in any column. Click the *submit* button to return to the main Gene Sorter page with the current filter settings applied.

Quickly obtain a list of gene names that pass the filter:

Filter Controls for Displayed Columns:

Name - Gene Name/Select Gene

Name search (including * and ? wildcards):

Include if any words in search term match.

Limit to items (no wildcards) in list:

VisiGene - UCSC VisiGene In Situ Image Browser

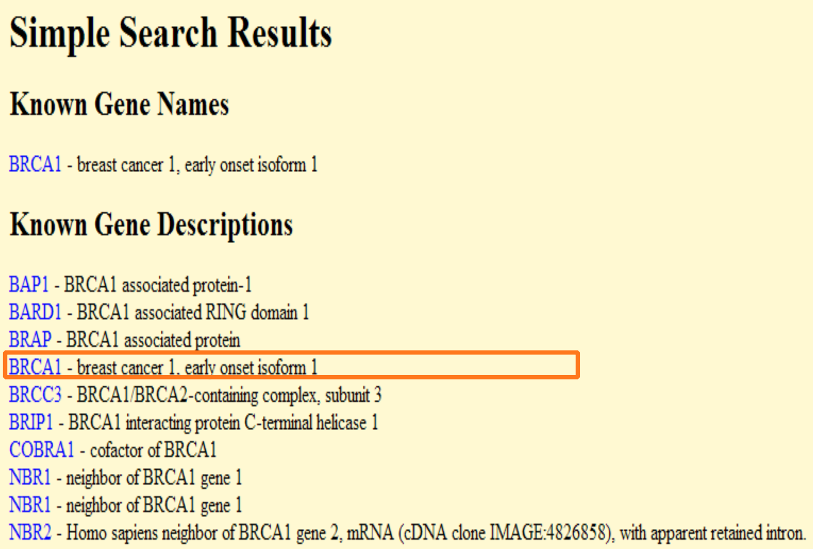
VisiGene search (including * and ? wildcards):

Include if any words in search term match.

Limit to items (no wildcards) in list:

UCSC Genome Bioinformatics

Gene Sorter 界面



Simple Search Results

Known Gene Names

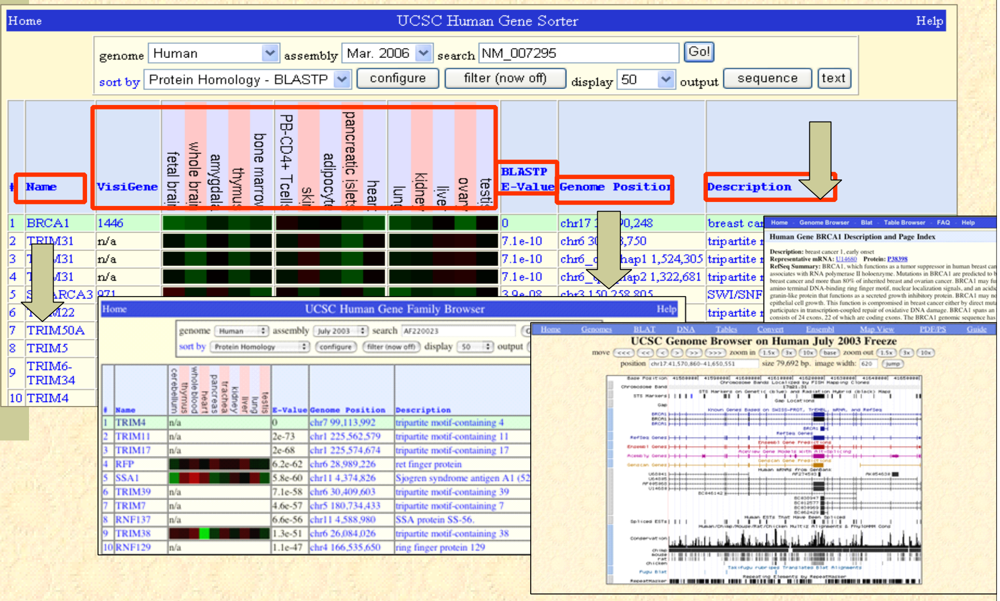
BRCA1 - breast cancer 1, early onset isoform 1

Known Gene Descriptions

BAP1 - BRCA1 associated protein-1
BARD1 - BRCA1 associated RING domain 1
BRAP - BRCA1 associated protein
BRCA1 - breast cancer 1, early onset isoform 1
BRCC3 - BRCA1/BRCA2-containing complex, subunit 3
BRIP1 - BRCA1 interacting protein C-terminal helicase 1
COBRA1 - cofactor of BRCA1
NBR1 - neighbor of BRCA1 gene 1
NBR1 - neighbor of BRCA1 gene 1
NBR2 - Homo sapiens neighbor of BRCA1 gene 2, mRNA (cDNA clone IMAGE:4826858), with apparent retained intron.

