Free Software In Bioinformatics

by Wises Namwat

Department of Microbiology,

Faculty of Medicine, Khon Kaen University

Learning objectives

1. Describe types and characteristics of bioinformatics free-software which available in internet
2. How to access to sources of the bioinformatics free-softwares
3. How to use Bioedit for basic bioinformatics application.

Outline

- Web-based free-software
- Stand-alone free-software
- Practice on “Bioedit” and “ImageJ”
- Practice on web-based free-software

Example of the Free software

Stand-alone software

- Bioedit
- PerlPrimer
- ImageJ

Web-bases software

- ClustalW
- WebCutter site
- Gene Fisher primer design
- Expasy-base software
- EBI-base software
- NCBI-base software

Characteristics of the softwares

Stand-alone software

- All process in your PC
- Smaller size
- Update new version by user
- Construct your own database
- Simple algorithm or function
- Rapid processing
- Internet independence during work

Web-bases software

- Input and display result in your PC by process analysis in server (mainframe computer) somewhere in the network
- Larger size
- Update by owner
- Link to large public database in WWW.
- Complicate and sophisticated algorithm
- Network traffic dependent processing (online during work)

Web-base resources

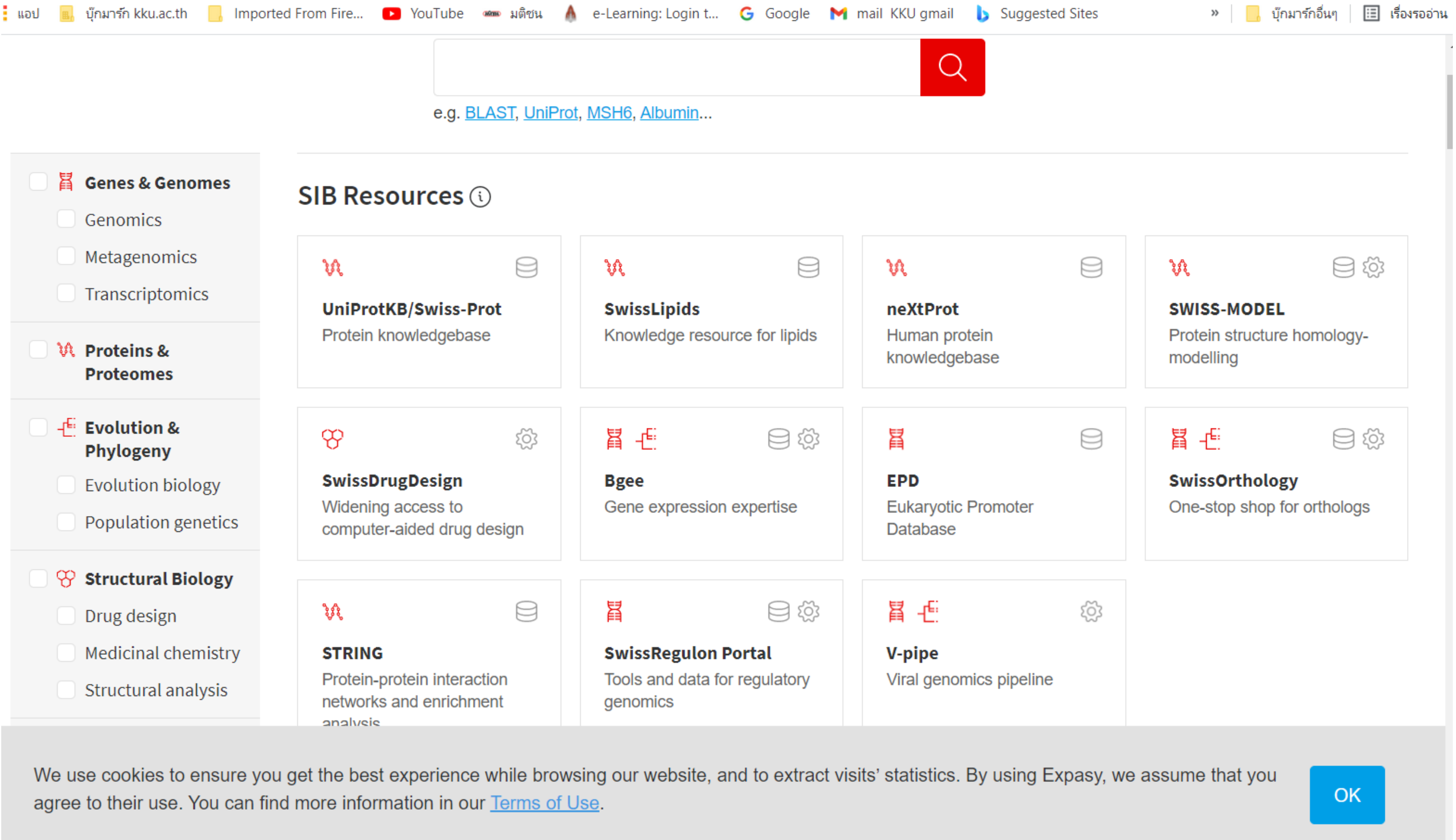
Classic home of free software

- http://expasy.org/
- http://www.ebi.ac.uk/
- http://www.bioinformatics.org/

Google search “bioinformatics free software”

- https://www.google.com/search?q=free+software+bioinformatics&oq=free+software+bioinformatics&aqs=chrome..69i57j0i22i30l2j0i390l5.10294j0j15&sourceid=chrome&ie=UTF-8
- https://listoffreeware.com/free-bioinformatics-software-windows/
- https://www.techjockey.com/blog/bioinformatics-tools

http://expasy.org/



e.g. BLAST, UniProt, MSH6, Albumin...

☐ **Genes & Genomes**
- ☐ Genomics
- ☐ Metagenomics
- ☐ Transcriptomics

☐ **Proteins & Proteomes**

☐ **Evolution & Phylogeny**
- ☐ Evolution biology
- ☐ Population genetics

☐ **Structural Biology**
- ☐ Drug design
- ☐ Medicinal chemistry
- ☐ Structural analysis

