Bioinformatics: Alive and Kicking

David L. Osterbur
Harvard Medical School

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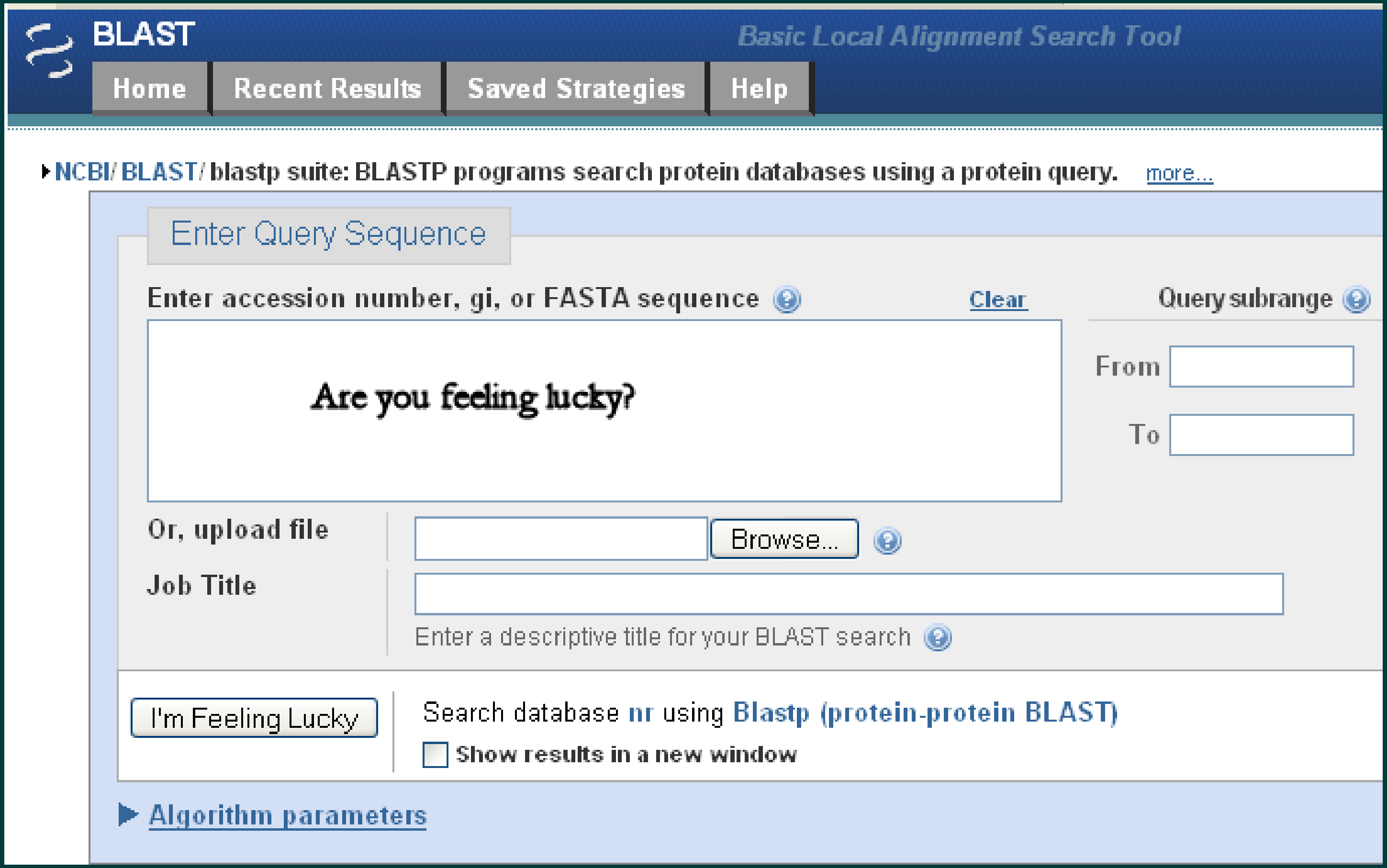
Too Central

- “Bioinformatics has become too central to biology to be left to specialist bioinformaticians. Biologists are all bioinformaticians now.”

Taken from Stein, L.D. (2008). Bioinformatics: alive and kicking. Genome Biol *9, 114.*

Google Generation



NCBI/ BLAST/ blastp suite: BLASTP programs search protein databases using a protein query. more...

Enter Query Sequence

Enter accession number, gi, or FASTA sequence Clear

Are you feeling lucky?

Query subrange

From

To

Or, upload file Browse...

Job Title

Enter a descriptive title for your BLAST search

I'm Feeling Lucky

Search database nr using Blastp (protein-protein BLAST)