UCSC Genome Bioinformatics

Gene Sorter 结果



genome Human assembly Mar. 2006 search NM_007295
sort by Protein Homology - BLASTP display 50 output

#	Name	VisiGene	BLASTP E-Value	Genome Position	Description
1	BRCA1	1446	0	chr17 1 0,248	breast ca
2	TRIM31	n/a	7.1e-10	chr6 3 ,750	tripartite
3	T M31	n/a	7.1e-10	chr6_ hap1 1,524,305	tripartite
4	T M31	n/a	7.1e-10	chr6_ ap2 1,322,681	tripartite
5	S ARCA3	971	3.9e-08	chr3 150,258,805	SWI/SNF
6	T M22				tripartite
7	TRIM50A				
8	TRIM5				
9	TRIM6-TRIM34				
10	TRIM4				

genome Human assembly July 2003 search AF220023
sort by Protein Homology display 50 output

#	Name	E-Value	Genome Position	Description
1	TRIM4	0	chr7 99,113,992	tripartite motif-containing 4
2	TRIM11	2e-73	chr1 225,562,579	tripartite motif-containing 11
3	TRIM17	2e-68	chr1 225,574,674	tripartite motif-containing 17
4	RFP	6.2e-62	chr6 28,989,226	ret finger protein
5	SSA1	5.8e-60	chr11 4,374,826	Sjogren syndrome antigen A1 (52
6	TRIM39	7.1e-58	chr6 30,409,603	tripartite motif-containing 39
7	TRIM7	4.6e-57	chr5 180,734,433	tripartite motif-containing 7
8	RNF137	6.6e-56	chr11 4,588,980	SSA protein SS-56.
9	TRIM38	1.3e-51	chr6 26,084,026	tripartite motif-containing 38
10	RNF129	1.1e-47	chr4 166,535,650	ring finger protein 129

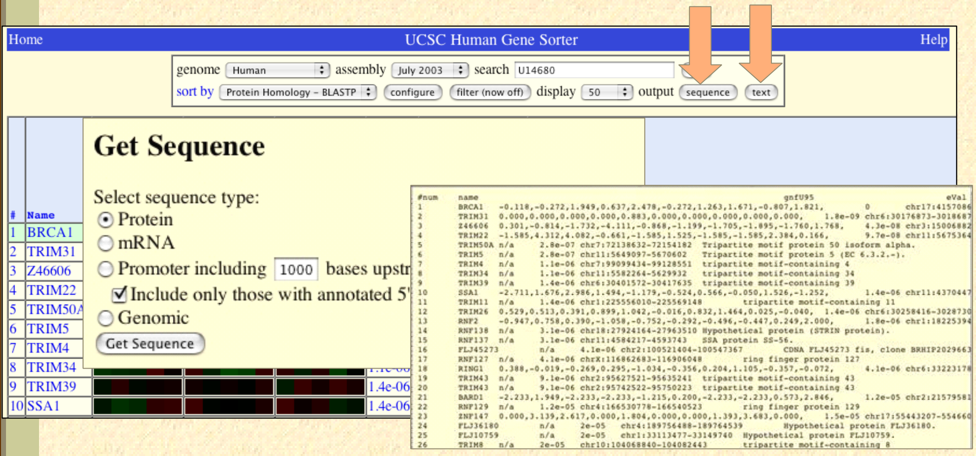
Human Gene BRCA1 Description and Page Index

Description: breast cancer 1, early onset
Representative mRNA: U14680 Protein: P38398
RefSeq Summary: BRCA1, which functions as a tumor suppressor in human breast c
associates with RNA polymerase II holoenzyme. Mutations in BRCA1 are predicted t
breast cancer and more than 80% of inherited breast and ovarian cancer. BRCA1 may
amino terminal DNA-binding ring finger motif, nuclear localization signals, and an aci
granin-like protein that functions as a secreted growth inhibitory protein. BRCA1 may
epithelial cell growth. This function is compromised in breast cancer either by direct m
participates in transcription-coupled repair of oxidative DNA damage. BRCA1 spans a
consists of 24 exons, 22 of which are coding exons. The BRCA1 genomic sequence h