SIB Resources ⓘ

UniProtKB/Swiss-Prot
Protein knowledgebase

SwissLipids
Knowledge resource for lipids

neXtProt
Human protein knowledgebase

SWISS-MODEL
Protein structure homology-modelling

SwissDrugDesign
Widening access to computer-aided drug design

Bgee
Gene expression expertise

EPD
Eukaryotic Promoter Database

SwissOrthology
One-stop shop for orthologs

STRING
Protein-protein interaction networks and enrichment analysis

SwissRegulon Portal
Tools and data for regulatory genomics

V-pipe
Viral genomics pipeline

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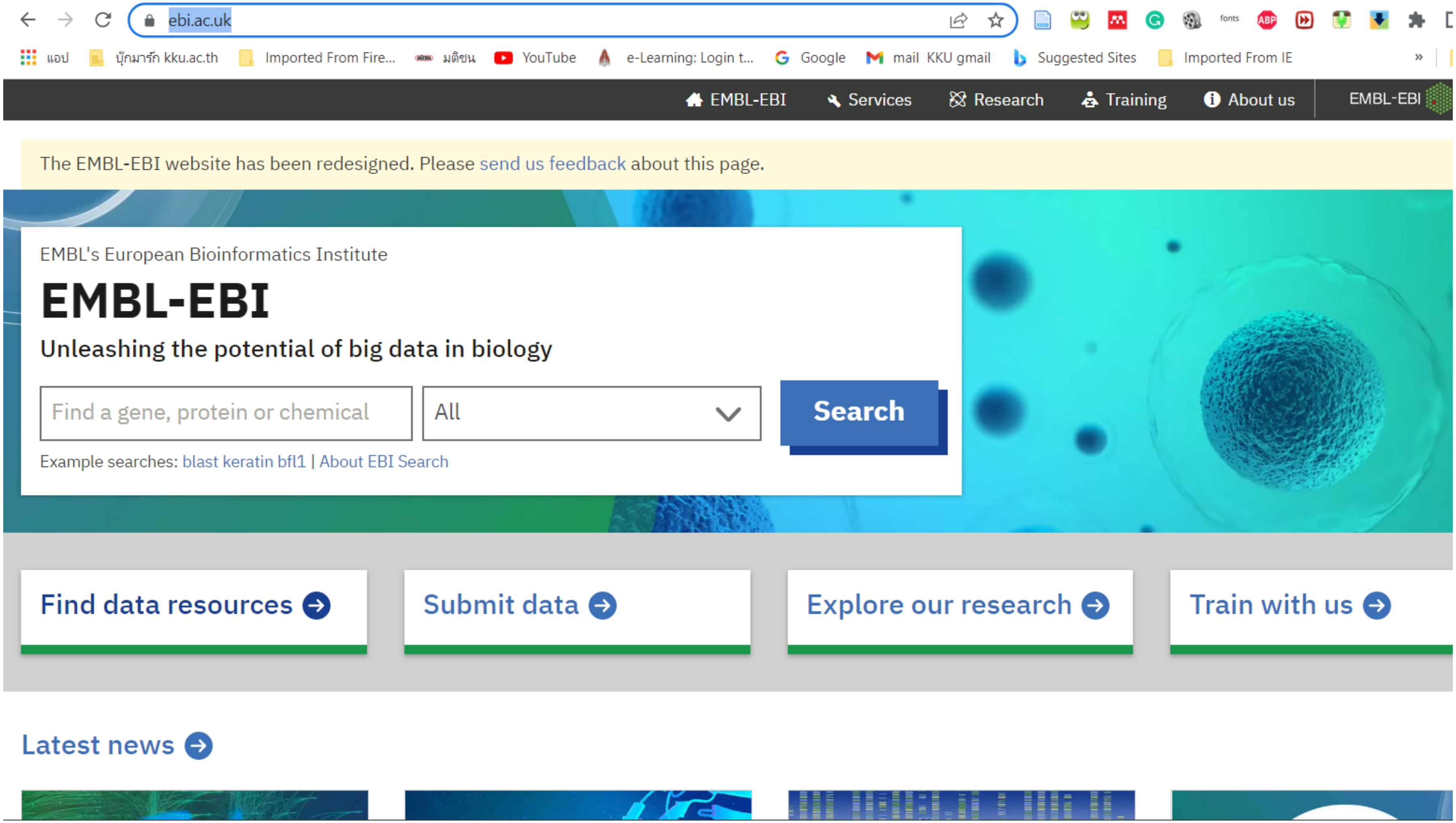
OK

https://www.ebi.ac.uk/



The EMBL-EBI website has been redesigned. Please send us feedback about this page.

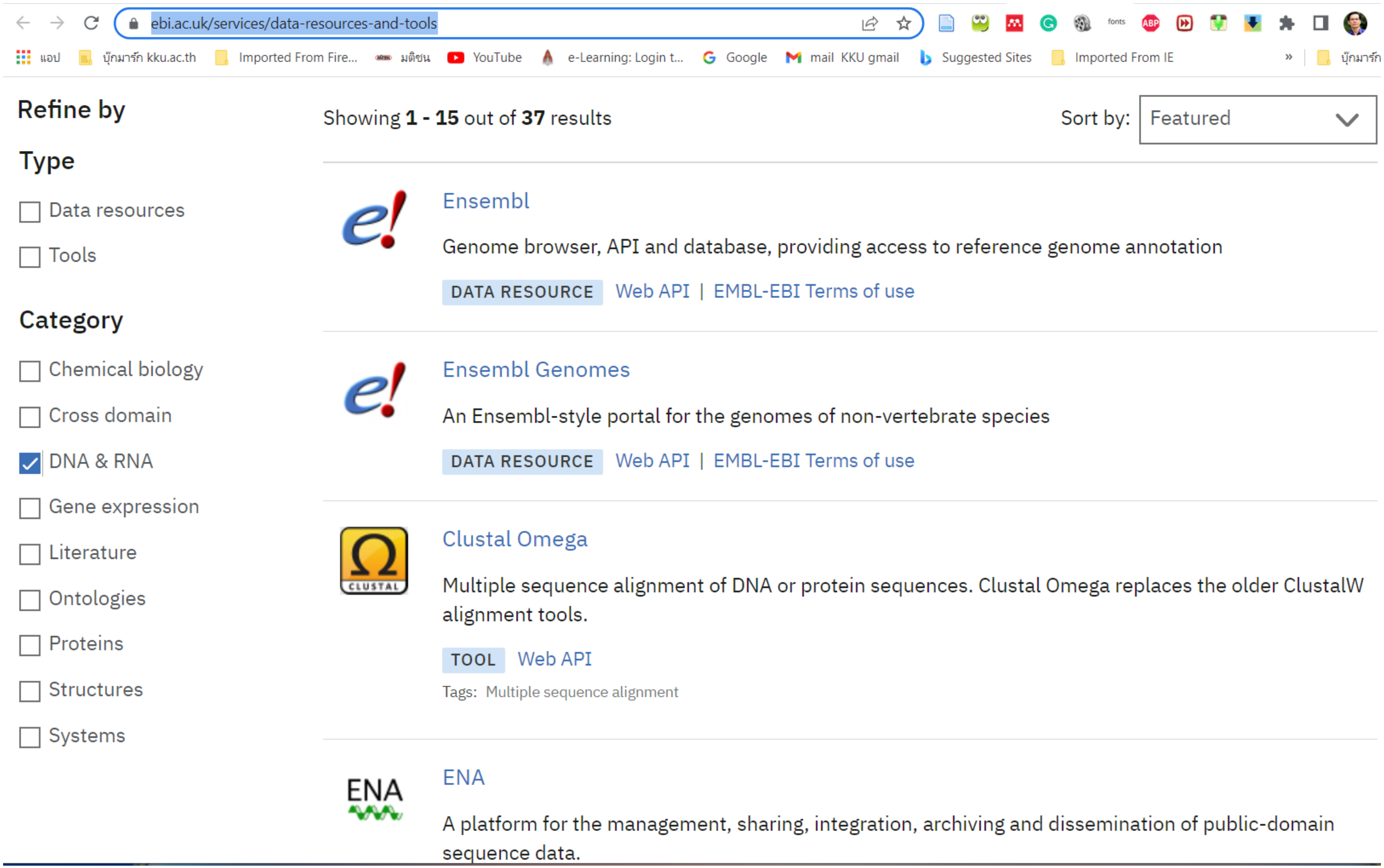
EMBL's European Bioinformatics Institute

EMBL-EBI

Unleashing the potential of big data in biology

Example searches: blast keratin bfl1 | About EBI Search

https://www.ebi.ac.uk/services/data-resources-and-tools



Refine by

Type

☐ Data resources

☐ Tools

Category

☐ Chemical biology

☐ Cross domain

☑ DNA & RNA

☐ Gene expression

☐ Literature

☐ Ontologies

☐ Proteins

☐ Structures

☐ Systems

Showing **1 - 15** out of **37** results

Sort by: Featured

Ensembl

Genome browser, API and database, providing access to reference genome annotation

DATA RESOURCE Web API | EMBL-EBI Terms of use

Ensembl Genomes

An Ensembl-style portal for the genomes of non-vertebrate species

DATA RESOURCE Web API | EMBL-EBI Terms of use

Clustal Omega

Multiple sequence alignment of DNA or protein sequences. Clustal Omega replaces the older ClustalW alignment tools.