□ Show results in a new window

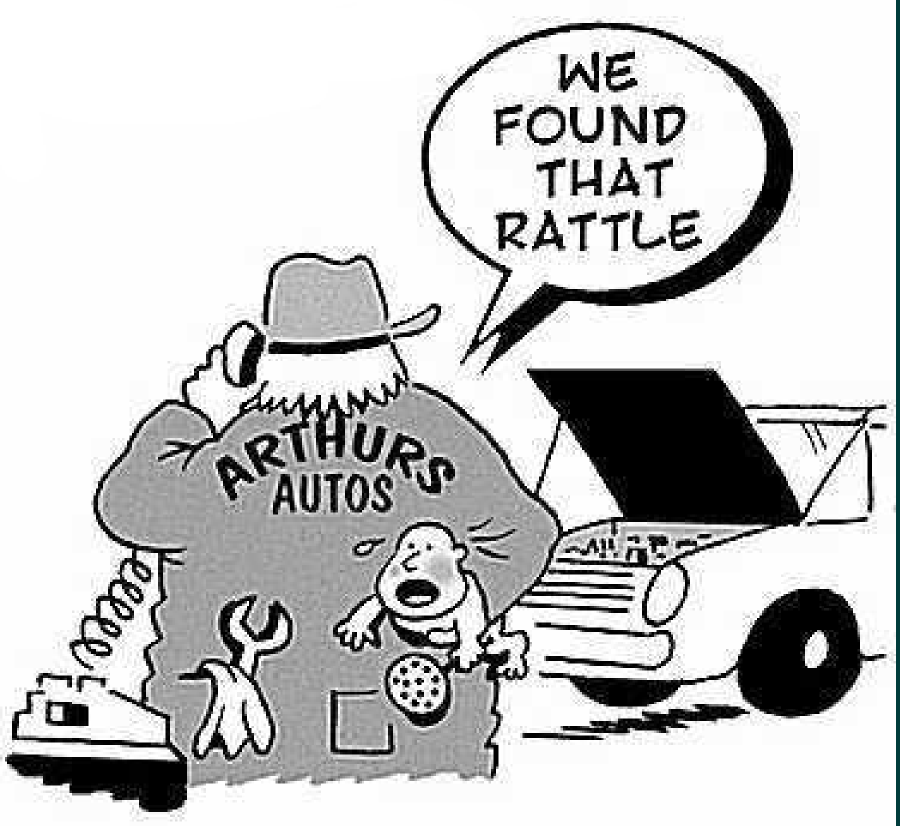
Algorithm parameters

History

Lister Hill
Auditorium
38A
LISTER HILL
AUDITORIUM
Visitor

Auto Designers

Auto Mechanics



Driver’s Ed

Keeping up to speed…

Not just how to drive but choosing the right tools.

…to reach your goal on time.

The Library’s Role

Why Libraries?

- We are a service organization.

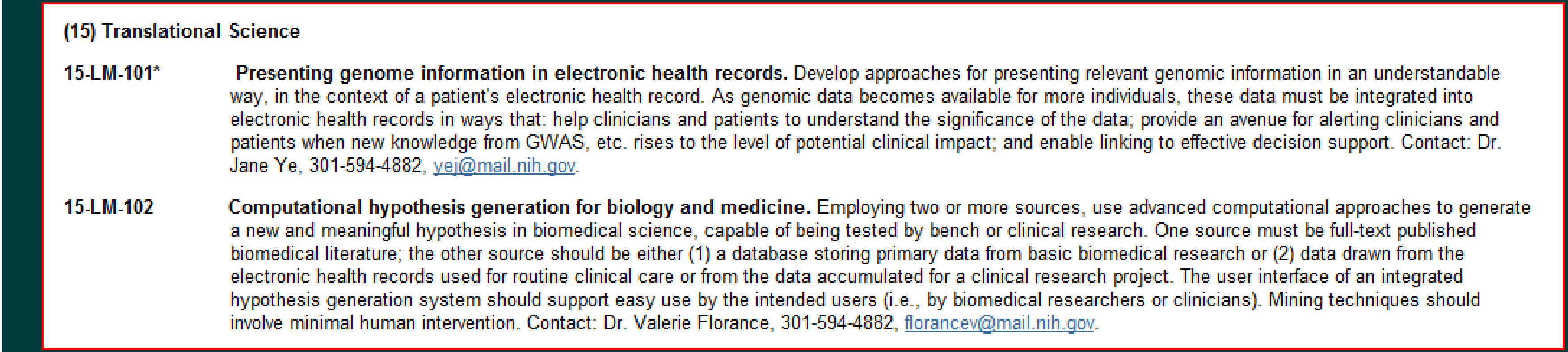
- We are already good at organizing, distributing and teaching access to many different types of information.

- We are a shared organization, not “owned” by any one department or unit.

- “Librarians like to search…

  …everyone else likes to find”

Why Your Library?

