

Celera Quick Guide

First let me say that this stuff works more reliably on a Windows machine. Has nothing to do with what Celera has done or did not do. Apple's support for JAVA is at present atrocious. Also, Netscape on a Mac will pretty much guarantee that CDS will not work. So stick with Microsoft's Internet Explorer 5.0(or better) for Mac. (Also be aware that you need at least MRJ 2.1 to work properly on the Mac. However, the version of MRJ 2.2.3 that gives you the best performance for JaVa on a Mac also has a security hole in it. So pick your poison. For instructions on how to install MRJ on your Mac, see Appendix I).

Minimum Requirements (from The Celera Website)

*The **Celera Discovery System** requires one of the following internet browsers, [Microsoft Internet Explorer 5](#) or higher or [Netscape Navigator 4.7](#).*

In addition, your browser must have JavaScript, Java applets and cookies enabled. The default installation for both Internet Explorer and Netscape Navigator enables JavaScript, Java applets and cookies. A screen resolution of at least 800 x 600 is strongly recommended.

Macintosh Users: IE 5 or higher is recommended for optimal site usage with a memory allocation of 8000k (minimum) and 16,000k (preferred). The Mac Runtime for Java (MRJ) version 2.2 or greater is also required and can be downloaded by [clicking here](#).

PCs need Windows 95/98/NT/2000 running on their systems with a minimum of 64MB of RAM and at least 40MB of free hard disk space. For satisfactory performance, at least a Pentium II class machine is preferred. You will also need a high speed connection (ie, LAN, DSL, Cable. 56K is OK).

Macs need to be running at least OS 8.6. 8.1 has been reported to be unstable but works. OS 9 doesn't seem to present any problems. Don't know about OS X.

Mac hardware should at least be 68040 class machines. PowerPC class machines are preferable.

Login Procedure

Point your browser to <http://cds.celera.com/cds/login.cfm>



CELERA Company Products & Services Genome News Celera Discovery System

Discovery can't wait.

Discovery System

Login
CDS Tour
Celera Publication Site
Contact Us

Celera Discovery System Login

User ID :

Password :

Forgot Your Password:

Subscribers: If you have forgotten your password please contact your Discovery System administrator with your 'password hint' requesting your password be reset. If you have a password and id, but are not a Celera Discovery System subscriber, please use Public Access Login.

You should have a username and password. If you don't contact your site administrator:

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When you login, you should be by default in the main *Biomolecule Library* page.



Live Home Page Apple Computer Apple Support Apple Store HSR Office for Macintosh Internet Explorer

Celera Discovery System

Biomolecule Library Text Search Sequence Analysis Workspace

Genome Maps

- [Search Celera human genome maps](#)
- [Search the human genome assembly](#)

Protein Family Classification

- [View genes by navigating and querying protein family and subfamily](#)
- [Text search Celera human genes & proteins \(Human genes\)](#)

Ontology

- [View genes by navigating and querying Gene Ontology classifications for biochemical function, biological process and cellular location.](#)

Biomolecule Library | Text Search | Sequence Analysis | Workspace
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The new version of CDS (3.0) has the following options:

Biomolecule Library

Genomic and protein information library and maps.

Text Search

Keyword searches in single or multi-source mode.

Sequence Analysis

Sequence homology and similarity type searches (ie. BLAST, HMM) against different subsets and databases.

Workspace

All cached results in your present session. (session means any environment that has “saved” all jobs and requests until you request a “new” session)

Queue

All jobs and searches you have submitted in your present session

Options

Where you can change your password and default start page. You can also specify default text search method.

Help

Online Help

Logoff

Ending your CDS session.

Biomolecule Library

The new Biomolecule Library in CDS 3.0 for the most part consists of 3 major sections:

Genome Maps

Protein Family Classifications

Gene Ontology

Genome Maps

Let's you navigate the Human Genome in two ways:

Map Query Tool

The "Gene List" button gives you all known "genes" found by Celera. The "Map" button shows you a graphic display where a specific gene sequence, transcript or protein may be as it is cross-referenced with respect to the genome assembly.

The Map Query Tool displays information in two panels. The top(upper) panel gives you "global" view of the sequence range of interest – normally at the chromosomal level. The second(lower) panel gives you a "zoom" or a close up look of the range highlighted by the red select region in the upper panel.

No matter which option is chosen from the list below, all the other display panels are also present. So if you choose Celera Gene view, the other panels for CytoGenetic band etc. will also be present. This let's you cross reference across different kinds of information.

Options include

a) Whole Chromosome View

Just choose the Chromosome number you would like information on. Useful when you don't know what Celera gene ID denotes a specific gene.

b) Celera Gene

Only works with Celera Gene Ids. Can't use Genbank Accession Numbers or LocusNames. Use Chromosome View to find likely Celera Gene ID. You can also a BLAST Search of **Human Genes** in the Celera Database

c) CytoGenetic Band

Self explanatory but essentially you can give a coordinate or a range of coordinates for the Human Genome and look at the Map or Gene List display.

d) Position

Let's you specify the Megabase position for specific locations on a chromosome

e) STS marker

STS marker locations as mapped to the Celera Genome Assembly

f) BAC Tile Map

Bacterial Artificial Chromosomal information as mapped to the Celera Genome Assembly

Each point on a BAC clone or STS marker for example, is hyperlinked to a specific file or sequence.