UCSC Genome Browser on Human July 2003 Freeze

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x
position chr17:41,570,860-41,650,551 size 79,692 bp. image width: 620 jump

Gene Sorter results



genome Human assembly July 2003 search U14680
sort by Protein Homology - BLASTP display 50 output

Get Sequence

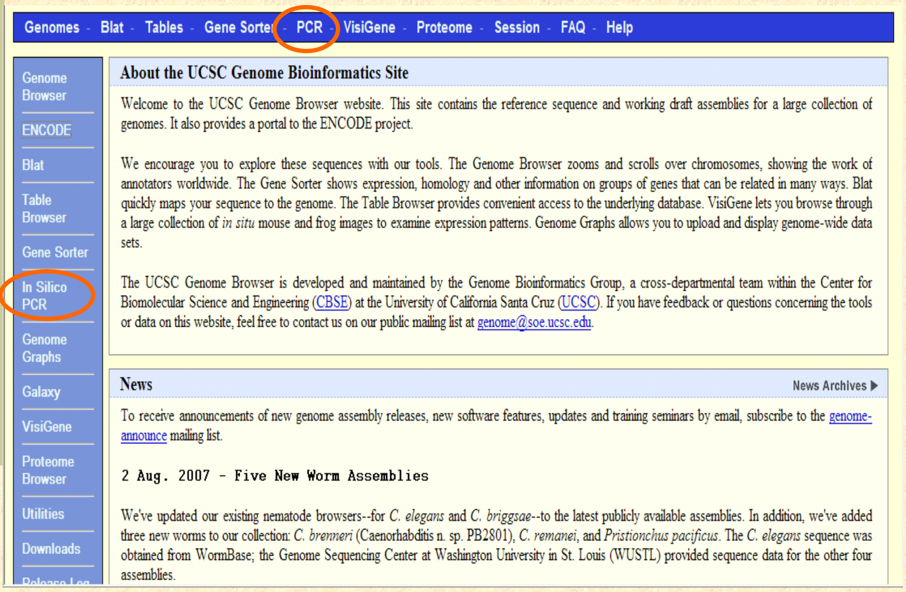
Select sequence type:
● Protein
○ mRNA
○ Promoter including 1000 bases upstr
☑ Include only those with annotated 5'
○ Genomic