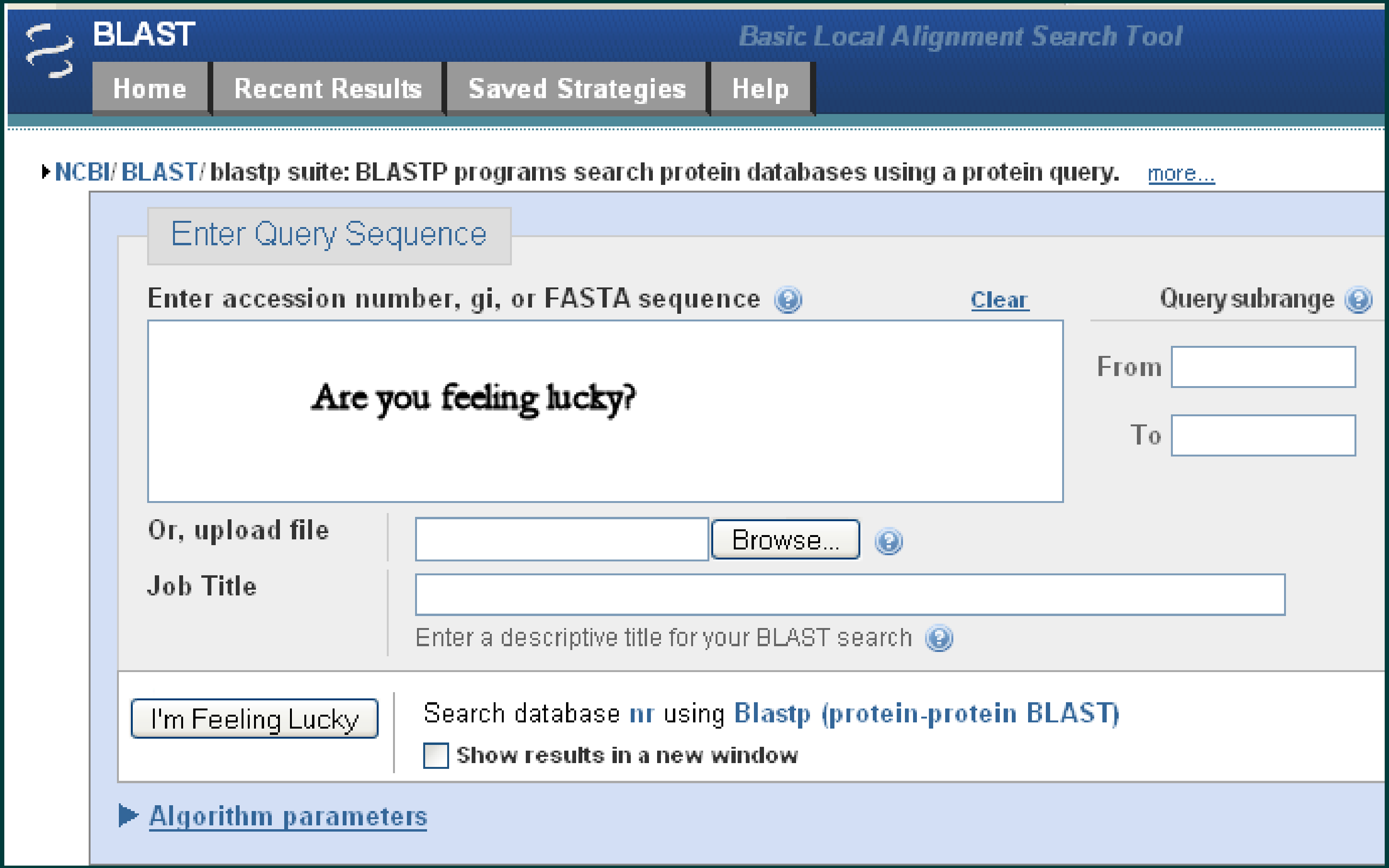


(15) Translational Science

15-LM-101* **Presenting genome information in electronic health records.** Develop approaches for presenting relevant genomic information in an understandable way, in the context of a patient's electronic health record. As genomic data becomes available for more individuals, these data must be integrated into electronic health records in ways that: help clinicians and patients to understand the significance of the data; provide an avenue for alerting clinicians and patients when new knowledge from GWAS, etc. rises to the level of potential clinical impact; and enable linking to effective decision support. Contact: Dr. Jane Ye, 301-594-4882, yej@mail.nih.gov.

15-LM-102 **Computational hypothesis generation for biology and medicine.** Employing two or more sources, use advanced computational approaches to generate a new and meaningful hypothesis in biomedical science, capable of being tested by bench or clinical research. One source must be full-text published biomedical literature; the other source should be either (1) a database storing primary data from basic biomedical research or (2) data drawn from the electronic health records used for routine clinical care or from the data accumulated for a clinical research project. The user interface of an integrated hypothesis generation system should support easy use by the intended users (i.e., by biomedical researchers or clinicians). Mining techniques should involve minimal human intervention. Contact: Dr. Valerie Florance, 301-594-4882, florancev@mail.nih.gov.