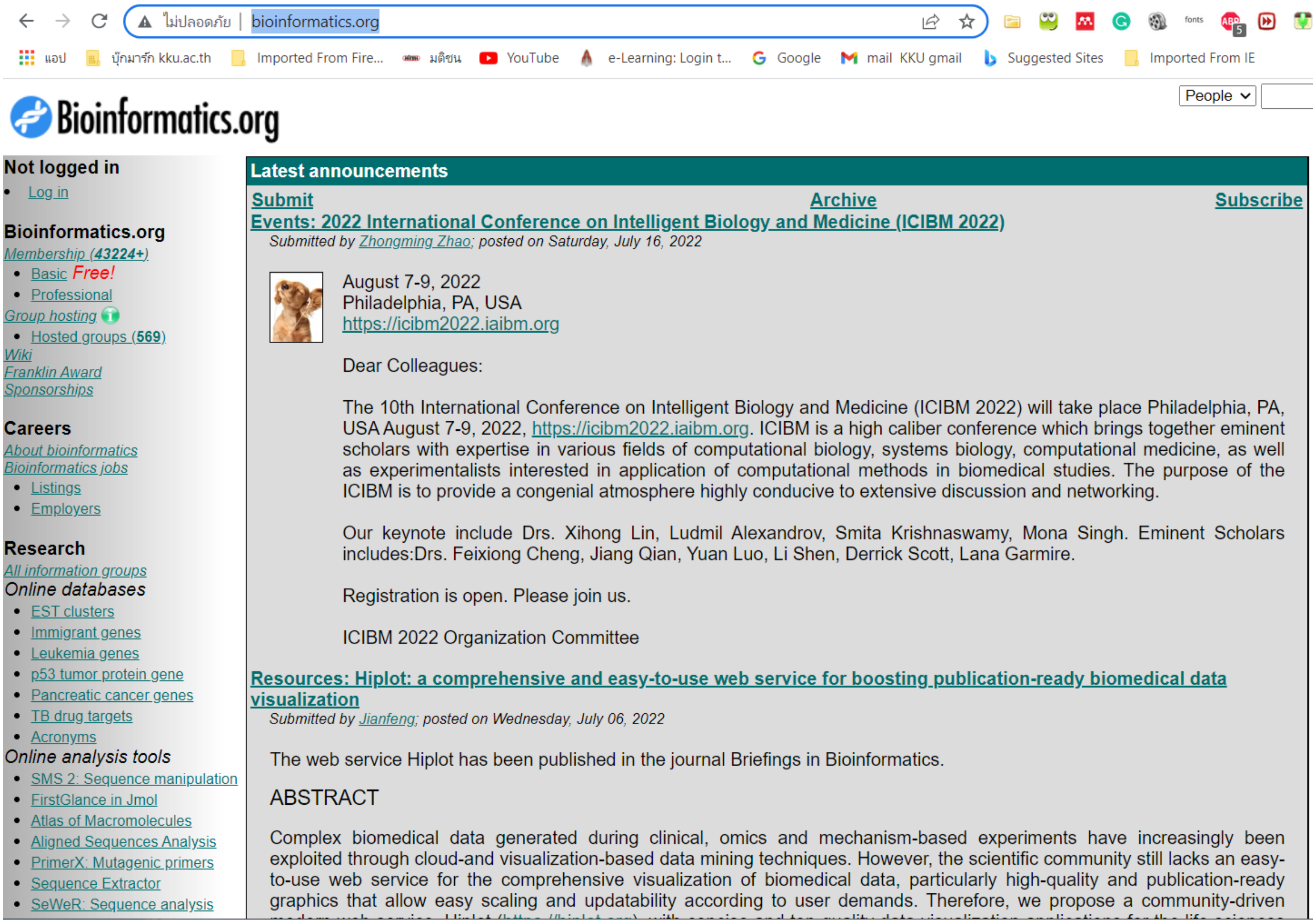
TOOL Web API

Tags: Multiple sequence alignment

ENA

A platform for the management, sharing, integration, archiving and dissemination of public-domain sequence data.

http://www.bioinformatics.org/



Bioinformatics.org

Not logged in

- Log in

Bioinformatics.org

*Membership (**43224+**)*

- Basic *Free!*
- Professional

Group hosting

- Hosted groups (**569**)

Wiki

Franklin Award

Sponsorships

Careers

About bioinformatics

Bioinformatics jobs

- Listings
- Employers

Research

All information groups

Online databases

- EST clusters
- Immigrant genes
- Leukemia genes
- p53 tumor protein gene
- Pancreatic cancer genes
- TB drug targets
- Acronyms

Online analysis tools

- SMS 2: Sequence manipulation
- FirstGlance in Jmol
- Atlas of Macromolecules
- Aligned Sequences Analysis
- PrimerX: Mutagenic primers
- Sequence Extractor
- SeWeR: Sequence analysis

Latest announcements

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Events: 2022 International Conference on Intelligent Biology and Medicine (ICIBM 2022)

Submitted by Zhongming Zhao; posted on Saturday, July 16, 2022

August 7-9, 2022
Philadelphia, PA, USA
https://icibm2022.iaibm.org

Dear Colleagues:

The 10th International Conference on Intelligent Biology and Medicine (ICIBM 2022) will take place Philadelphia, PA, USA August 7-9, 2022, https://icibm2022.iaibm.org. ICIBM is a high caliber conference which brings together eminent scholars with expertise in various fields of computational biology, systems biology, computational medicine, as well as experimentalists interested in application of computational methods in biomedical studies. The purpose of the ICIBM is to provide a congenial atmosphere highly conducive to extensive discussion and networking.

Our keynote include Drs. Xihong Lin, Ludmil Alexandrov, Smita Krishnaswamy, Mona Singh. Eminent Scholars includes:Drs. Feixiong Cheng, Jiang Qian, Yuan Luo, Li Shen, Derrick Scott, Lana Garmire.

Registration is open. Please join us.

ICIBM 2022 Organization Committee

Resources: Hiplot: a comprehensive and easy-to-use web service for boosting publication-ready biomedical data visualization

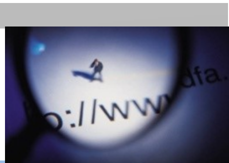
Submitted by Jianfeng; posted on Wednesday, July 06, 2022

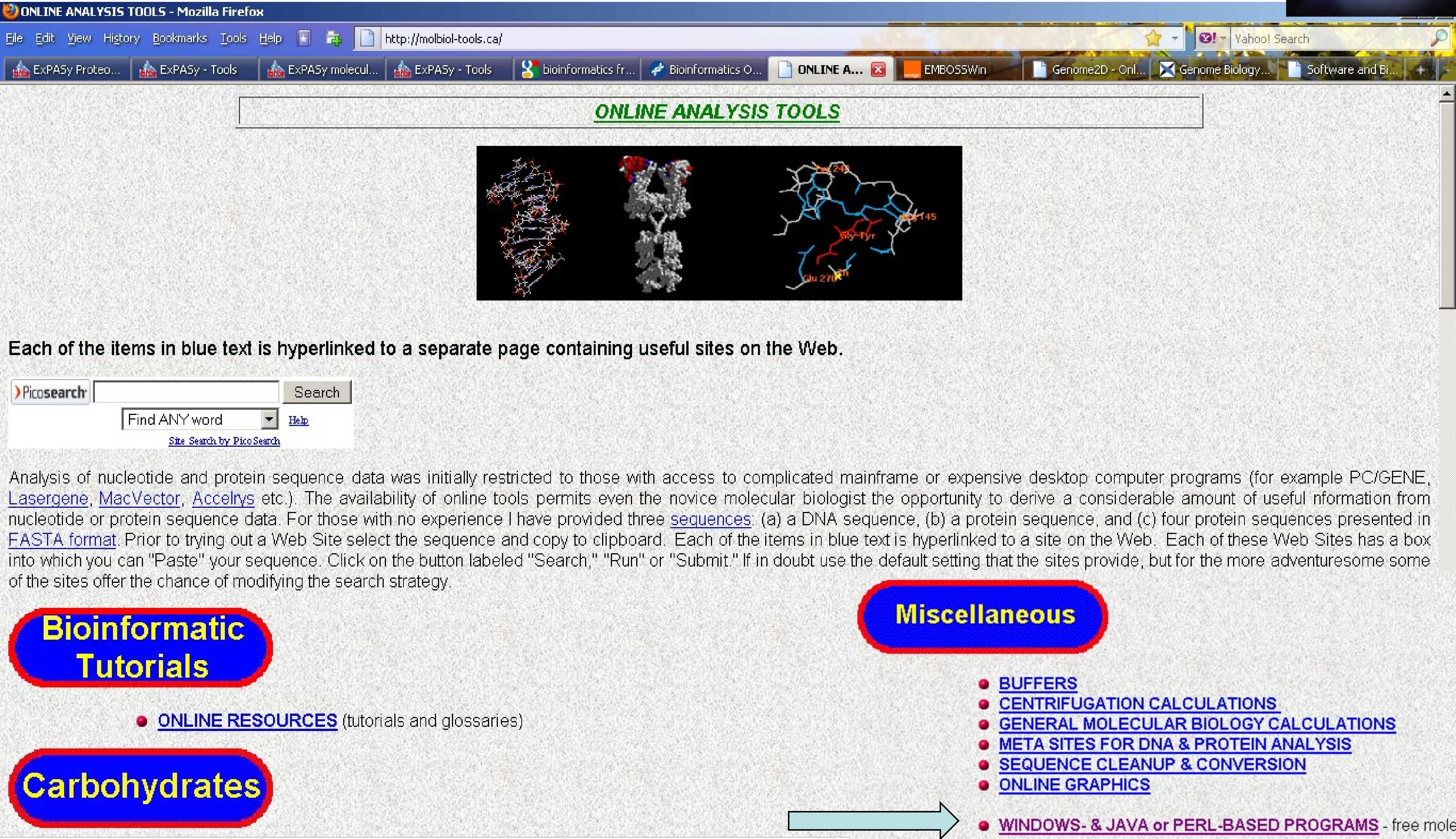
The web service Hiplot has been published in the journal Briefings in Bioinformatics.