#	Name
1	BRCA1
2	TRIM31
3	Z46606
4	TRIM22
5	TRIM50A
6	TRIM5
7	TRIM4
8	TRIM34
9	TRIM39
10	SSA1

```
#num    name                                                                    gnfU95                eVal
1       BRCA1   -0.118,-0.272,1.949,0.637,2.478,-0.272,1.263,1.671,-0.807,1.821,        0       chr17:4157086
2       TRIM31  0.000,0.000,0.000,0.000,0.883,0.000,0.000,0.000,0.000,0.000,    1.8e-09 chr6:30176873-3018687
3       Z46606  0.301,-0.814,-1.732,-4.111,-0.868,-1.199,-1.705,-1.895,-1.760,1.768,    4.3e-08 chr3:15006882
4       TRIM22  -1.585,4.312,4.082,-0.661,-1.585,1.525,-1.585,-1.585,2.384,0.166,       9.7e-08 chr11:5675364
5       TRIM50A n/a     2.8e-07 chr7:72138632-72154182  Tripartite motif protein 50 isoform alpha.
6       TRIM5   n/a     2.8e-07 chr11:5649097-5670602   Tripartite motif protein 5 (EC 6.3.2.-).
7       TRIM4   n/a     1.1e-06 chr7:99099434-99128551  tripartite motif-containing 4
8       TRIM34  n/a     1.1e-06 chr11:5582264-5629932   tripartite motif-containing 34
9       TRIM39  n/a     1.4e-06 chr6:30401572-30417635  tripartite motif-containing 39
10      SSA1    -2.711,1.676,2.986,1.494,-1.179,-0.524,0.566,-0.050,1.526,-1.252,       1.4e-06 chr11:4370447
11      TRIM11  n/a     1.4e-06 chr1:225556010-225569148        tripartite motif-containing 11
12      TRIM26  0.529,0.513,0.391,0.899,1.042,-0.016,0.832,1.464,0.025,-0.040,  1.4e-06 chr6:30258416-3028730
13      RNF2    -0.947,0.758,0.390,-1.058,-0.752,-0.292,-0.496,-0.447,0.249,2.000,      1.8e-06 chr1:18225394
14      RNF138  n/a     3.1e-06 chr18:27924164-27963510 Hypothetical protein (STRIN protein).
15      RNF137  n/a     3.1e-06 chr11:4584217-4593743   SSA protein SS-56.
16      FLJ45273        n/a     4.1e-06 chr2:100521404-100547367        CDNA FLJ45273 fis, clone BRHIP2029663
17      RNF127  n/a     4.1e-06 chrX:116862683-116906048        ring finger protein 127
18      RING1   0.388,-0.019,-0.269,0.295,-1.034,-0.356,0.204,1.105,-0.357,-0.072,      4.1e-06 chr6:3322317
19      TRIM43  n/a     9.1e-06 chr2:95627521-95635241  tripartite motif-containing 43
20      TRIM43  n/a     9.1e-06 chr2:95742522-95750223  tripartite motif-containing 43
21      BARD1   -2.233,1.949,-2.233,-2.233,-1.215,0.200,-2.233,-2.233,0.573,2.846,      1.2e-05 chr2:21579581
22      RNF129  n/a     1.2e-05 chr4:166530778-166540523        ring finger protein 129
23      ZNF147  0.000,3.139,2.617,0.000,1.804,0.000,0.000,1.393,3.683,0.000,    1.5e-05 chr17:55443207-554660
24      FLJ36180        n/a     2e-05   chr4:189756488-189764539        Hypothetical protein FLJ36180.
25      FLJ10759        n/a     2e-05   chr1:33113477-33149740  Hypothetical protein FLJ10759.
26      TRIM8   n/a     2e-05   chr10:104068840-104082443       tripartite motif-containing 8
```

Obtain file of gene sequences or tab-delineated file of data

In Silico PCR



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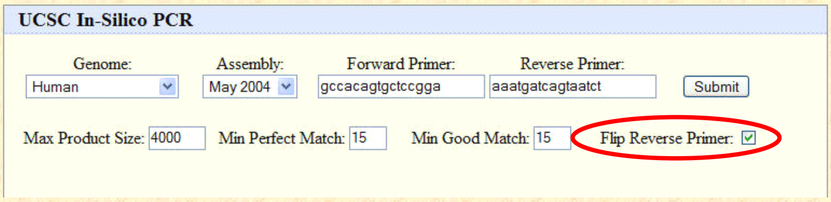
- From the Genome Browser home page, select Table Browser

In Silico PCR

- In-Silico PCR: 电子PCR，模拟PCR。
- 用一组序列作为PCR引物来搜索数据库，返回相关的序列。

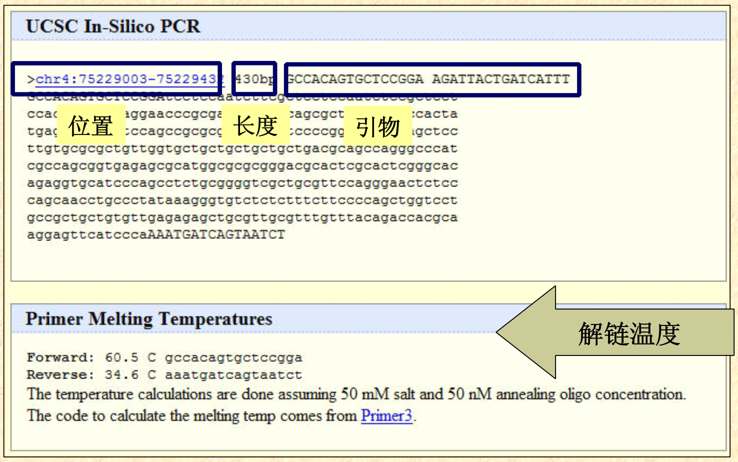


UCSC In-Silico PCR

Genome: Human
Assembly: May 2004
Forward Primer: gccacagtgctccgga
Reverse Primer: aaatgatcagtaatct
Max Product Size: 4000
Min Perfect Match: 15
Min Good Match: 15
Flip Reverse Primer: ☑