Google Generation



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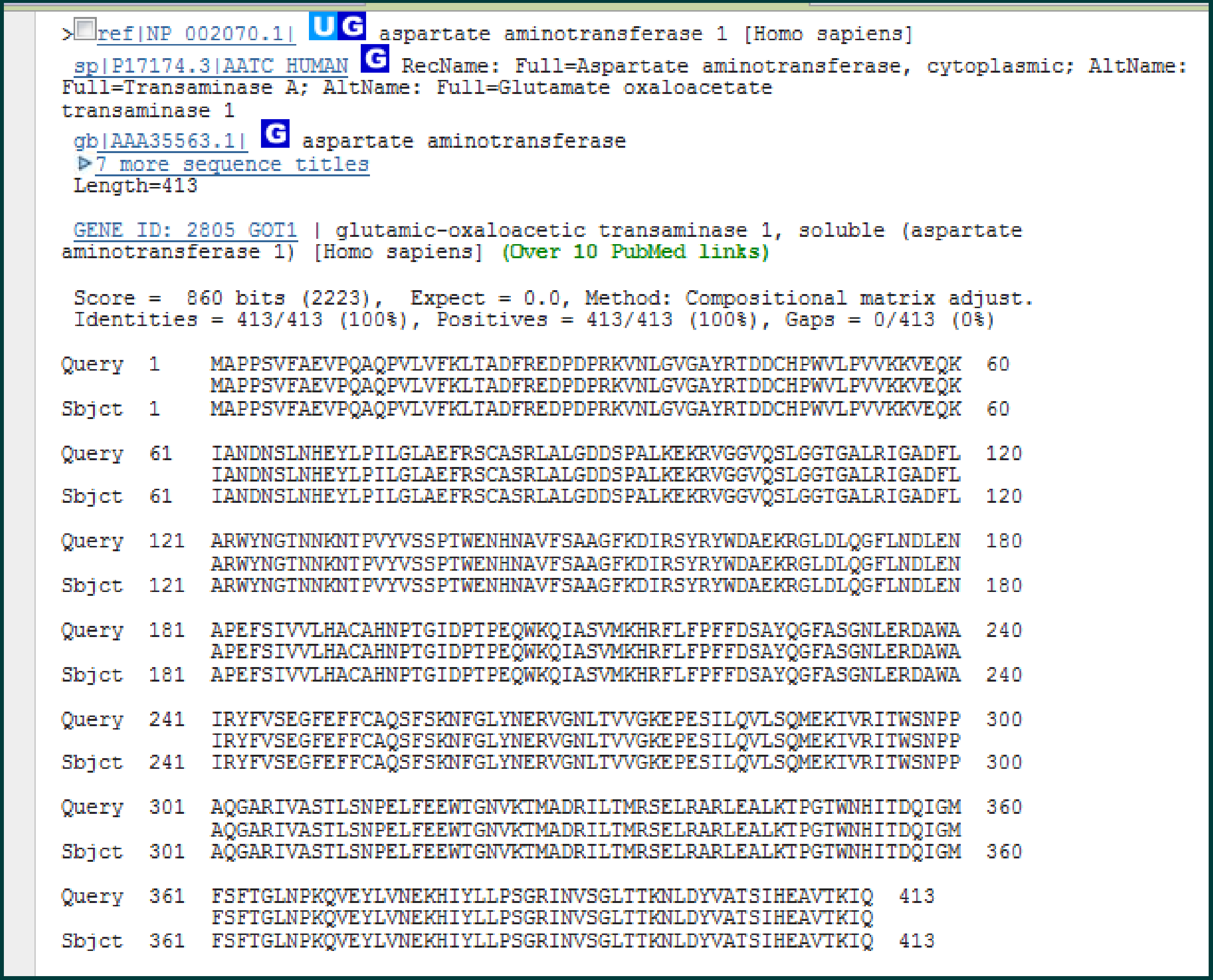
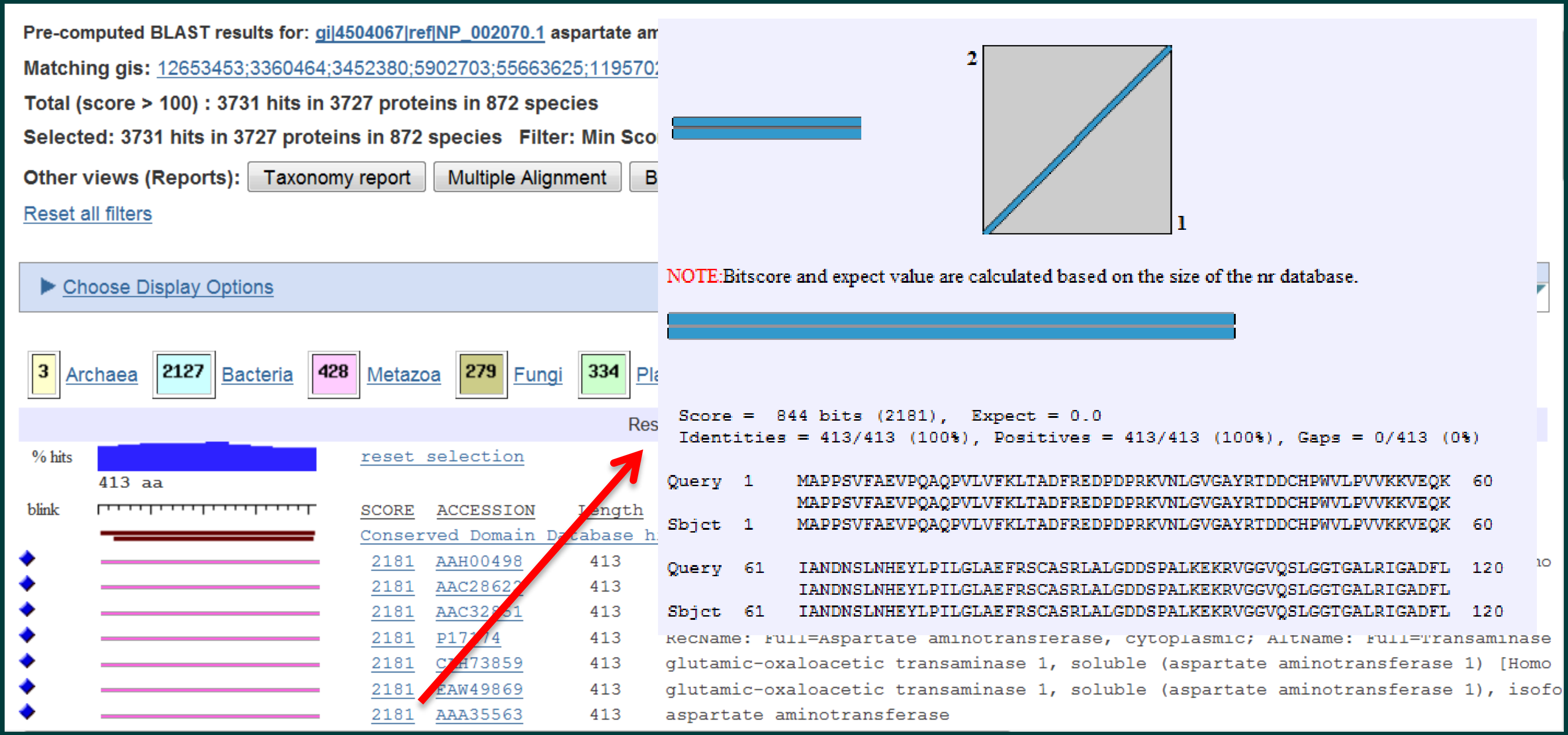
▶ Algorithm parameters