ABSTRACT

Complex biomedical data generated during clinical, omics and mechanism-based experiments have increasingly been exploited through cloud-and visualization-based data mining techniques. However, the scientific community still lacks an easy-to-use web service for the comprehensive visualization of biomedical data, particularly high-quality and publication-ready graphics that allow easy scaling and updatability according to user demands. Therefore, we propose a community-driven

http://molbiol-tools.ca/





ONLINE ANALYSIS TOOLS

Each of the items in blue text is hyperlinked to a separate page containing useful sites on the Web.

Analysis of nucleotide and protein sequence data was initially restricted to those with access to complicated mainframe or expensive desktop computer programs (for example PC/GENE, Lasergene, MacVector, Accelrys etc.). The availability of online tools permits even the novice molecular biologist the opportunity to derive a considerable amount of useful nformation from nucleotide or protein sequence data. For those with no experience I have provided three sequences: (a) a DNA sequence, (b) a protein sequence, and (c) four protein sequences presented in FASTA format. Prior to trying out a Web Site select the sequence and copy to clipboard. Each of the items in blue text is hyperlinked to a site on the Web. Each of these Web Sites has a box into which you can "Paste" your sequence. Click on the button labeled "Search," "Run" or "Submit." If in doubt use the default setting that the sites provide, but for the more adventuresome some of the sites offer the chance of modifying the search strategy.

Bioinformatic Tutorials

- ONLINE RESOURCES (tutorials and glossaries)

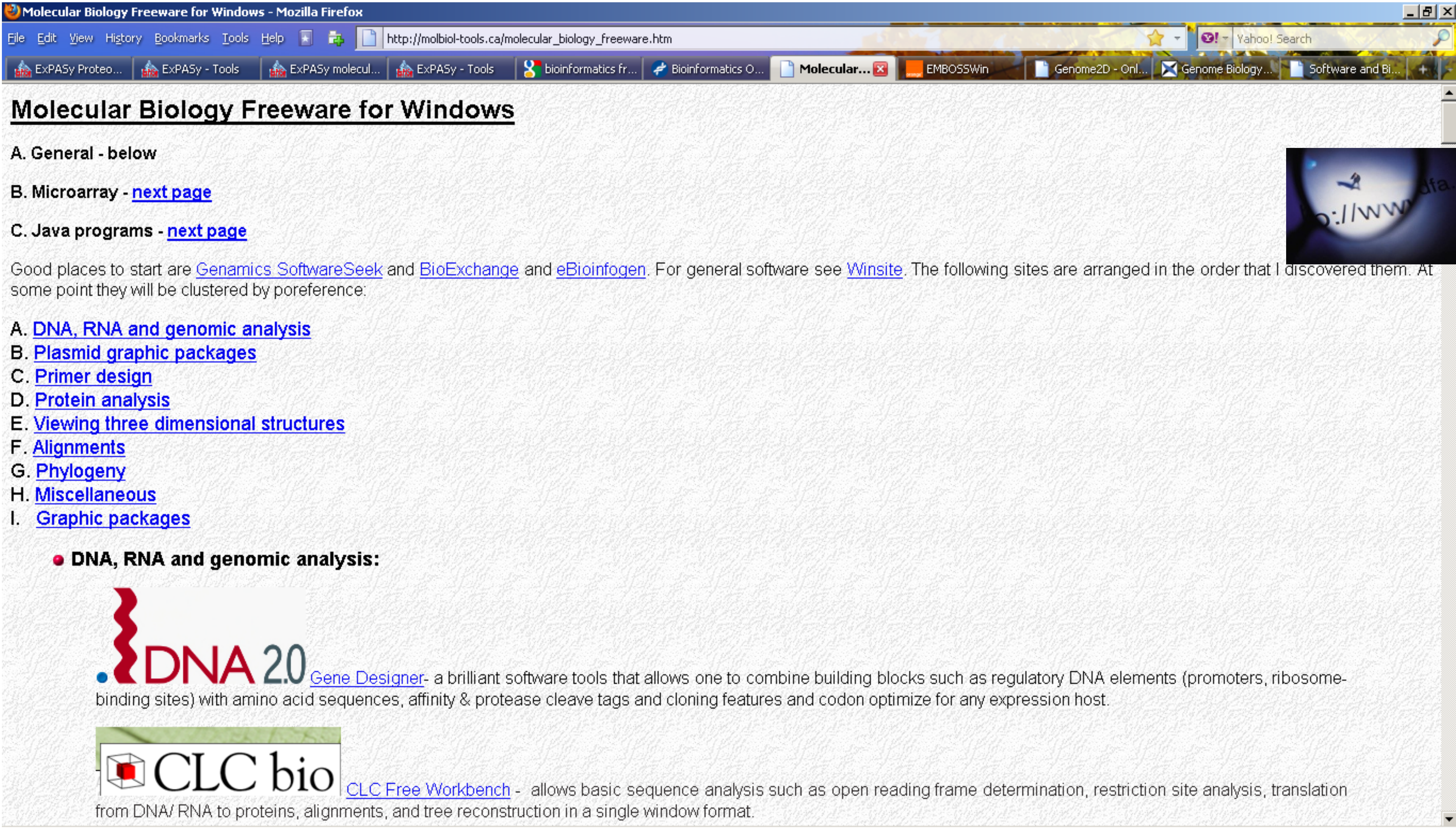
Carbohydrates

Miscellaneous

- BUFFERS
- CENTRIFUGATION CALCULATIONS
- GENERAL MOLECULAR BIOLOGY CALCULATIONS
- META SITES FOR DNA & PROTEIN ANALYSIS
- SEQUENCE CLEANUP & CONVERSION
- ONLINE GRAPHICS
- WINDOWS- & JAVA or PERL-BASED PROGRAMS - free mole