Max Product Size: 被放大区域的最大长度.
Min Perfect Match: 和引物的3’端Perfect Match的最小碱基数目。
Min Good Match: 和引物的3’端Good Match的最小碱基数目，Good Match指3个碱基里最少匹配2个。
Flip Reverse Primer: 反向引物反向互补。

In Silico PCR: 结果



UCSC In-Silico PCR

```
>chr4:75229003-75229432 430bp GCCACAGTGCTCCGGA AGATTACTGATCATTT
ttgtgcgcgctgttggtgctgctgctgctgacgcagccagggcccat
cgccagcggtgagagcgcatggcgcgcgggacgcactcgcactcgggcac
agaggtgcatcccagcctctgcggggtcgctgcgttccagggaactctcc
cagcaacctgccctataaagggtgtctctctttcttccccagctggtcct
gccgctgctgtgttgagagagctgcgttgcgtttgtttacagaccacgca
aggagttcatcccaAAATGATCAGTAATCT
```

Primer Melting Temperatures

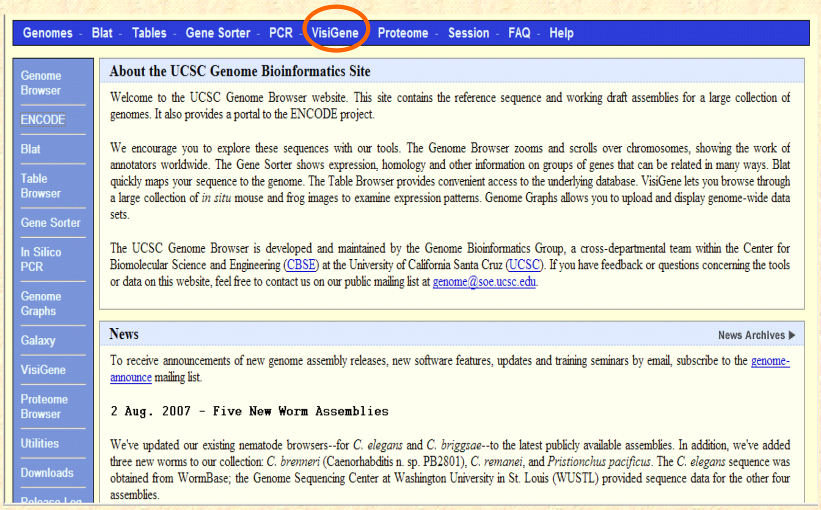
```
Forward: 60.5 C gccacagtgctccgga
Reverse: 34.6 C aaatgatcagtaatct
```

The temperature calculations are done assuming 50 mM salt and 50 nM annealing oligo concentration. The code to calculate the melting temp comes from Primer3.

其它部分简介

- 其它部分：VisiGene, Proteome, Session和Custome tracks。

VisiGene



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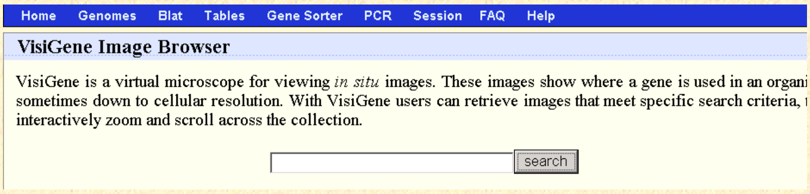
VisiGene Image Browser