BLAST Results



```
>□ref|NP_002070.1| U G aspartate aminotransferase 1 [Homo sapiens]
 sp|P17174.3|AATC_HUMAN G RecName: Full=Aspartate aminotransferase, cytoplasmic; AltName:
Full=Transaminase A; AltName: Full=Glutamate oxaloacetate
transaminase 1
 gb|AAA35563.1| G aspartate aminotransferase
 ▶7 more sequence titles
 Length=413

 GENE ID: 2805 GOT1 | glutamic-oxaloacetic transaminase 1, soluble (aspartate
aminotransferase 1) [Homo sapiens] (Over 10 PubMed links)

 Score =  860 bits (2223),  Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 413/413 (100%), Positives = 413/413 (100%), Gaps = 0/413 (0%)

Query  1    MAPPSVFAEVPQAQPVLVFKLTADFREDPDPRKVNLGVGAYRTDDCHPWVLPVVKKVEQK  60
            MAPPSVFAEVPQAQPVLVFKLTADFREDPDPRKVNLGVGAYRTDDCHPWVLPVVKKVEQK
Sbjct  1    MAPPSVFAEVPQAQPVLVFKLTADFREDPDPRKVNLGVGAYRTDDCHPWVLPVVKKVEQK  60

Query  61   IANDNSLNHEYLPILGLAEFRSCASRLALGDDSPALKEKRVGGVQSLGGTGALRIGADFL  120
            IANDNSLNHEYLPILGLAEFRSCASRLALGDDSPALKEKRVGGVQSLGGTGALRIGADFL
Sbjct  61   IANDNSLNHEYLPILGLAEFRSCASRLALGDDSPALKEKRVGGVQSLGGTGALRIGADFL  120

Query  121  ARWYNGTNNKNTPVYVSSPTWENHNAVFSAAGFKDIRSYRYWDAEKRGLDLQGFLNDLEN  180
            ARWYNGTNNKNTPVYVSSPTWENHNAVFSAAGFKDIRSYRYWDAEKRGLDLQGFLNDLEN
Sbjct  121  ARWYNGTNNKNTPVYVSSPTWENHNAVFSAAGFKDIRSYRYWDAEKRGLDLQGFLNDLEN  180

Query  181  APEFSIVVLHACAHNPTGIDPTPEQWKQIASVMKHRFLFPFFDSAYQGFASGNLERDAWA  240
            APEFSIVVLHACAHNPTGIDPTPEQWKQIASVMKHRFLFPFFDSAYQGFASGNLERDAWA
Sbjct  181  APEFSIVVLHACAHNPTGIDPTPEQWKQIASVMKHRFLFPFFDSAYQGFASGNLERDAWA  240

Query  241  IRYFVSEGFEFFCAQSFSKNFGLYNERVGNLTVVGKEPESILQVLSQMEKIVRITWSNPP  300
            IRYFVSEGFEFFCAQSFSKNFGLYNERVGNLTVVGKEPESILQVLSQMEKIVRITWSNPP
Sbjct  241  IRYFVSEGFEFFCAQSFSKNFGLYNERVGNLTVVGKEPESILQVLSQMEKIVRITWSNPP  300

Query  301  AQGARIVASTLSNPELFEEWTGNVKTMADRILTMRSELRARLEALKTPGTWNHITDQIGM  360
            AQGARIVASTLSNPELFEEWTGNVKTMADRILTMRSELRARLEALKTPGTWNHITDQIGM
Sbjct  301  AQGARIVASTLSNPELFEEWTGNVKTMADRILTMRSELRARLEALKTPGTWNHITDQIGM  360

Query  361  FSFTGLNPKQVEYLVNEKHIYLLPSGRINVSGLTTKNLDYVATSIHEAVTKIQ  413
            FSFTGLNPKQVEYLVNEKHIYLLPSGRINVSGLTTKNLDYVATSIHEAVTKIQ
Sbjct  361  FSFTGLNPKQVEYLVNEKHIYLLPSGRINVSGLTTKNLDYVATSIHEAVTKIQ  413
```