http://molbiol-tools.ca/molecular_biology_freeware.htm

- Look at DNA for windows



Molecular Biology Freeware for Windows

A. General - below

B. Microarray - next page

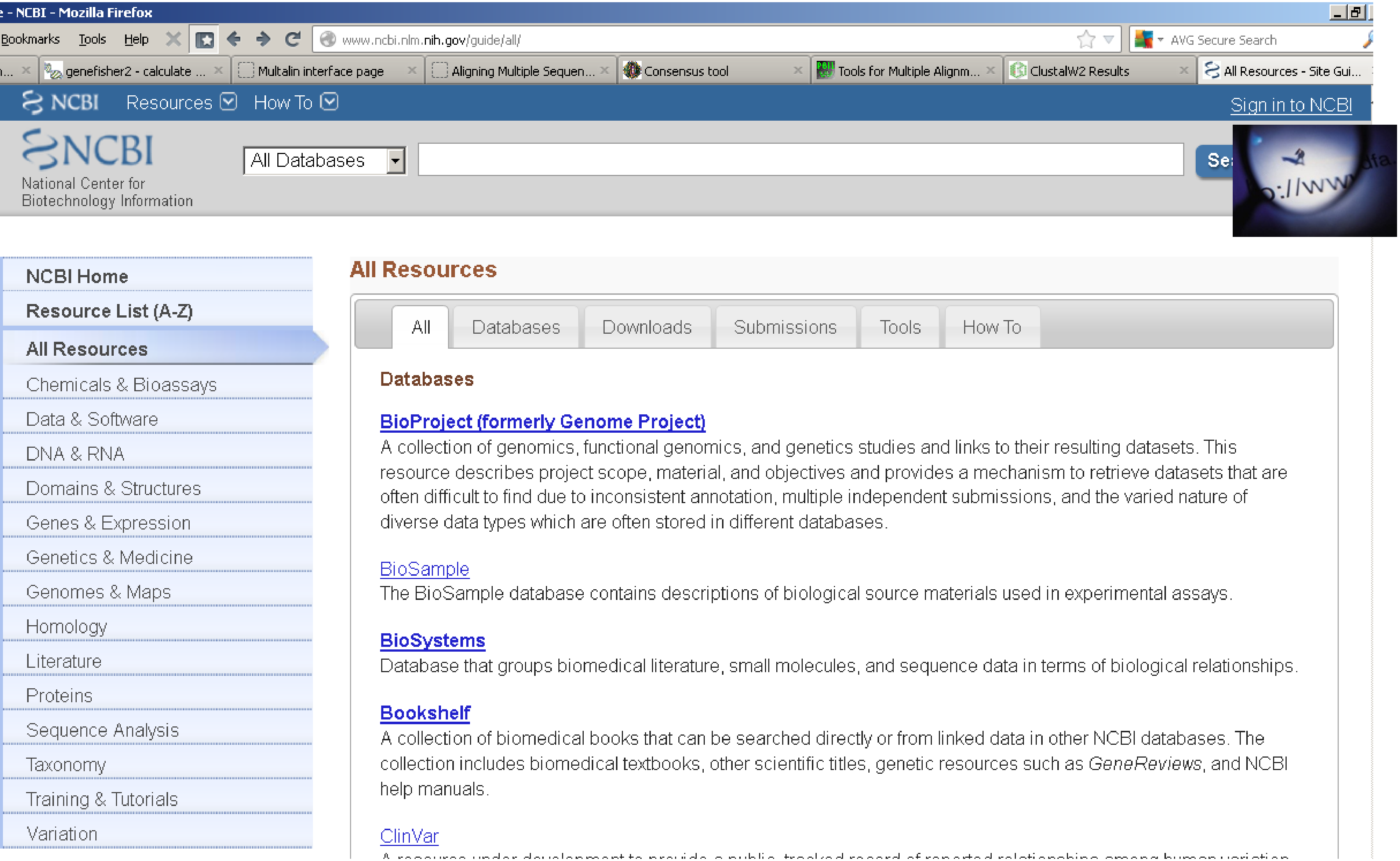
C. Java programs - next page

Good places to start are Genamics SoftwareSeek and BioExchange and eBioinfogen. For general software see Winsite. The following sites are arranged in the order that I discovered them. At some point they will be clustered by poreference:

A. DNA, RNA and genomic analysis
B. Plasmid graphic packages
C. Primer design
D. Protein analysis
E. Viewing three dimensional structures
F. Alignments
G. Phylogeny
H. Miscellaneous
I. Graphic packages

- **DNA, RNA and genomic analysis:**
  - Gene Designer- a brilliant software tools that allows one to combine building blocks such as regulatory DNA elements (promoters, ribosome-binding sites) with amino acid sequences, affinity & protease cleave tags and cloning features and codon optimize for any expression host.
  - CLC Free Workbench - allows basic sequence analysis such as open reading frame determination, restriction site analysis, translation from DNA/ RNA to proteins, alignments, and tree reconstruction in a single window format.

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



All Resources

Databases

BioProject (formerly Genome Project)
A collection of genomics, functional genomics, and genetics studies and links to their resulting datasets. This resource describes project scope, material, and objectives and provides a mechanism to retrieve datasets that are often difficult to find due to inconsistent annotation, multiple independent submissions, and the varied nature of diverse data types which are often stored in different databases.

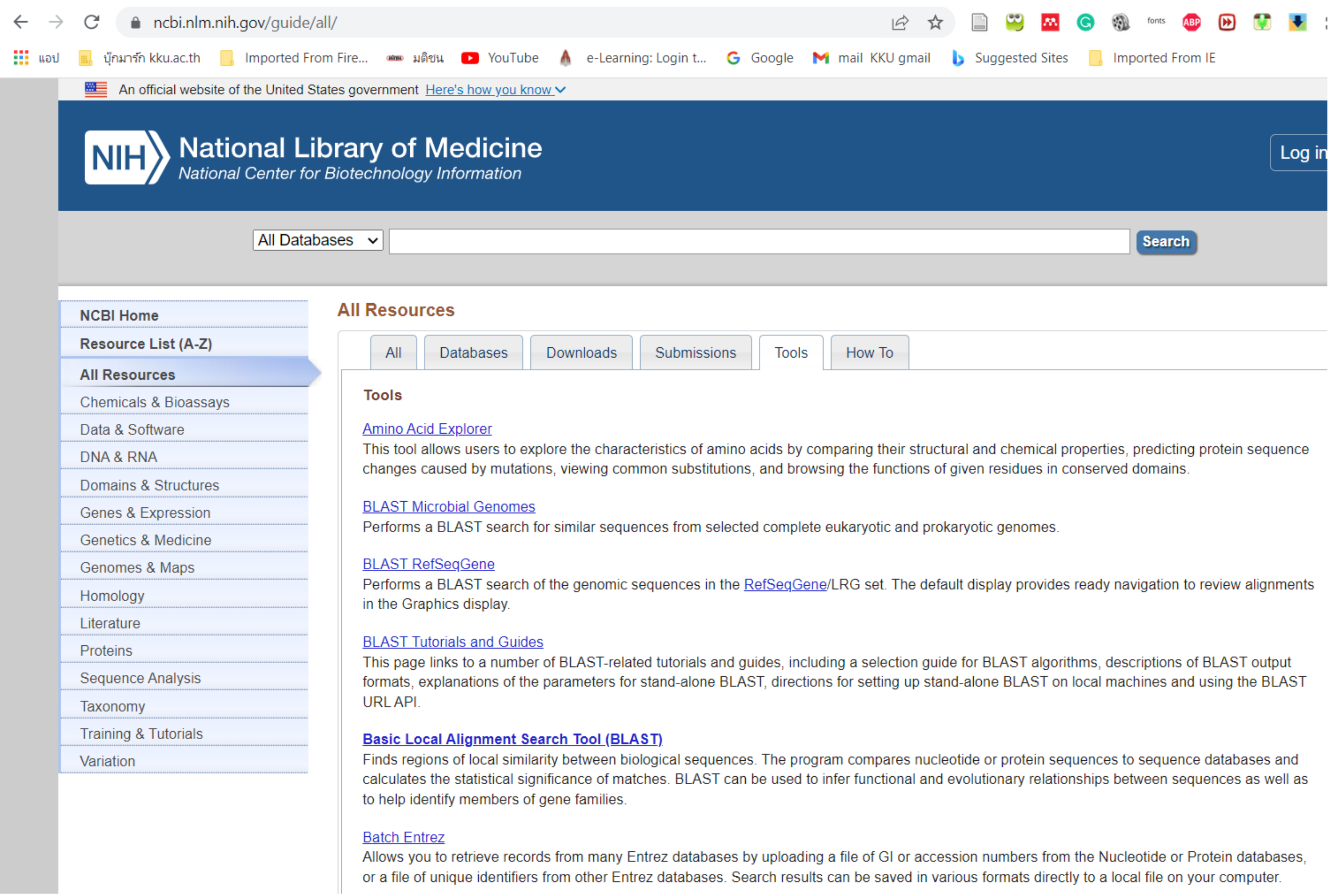
BioSample
The BioSample database contains descriptions of biological source materials used in experimental assays.

BioSystems
Database that groups biomedical literature, small molecules, and sequence data in terms of biological relationships.

Bookshelf
A collection of biomedical books that can be searched directly or from linked data in other NCBI databases. The collection includes biomedical textbooks, other scientific titles, genetic resources such as *GeneReviews*, and NCBI help manuals.

ClinVar
A resource under development to provide a public, tracked record of reported relationships among human variation

Tools at NCBI



An official website of the United States government Here's how you know

National Library of Medicine
National Center for Biotechnology Information

All Resources

Tools

Amino Acid Explorer
This tool allows users to explore the characteristics of amino acids by comparing their structural and chemical properties, predicting protein sequence changes caused by mutations, viewing common substitutions, and browsing the functions of given residues in conserved domains.

BLAST Microbial Genomes
Performs a BLAST search for similar sequences from selected complete eukaryotic and prokaryotic genomes.