- VisiGene是一个虚拟显微镜工具，用来 显示基因在物种内部的哪个部分被使用。

搜索界面

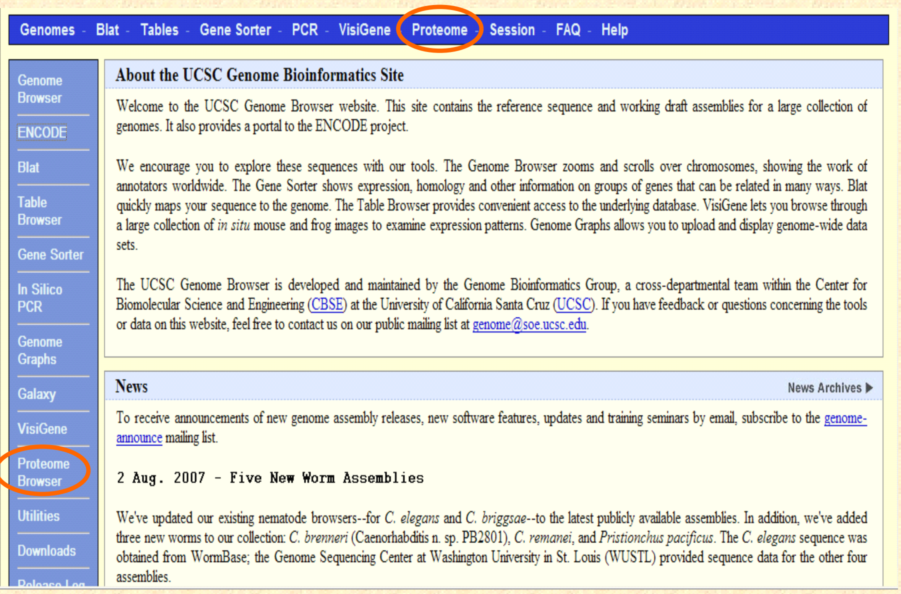


VisiGene Image Browser

VisiGene is a virtual microscope for viewing *in situ* images. These images show where a gene is used in an organi
sometimes down to cellular resolution. With VisiGene users can retrieve images that meet specific search criteria,
interactively zoom and scroll across the collection.

搜索关键词：基因代号，作者，年份，身体部位，物种，GenBank和UniProt收录号，以及对已知基因的描述词语。

Proteome



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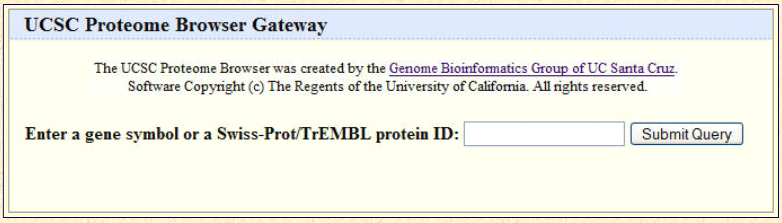
- From the Genome Browser home page, select Table Browser

Proteome Browser

- 输入一个基因代号或者Swiss-Prot/TrEMBL的蛋白ID号，Proteome就会以图片的形式提供丰富的蛋白信息和相关的到其它网站的链接。



UCSC Proteome Browser Gateway

The UCSC Proteome Browser was created by the Genome Bioinformatics Group of UC Santa Cruz.
Software Copyright (c) The Regents of the University of California. All rights reserved.

Enter a gene symbol or a Swiss-Prot/TrEMBL protein ID:

Custome Tracks

- 把自己的数据放在Genome Browser显示出来。

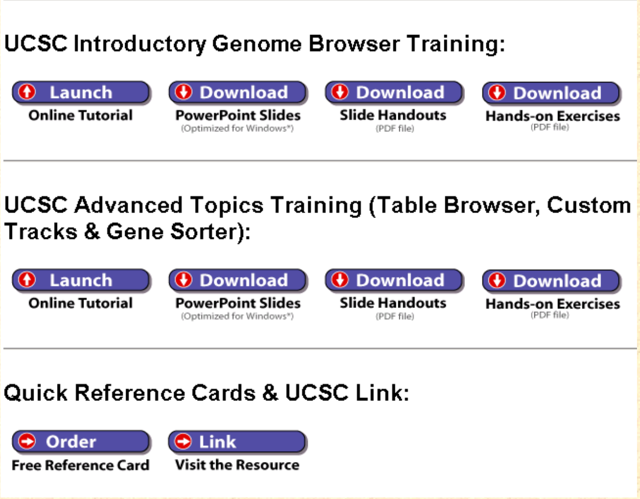
实现步骤：

- 把数据格式化成UCSC Genome Browser支持的格式。
- 定义Genome Browser的显示选项。
- 定义该路径注释信息的显示方式。
- 把该路径添加到Genome Browser的显示选项里。
- 为该路径添加介绍详细情况的页面。（可选）
- 和别人分享该路径。 （可选）

参考资料

http://www.openhelix.com/downloads/ucsc/ucsc_home.shtml

提供PPT和PDF格式的说明文档，还有一些习题和相关答案。



UCSC Introductory Genome Browser Training:

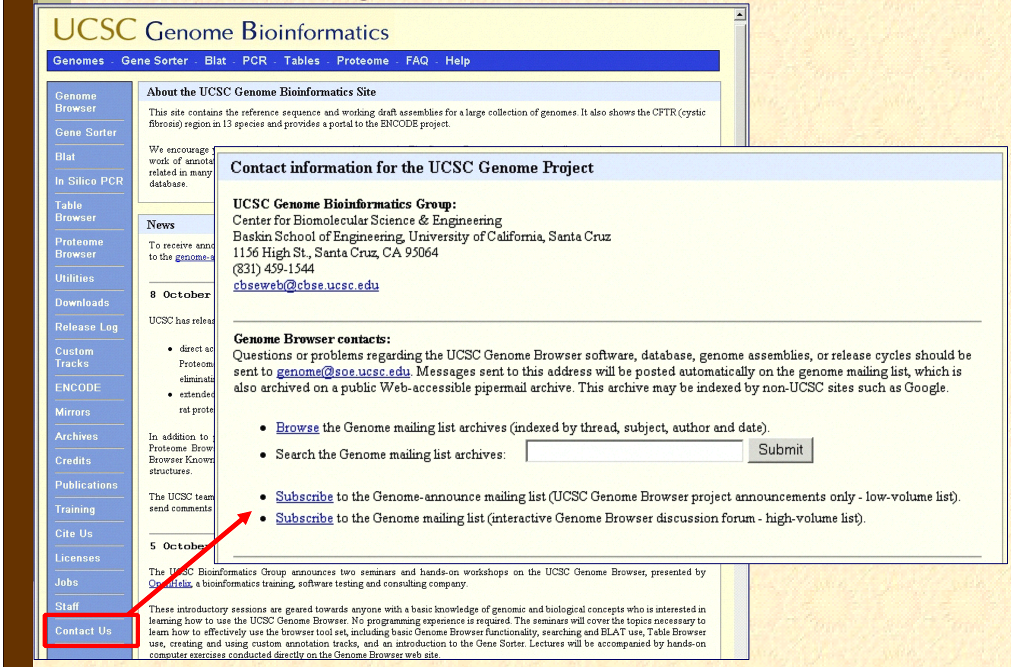
UCSC Advanced Topics Training (Table Browser, Custom Tracks & Gene Sorter):

Quick Reference Cards & UCSC Link:

Downloads

- Offers downloads to complete annotation sets
  - Human
  - Horse
  - Cat
  - Lizard
  - Medaka
  - Stickleback
  - Tetraodon
  - Chimpanzee
  - Rhesus
  - Dog
  - Cow
  - Fugu
  - Platypus
  - Zebrafish
  - Mouse
  - Rat
  - Opossum
  - Chicken
  - *X.tropicalis*

Join the mailing list!



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This site contains the reference sequence and working draft assemblies for a large collection of genomes. It also shows the CFTR (cystic fibrosis) region in 13 species and provides a portal to the ENCODE project.

Contact information for the UCSC Genome Project

UCSC Genome Bioinformatics Group:
Center for Biomolecular Science & Engineering
Baskin School of Engineering, University of California, Santa Cruz
1156 High St., Santa Cruz, CA 95064
(831) 459-1544
cbseweb@cbse.ucsc.edu

Genome Browser contacts:
Questions or problems regarding the UCSC Genome Browser software, database, genome assemblies, or release cycles should be sent to genome@soe.ucsc.edu. Messages sent to this address will be posted automatically on the Genome mailing list, which is also archived on a public Web-accessible pipermail archive. This archive may be indexed by non-UCSC sites such as Google.

- Browse the Genome mailing list archives (indexed by thread, subject, author and date).
- Search the Genome mailing list archives:

- Subscribe to the Genome-announce mailing list (UCSC Genome Browser project announcements only - low-volume list).
- Subscribe to the Genome mailing list (interactive Genome Browser discussion forum - high-volume list).

The UCSC Bioinformatics Group announces two seminars and hands-on workshops on the UCSC Genome Browser, presented by OpenHelix, a bioinformatics training, software testing and consulting company.

These introductory sessions are geared towards anyone with a basic knowledge of genomic and biological concepts who is interested in learning how to use the UCSC Genome Browser. No programming experience is required. The seminars will cover the topics necessary to learn how to effectively use the browser tool set, including basic Genome Browser functionality, searching and BLAT use, Table Browser use, creating and using custom annotation tracks, and an introduction to the Gene Sorter. Lectures will be accompanied by hands-on computer exercises conducted directly on the Genome Browser web site.

The End