NCBI has already done it…



Pre-computed BLAST results for: gi|4504067|ref|NP_002070.1 **aspartate am**

Matching gis: 12653453;3360464;3452380;5902703;55663625;119570

Total (score > 100) : 3731 hits in 3727 proteins in 872 species

Selected: 3731 hits in 3727 proteins in 872 species   Filter: Min Sco

Other views (Reports): Taxonomy report | Multiple Alignment | B

Reset all filters

▶ Choose Display Options

3	Archaea	2127	Bacteria	428	Metazoa	279	Fungi	334	Pl

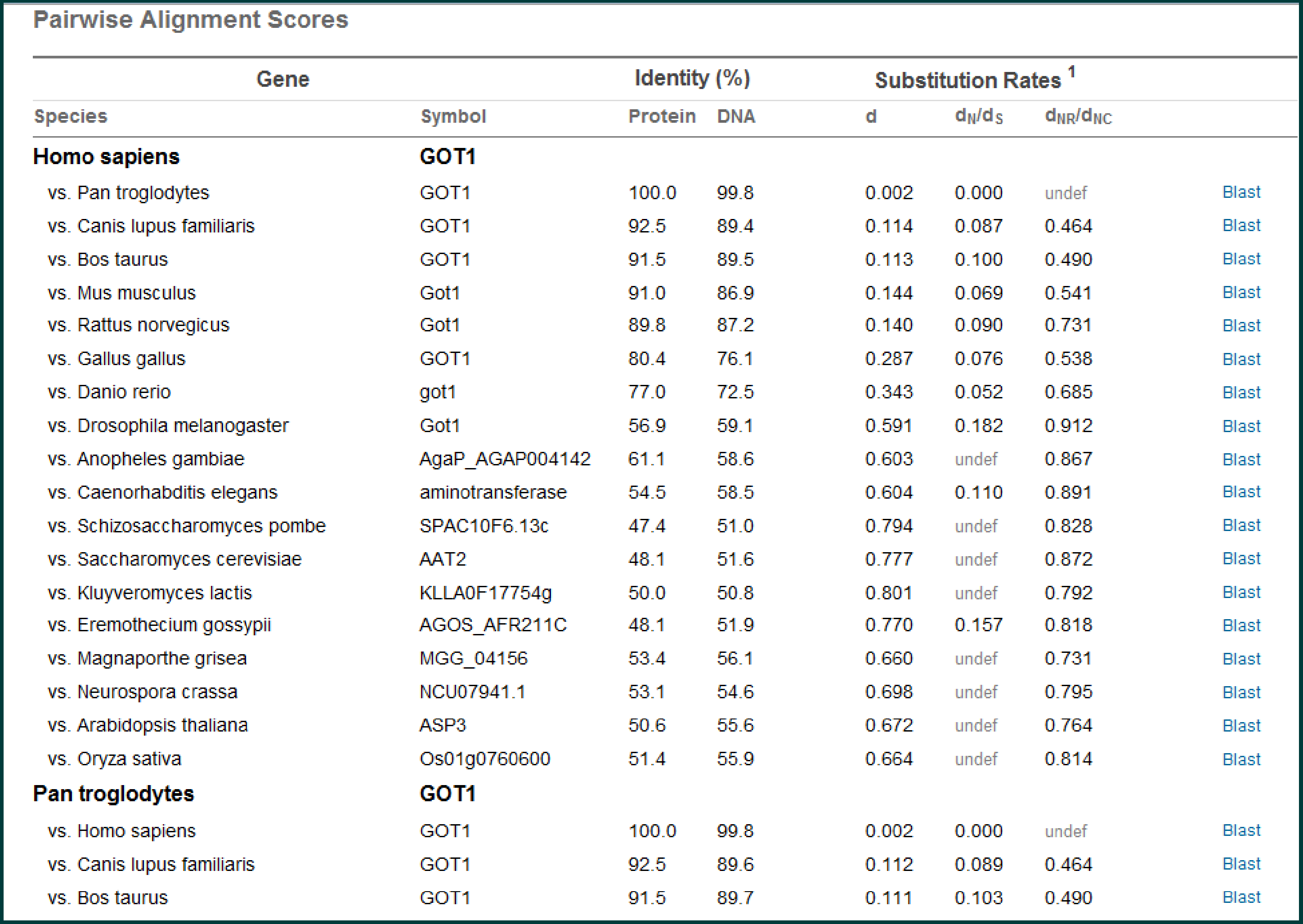
Conserved Domain Database hi

SCORE	ACCESSION	Length	
2181	AAH00498	413	
2181	AAC28622	413	
2181	AAC32851	413	
2181	P17174	413	RecName: Full=Aspartate aminotransferase, cytoplasmic; AltName: Full=Transaminase
2181	CAH73859	413	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) [Homo
2181	EAW49869	413	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1), isofo
2181	AAA35563	413	aspartate aminotransferase

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score =  844 bits (2181),  Expect = 0.0
 Identities = 413/413 (100%), Positives = 413/413 (100%), Gaps = 0/413 (0%)

Query  1    MAPPSVFAEVPQAQPVLVFKLTADFREDPDPRKVNLGVGAYRTDDCHPWVLPVVKKVEQK  60
            MAPPSVFAEVPQAQPVLVFKLTADFREDPDPRKVNLGVGAYRTDDCHPWVLPVVKKVEQK
Sbjct  1    MAPPSVFAEVPQAQPVLVFKLTADFREDPDPRKVNLGVGAYRTDDCHPWVLPVVKKVEQK  60