You ultimately can “drill down” to a Biomolecule page where information exists for the Gene Transcript (and related exons where applicable), Chromosomal Location & Reference and finally the related Protein Classifications & Ontologies.

Human Genome Assembly Search Tool

Celera uses it's own Chromosomal Location reference(surprise!) axis. The Chromosome axis was built from an assembly of Celera “scaffolds” or backbones. These scaffolds are in turn built from regional assemblies or contigs. Scaffolds are broken into 500kb segments (these may be where the sequences actually begin or end but in most cases these scaffolds are artificially broken. So, you may find a specific gene sequence span one or more scaffolds).

So in summary from small -> large

Sequence -> contig/assembly -> regional assembly -> scaffold -> chromosome

You can use a Celera GA reference number to determine where in the chromosome the gene or sequence is by using the Chromosome or Scaffold Report.

Protein Family Classification

The Panther Protein Classification system is a proprietary protein classification scheme, You can drill down into the various classes and associate proteins within specific families and their relationship to other protein families, as well, as by gene function.

You can search the PFC by family name or by keyword search. The keyword search is far more versatile (Option 2 in PFC).

Text Search

Text searches work better when you turn the wild card option on. It's also better to use the multi source search option.

Sequence Analysis

You can search Celera's Database in many ways. However the Complete Genomes, Transcripts or Known Genes are the most powerful options. These kind of searches require that you have a sequence to work with.

Saving Files on the Celera System

- 1) Click on Text Search tab
- 2) Click on User Defined Sources icon (+ symbol)
- 3) Under User Owned Databanks click on ADD DATA for appropriate category
- 4) Manually enter sequence or browse for file
- 5) Click on Submit

Retrieving Files from The Celera System

- 6) Click on Text Search tab
- 7) Click on User Defined Sources icon (+ symbol)
- 8) Under User Owned Databanks click on USERDNA OR USERPROTEIN for appropriate category
- 9) Do a text search for filename with the wildcard option turned on. Entering "*" lists all files.

Saving Results

BLAST

Use the BLAST View Display option and you have the option to use any data format. Use "Not" if you want to save in Web Archive or Source format. Saving these results only works for reference. The application gets really confused sometimes since it requires authentication when you want to see the document at a later time.

Printing Graphics

The graphics in CDS are mostly JaVa Applets. In the JaVa standards there is no print support for applets. Typically you don't need it since for all intents and purposes they're executable programs. But since in our case we do need to print them to look at results, here's a work around.

Here's how you get screen prints of JAVA Applets

For Microsoft machines,

- 1) While looking at your output in your browser window, click on the window with your mouse.
- 2) Hold down the Alt and PrintScreen keys to capture the browser window.(you can also use Shift-Alt-PrintScreen to give you finer control, but the output look nasty)
- 3) Open a application like Paint, Word or any other word processing/graphic application. You can also use Photoshop but that will pixelate the graphic and make it look "grainy."
- 4) Click mouse anywhere in an empty document and Paste
- 5) View (or Edit) and Print like you would a regular document.

For Macintosh,

There's a freeware utility out there called Pictify that gives you really nice control over screen dumps. I use it and love it. It's available from www.download.com and other software web sites.

if you don't have Pictify.

1) To capture the browser window in PICT format, click on window and hold Command-Shift-CapsLock-4 (you have to be an Octopus!) On your Main HD directory you should be able to see a file called Picture1 etc. etc.

2) You can then edit this file with any drawing or word-processing program like Word or Illustrator. You can also use Photoshop but that will pixelate the graphic and make it look "grainy."

Note: Command-Shift-4 lets you select a part of a browser window but I don't get very good selection control. Your mileage may vary.

Charles Alexander – Celera Quick Guide rev.02/15/01

Appendix I

Mac Run Time Java Install Instructions

If you are on a Macintosh, please use only Internet Explorer 5.0 or higher. you might also need to upgrade your Apple Macintosh Runtime Java (MRJ) engine. This is necessary to optimize the performance of a lot of JAVA type displays and graphics.

Go to <http://asu.info.apple.com/swupdates.nsf/artnum/n11572> and download the MRJ v. 2.2.3 Follow instructions on how to install it. It's very straightforward.

Once you've installed the MRJ, reboot your Mac. Then reboot your Mac once again (just superstition) and rebuild the desktop (Hold down Command-Option keys while rebooting).

With IE 5.0 and with (at least) Mac OS 8.5.1, your CDS experience should be stable. But you will need at least 40 MB (preferably 64 MB) of RAM. You'll also need about 15MB of free disk space. You might need to turn Virtual Memory "On". If you have 64MB of RAM, start with about 128 MB of VM. Your mileage here may vary.