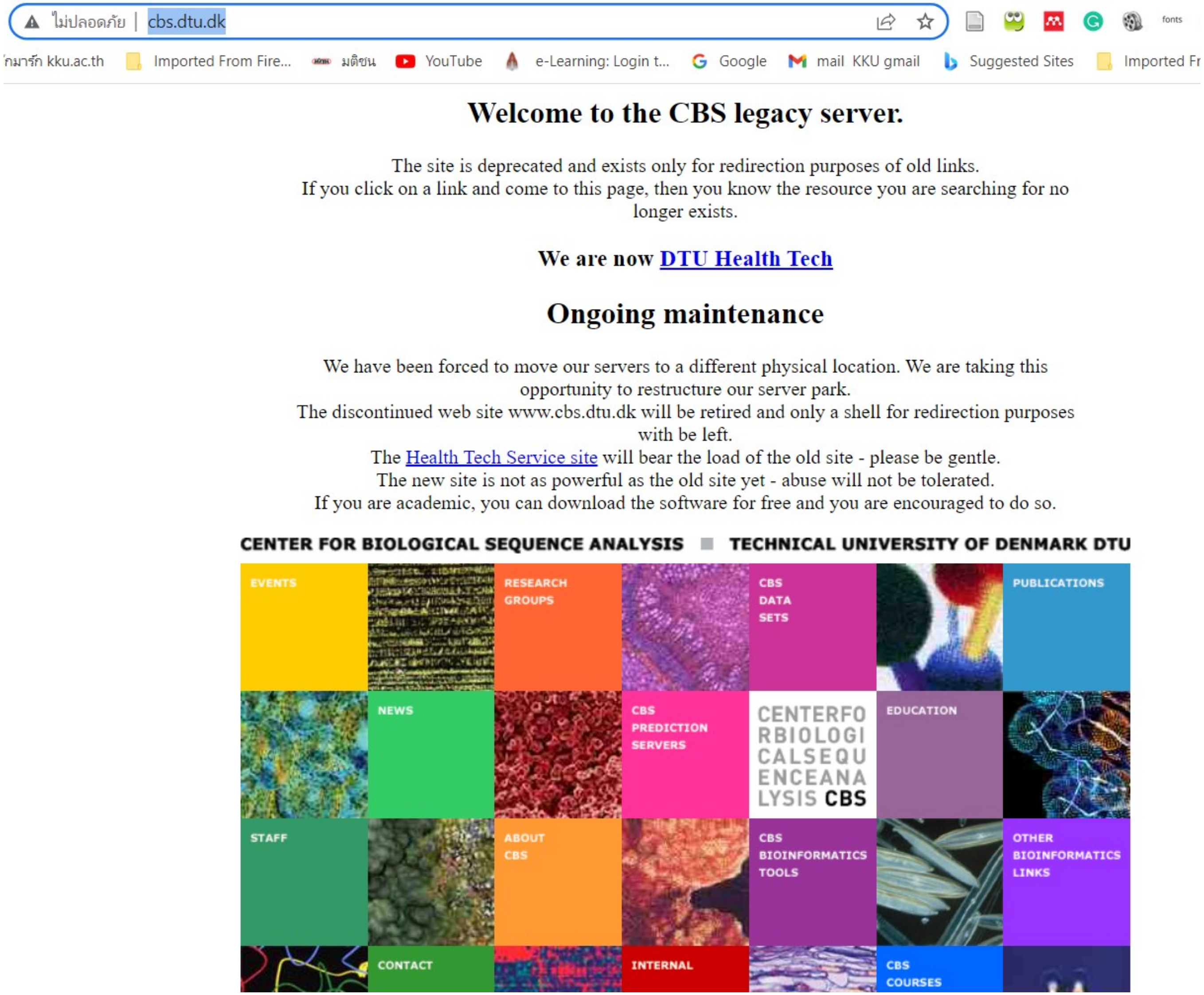
BLAST RefSeqGene
Performs a BLAST search of the genomic sequences in the RefSeqGene/LRG set. The default display provides ready navigation to review alignments in the Graphics display.

BLAST Tutorials and Guides
This page links to a number of BLAST-related tutorials and guides, including a selection guide for BLAST algorithms, descriptions of BLAST output formats, explanations of the parameters for stand-alone BLAST, directions for setting up stand-alone BLAST on local machines and using the BLAST URL API.

Basic Local Alignment Search Tool (BLAST)
Finds regions of local similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches. BLAST can be used to infer functional and evolutionary relationships between sequences as well as to help identify members of gene families.

Batch Entrez
Allows you to retrieve records from many Entrez databases by uploading a file of GI or accession numbers from the Nucleotide or Protein databases, or a file of unique identifiers from other Entrez databases. Search results can be saved in various formats directly to a local file on your computer.

http://www.cbs.dtu.dk/



Welcome to the CBS legacy server.

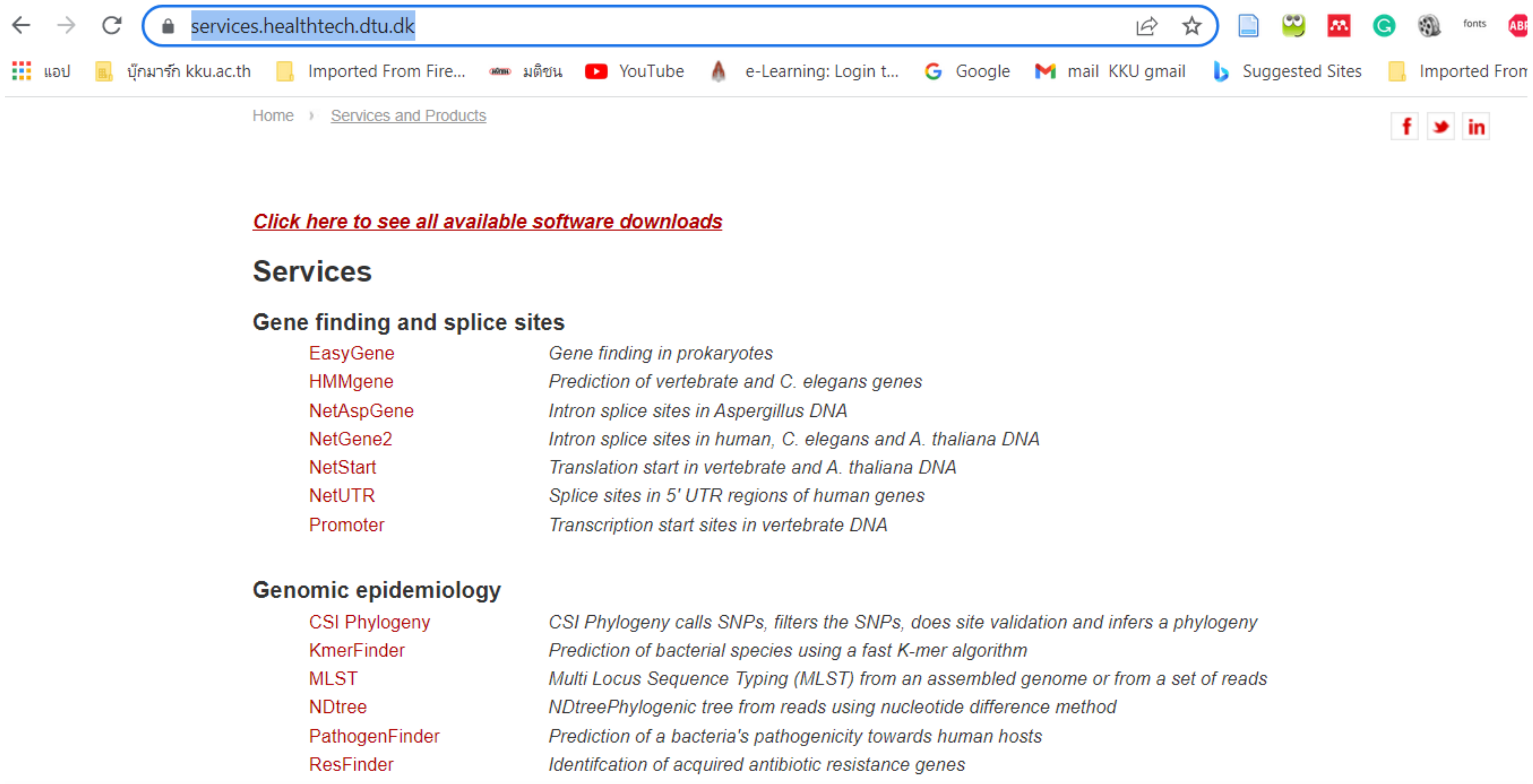
The site is deprecated and exists only for redirection purposes of old links.
If you click on a link and come to this page, then you know the resource you are searching for no longer exists.