Query  61   IANDNSLNHEYLPILGLAEFRSCASRLALGDDSPALKEKRVGGVQSLGGTGALRIGADFL  120
            IANDNSLNHEYLPILGLAEFRSCASRLALGDDSPALKEKRVGGVQSLGGTGALRIGADFL
Sbjct  61   IANDNSLNHEYLPILGLAEFRSCASRLALGDDSPALKEKRVGGVQSLGGTGALRIGADFL  120
```

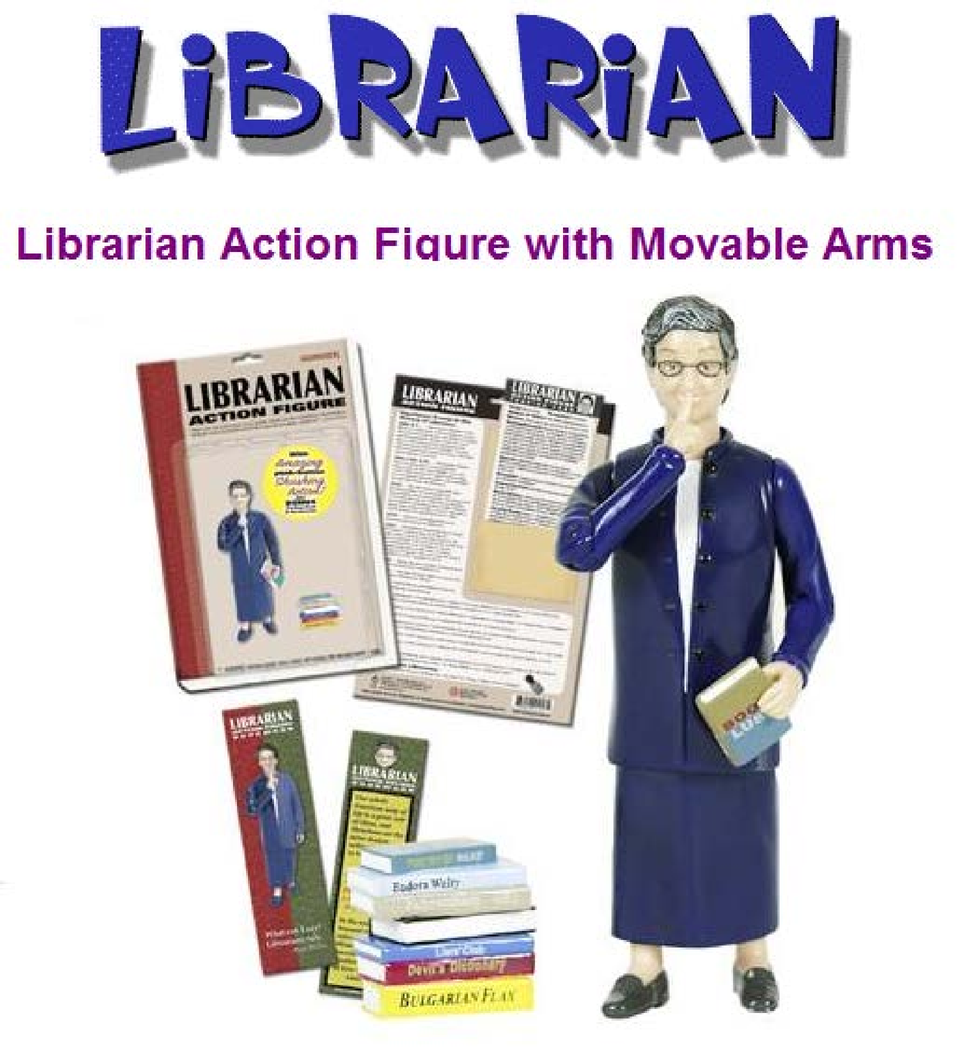
…and more.



Pairwise Alignment Scores

Gene		Identity (%)		Substitution Rates [1]			
Species	Symbol	Protein	DNA	d	d_N/d_S	d_{NR}/d_{NC}	
Homo sapiens	**GOT1**						
vs. Pan troglodytes	GOT1	100.0	99.8	0.002	0.000	undef	Blast
vs. Canis lupus familiaris	GOT1	92.5	89.4	0.114	0.087	0.464	Blast
vs. Bos taurus	GOT1	91.5	89.5	0.113	0.100	0.490	Blast
vs. Mus musculus	Got1	91.0	86.9	0.144	0.069	0.541	Blast
vs. Rattus norvegicus	Got1	89.8	87.2	0.140	0.090	0.731	Blast
vs. Gallus gallus	GOT1	80.4	76.1	0.287	0.076	0.538	Blast
vs. Danio rerio	got1	77.0	72.5	0.343	0.052	0.685	Blast
vs. Drosophila melanogaster	Got1	56.9	59.1	0.591	0.182	0.912	Blast
vs. Anopheles gambiae	AgaP_AGAP004142	61.1	58.6	0.603	undef	0.867	Blast
vs. Caenorhabditis elegans	aminotransferase	54.5	58.5	0.604	0.110	0.891	Blast
vs. Schizosaccharomyces pombe	SPAC10F6.13c	47.4	51.0	0.794	undef	0.828	Blast
vs. Saccharomyces cerevisiae	AAT2	48.1	51.6	0.777	undef	0.872	Blast
vs. Kluyveromyces lactis	KLLA0F17754g	50.0	50.8	0.801	undef	0.792	Blast
vs. Eremothecium gossypii	AGOS_AFR211C	48.1	51.9	0.770	0.157	0.818	Blast
vs. Magnaporthe grisea	MGG_04156	53.4	56.1	0.660	undef	0.731	Blast
vs. Neurospora crassa	NCU07941.1	53.1	54.6	0.698	undef	0.795	Blast
vs. Arabidopsis thaliana	ASP3	50.6	55.6	0.672	undef	0.764	Blast
vs. Oryza sativa	Os01g0760600	51.4	55.9	0.664	undef	0.814	Blast
Pan troglodytes	**GOT1**						
vs. Homo sapiens	GOT1	100.0	99.8	0.002	0.000	undef	Blast
vs. Canis lupus familiaris	GOT1	92.5	89.6	0.112	0.089	0.464	Blast
vs. Bos taurus	GOT1	91.5	89.7	0.111	0.103	0.490	Blast

Why not Libraries?



Criteria for Success

- Bioinformaticist interested in service
- Money to support software licensing
- No micromanaging