We are now DTU Health Tech

Ongoing maintenance

We have been forced to move our servers to a different physical location. We are taking this opportunity to restructure our server park.
The discontinued web site www.cbs.dtu.dk will be retired and only a shell for redirection purposes with be left.
The Health Tech Service site will bear the load of the old site - please be gentle.
The new site is not as powerful as the old site yet - abuse will not be tolerated.
If you are academic, you can download the software for free and you are encouraged to do so.

https://services.healthtech.dtu.dk/



Home › Services and Products

Click here to see all available software downloads

Services

Gene finding and splice sites

EasyGene	*Gene finding in prokaryotes*
HMMgene	*Prediction of vertebrate and C. elegans genes*
NetAspGene	*Intron splice sites in Aspergillus DNA*
NetGene2	*Intron splice sites in human, C. elegans and A. thaliana DNA*
NetStart	*Translation start in vertebrate and A. thaliana DNA*
NetUTR	*Splice sites in 5' UTR regions of human genes*
Promoter	*Transcription start sites in vertebrate DNA*

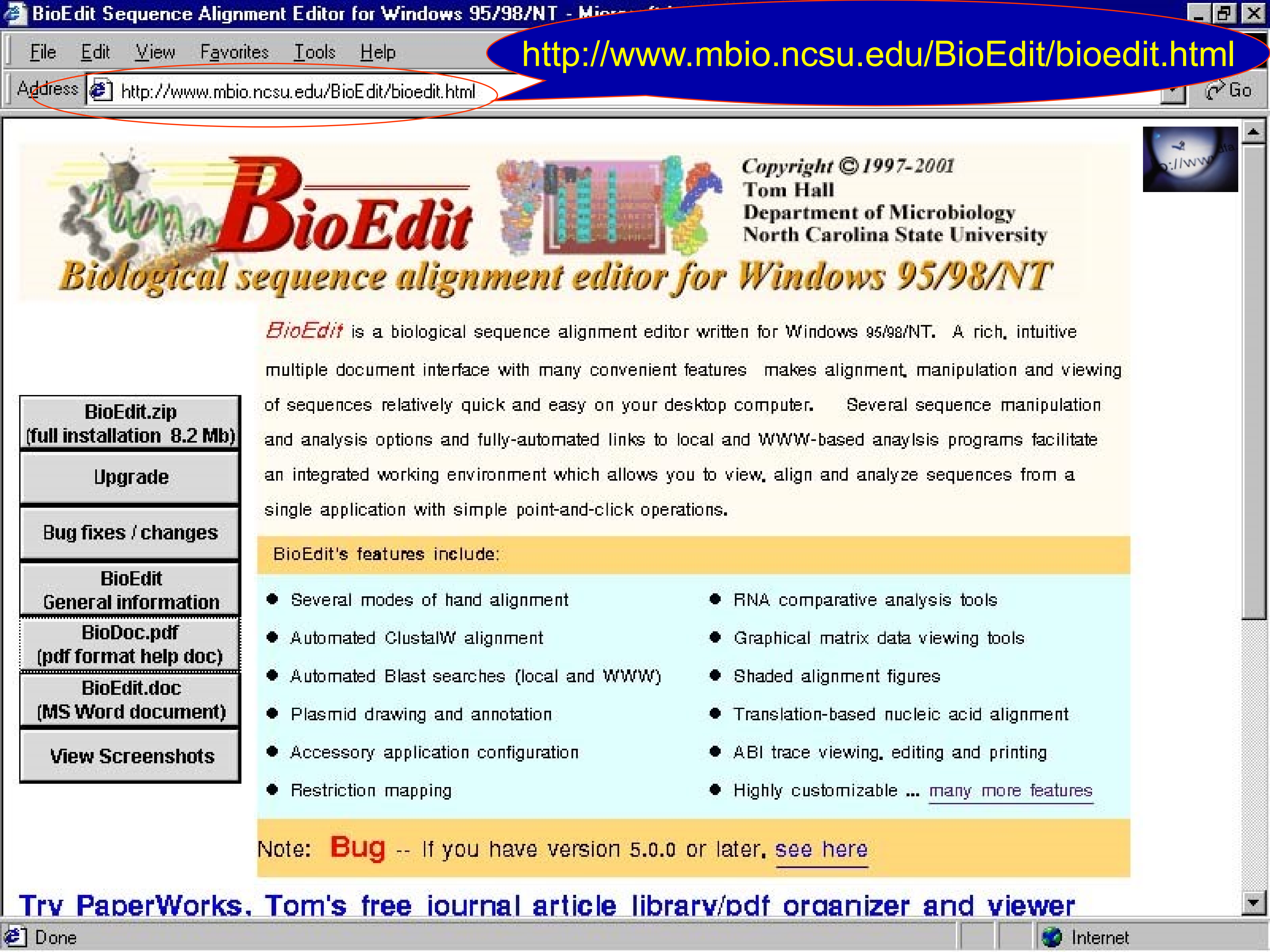
Genomic epidemiology

CSI Phylogeny	*CSI Phylogeny calls SNPs, filters the SNPs, does site validation and infers a phylogeny*
KmerFinder	*Prediction of bacterial species using a fast K-mer algorithm*
MLST	*Multi Locus Sequence Typing (MLST) from an assembled genome or from a set of reads*
NDtree	*NDtreePhylogenic tree from reads using nucleotide difference method*
PathogenFinder	*Prediction of a bacteria's pathogenicity towards human hosts*
ResFinder	*Identifcation of acquired antibiotic resistance genes*

What are common functions used in the bioinformatics-related software?

- DNA sequence
  - ✓ edit/search
  - ✓ translate
  - ✓ ORF search
  - ✓ Restricted endonuclease site search
  - ✓ plasmid drawing
  - ✓ alignment
- Protein's characteristics, enzymology
- PCR primer/ probe design
- etc.

http://www.mbio.ncsu.edu/BioEdit/bioedit.html



Copyright © 1997-2001
Tom Hall
Department of Microbiology
North Carolina State University

Biological sequence alignment editor for Windows 95/98/NT

BioEdit is a biological sequence alignment editor written for Windows 95/98/NT. A rich, intuitive multiple document interface with many convenient features makes alignment, manipulation and viewing of sequences relatively quick and easy on your desktop computer. Several sequence manipulation and analysis options and fully-automated links to local and WWW-based anaylsis programs facilitate an integrated working environment which allows you to view, align and analyze sequences from a single application with simple point-and-click operations.

BioEdit's features include:

- Several modes of hand alignment
- Automated ClustalW alignment
- Automated Blast searches (local and WWW)
- Plasmid drawing and annotation
- Accessory application configuration
- Restriction mapping
- RNA comparative analysis tools
- Graphical matrix data viewing tools
- Shaded alignment figures
- Translation-based nucleic acid alignment
- ABI trace viewing, editing and printing
- Highly customizable ... many more features

Note: **Bug** -- If you have version 5.0.0 or later, see here

Try PaperWorks, Tom's free journal article library/pdf organizer and viewer

http://www.mbio.ncsu.edu/BioEdit/bioedit.html

BioEdit

Biological sequence alignment editor for Win95/98/NT/2K/XP

Copyright © 1997-2005
Tom Hall
Ibis Therapeutics
Carlsbad, CA 92008

BioEdit is a biological sequence alignment editor written for Windows 95/98/NT/2000/XP. An intuitive multiple document interface with convenient features makes alignment and manipulation of sequences relatively easy on your desktop computer. Several sequence manipulation and analysis options and links to external anaylsis programs facilitate a working environment which allows you to view and manipulate sequences with simple point-and-click operations.

BioEdit's features include: ***New version is WinXP compatible***

- Several modes of hand alignment
- Automated ClustalW alignment
- Automated Blast searches (local and WWW)
- Plasmid drawing and annotation
- Accessory application configuration
- Restriction mapping
- RNA comparative analysis tools
- Graphical matrix data viewing tools
- Shaded alignment figures
- Translation-based nucleic acid alignment
- ABI trace viewing, editing and printing
- Customizable ... other features

Note: Although BioEdit was recently updated, it is no longer being reliably maintained, and the documentation is out of date and no longer maintained. It is being updated slowly, but there is no guaranteed finish date. Until documentation is complete, play with the menus and see what happens, or email with a question.