Bioinformatics Support at Countway

Countway Bioinformatics Education Program

- **R/Bioconductor**
- **GeneGO - Metacore**
- **Biobase – ExPlain, TransFac and HGMD**
- **Ingenuity Pathway Analysis**
- **SNP Data**
- **Sequence Alignment – BLAST & Clustal**
- **Genome Browsing**
- **Beginning Unix**
- **ENSEMBL**
- **Matlab**
- **Rosetta Resolver**

Community

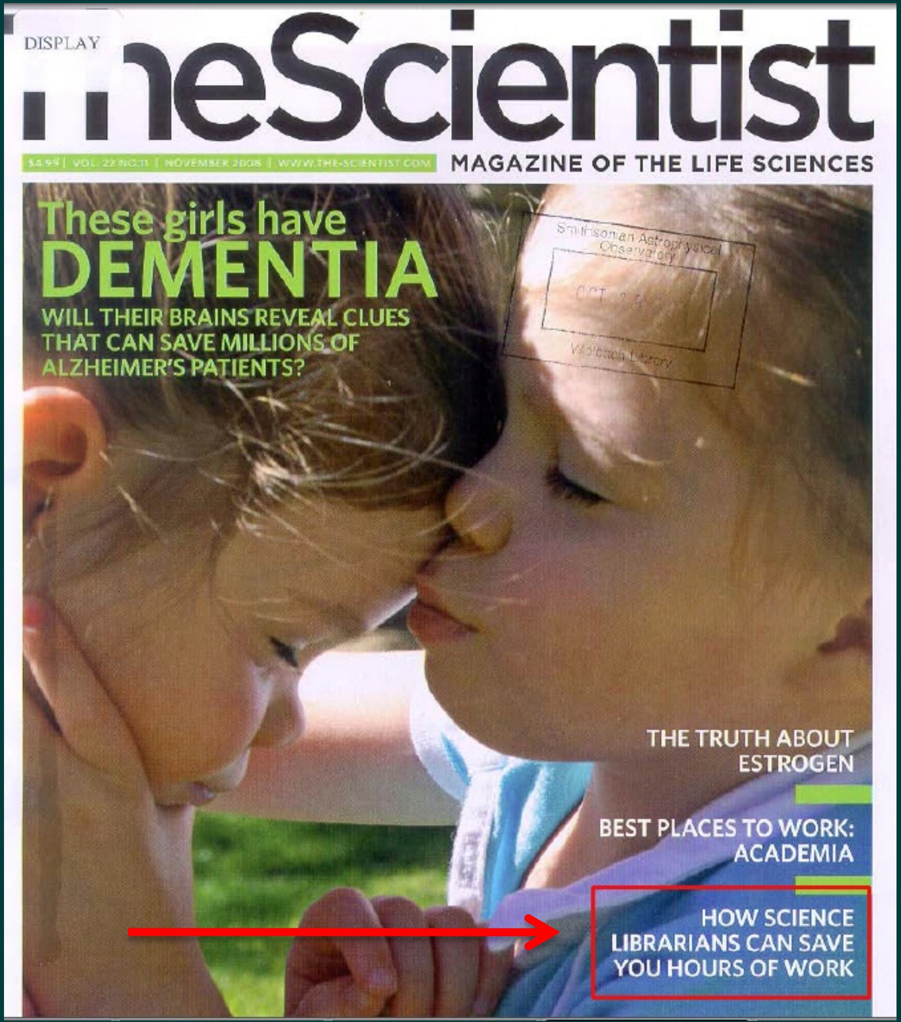
- BITS – Bioinformatics Tutorial Series – In collaboration with Courtney Crummett at MIT.
  - https://www.countway.harvard.edu/lenya/countway/live/menuNavigation/libraryServices/classes/videoTutorials.html
  - http://libguides.mit.edu/content.php?pid=14149&sid=145112

Harvard’s Favorites

- Survey to find out applications that are used by various labs around campus
  - This will inform us of what software we need to support if we are not already
  - It will help researchers to see what their colleagues are using
  - A way for others to see what Harvard is doing

Impact

For the Library



TheScientist

$4.99 | VOL. 22 NO.11 | NOVEMBER 2008 | WWW.THE-SCIENTIST.COM

MAGAZINE OF THE LIFE SCIENCES

These girls have DEMENTIA

WILL THEIR BRAINS REVEAL CLUES THAT CAN SAVE MILLIONS OF ALZHEIMER'S PATIENTS?

THE TRUTH ABOUT ESTROGEN

BEST PLACES TO WORK: ACADEMIA

HOW SCIENCE LIBRARIANS CAN SAVE YOU HOURS OF WORK

Impact

For the Library

- First time ever library invited to participate in both the graduate and medical curriculums.
- Collaborative opportunities
  - – MIT
  - – MLA – other libraries
  - – Across Harvard

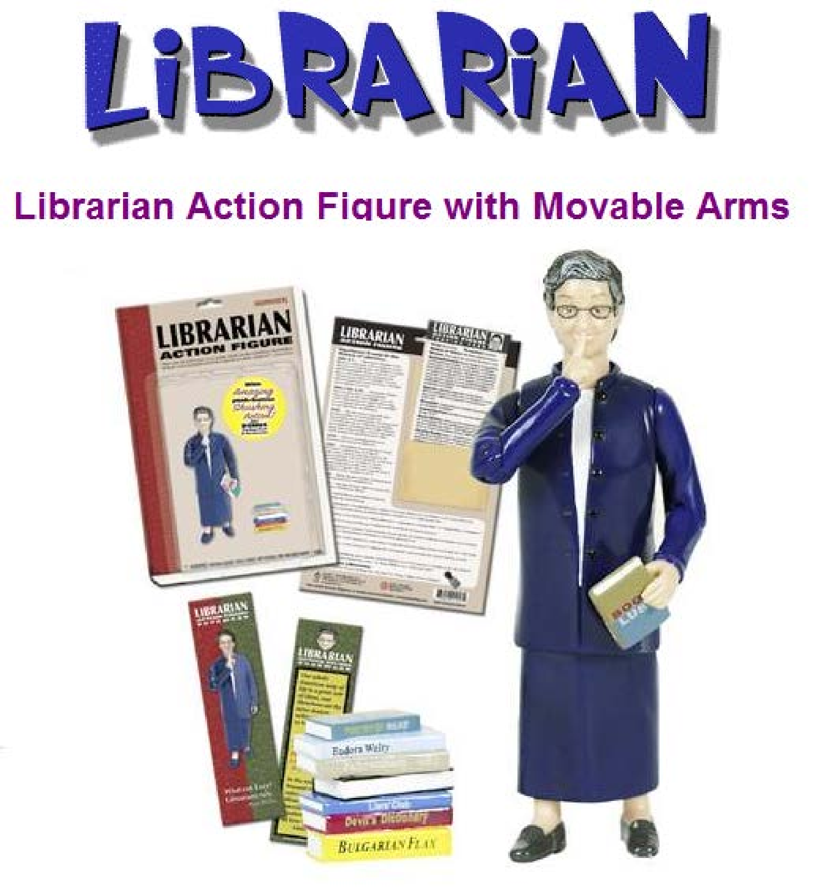
Impact

For HMS and the CTSA

- More productive researchers
- Better educated students and postdocs
- … (and faculty)

“The greatest obstacle to discovery is not ignorance - it is the illusion of knowledge.“ Daniel J. Boorstin (1914–2004) Historian and Librarian of Congress

When you think of libraries



Don’t think of Marian the Librarian

Think of Conan the Librarian

Bioinformatics: alive and kicking...

in the library.