Note: If you have trouble launching BioEdit on Windows NT, try replacing BioEdit.exe with this version

Sequence/contig assembly:

BioEdit does not directly do assemblies of sequencing data.

Bioedit characteristics

- Tom Hall, North Carolina Stage University
- 12 Mb Freeware; *Current version 7.2.6.1 Last updated 3/2/2021*
- Biological sequence alignment editor
- Sequence editor
- Basic function about DNA, RNA, amino acid sequence analysis
- Links to bioinformatics tools homepage
- Open source

Features of Bioedit

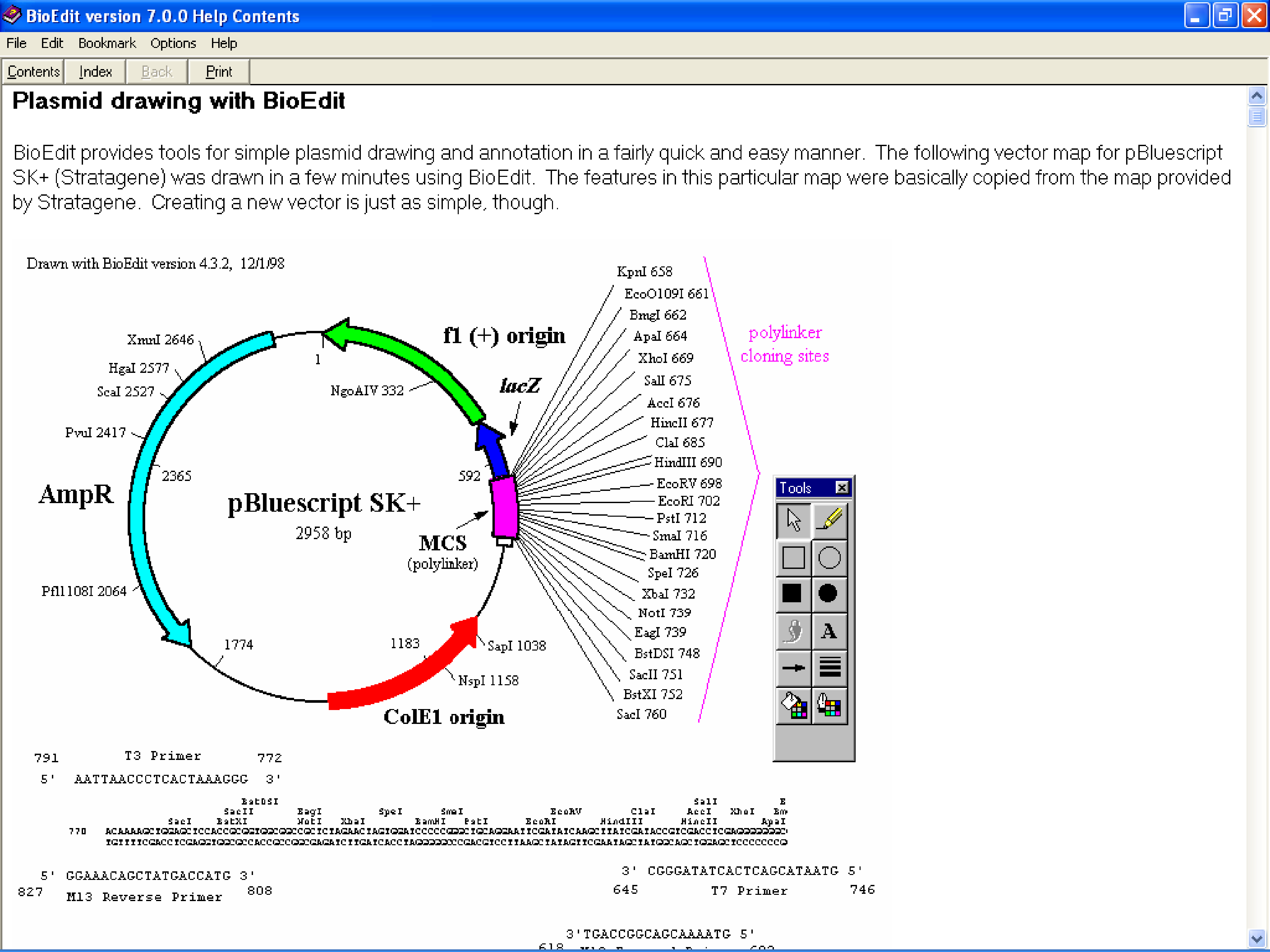
- Align >20,000 sequence
- Accept various sequence format
- Manual alignment mode
- Nice alignment result
- ClustalW and view phylogenic tree

Features about DNA

- Restriction enzymes mapping
- Nucleic acid composition
- complementary
- reverse complementary
- DNA-->RNA
- Translate
- Plasmid draw

Features about Protein

- Amino acid composition
- helical wheel diagram
- hydrophobicity



Plasmid drawing with BioEdit

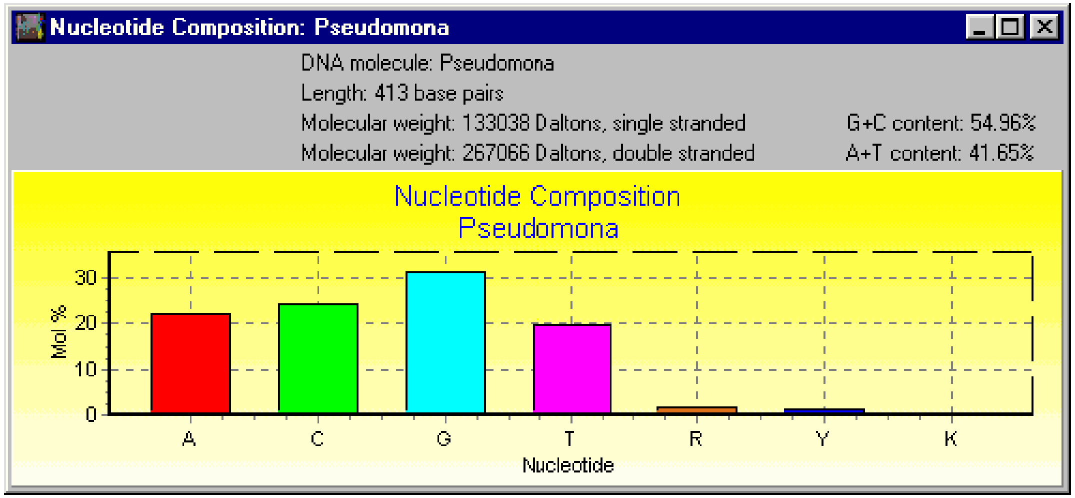
BioEdit provides tools for simple plasmid drawing and annotation in a fairly quick and easy manner. The following vector map for pBluescript SK+ (Stratagene) was drawn in a few minutes using BioEdit. The features in this particular map were basically copied from the map provided by Stratagene. Creating a new vector is just as simple, though.

Drawn with BioEdit version 4.3.2, 12/1/98

Amino Acid and Nucleotide Composition

Amino acid or nucleotide composition summaries and plots may be obtained by choosing "Amino Acid Composition" from the "Protein" submenu of the "Sequence" menu, or "Nucleotide Composition" form the "Nucleic Acid" submenu of the "Sequence" menu, respectively. Bar plots show the Molar percent of each residue in the sequence. For nucleic acids, degenerate nucleotide designations are added to the plot if and as they are encountered. For example, a sequence that has only A, G, C and T will have four bars on the graph, but if there are R's, Y's , M's, etc in the sequence, they will be added to the summary. For example, a nucleotide composition plot of the following sequence would look as follows

```
ATGAGCCAGGATTTTAGCCGTGAAAAACGTCTGCTGACCCCGCGTCATTTTAAAGCGGTGTTTGATAGCCCGACCGGC
AAAGTGCCGGGCAAAAACCTGCTGATTCTGGCGCGrTGAAAACGGCCTGGATCATCCGCGTCTGGGCCTGGTGyATTG
GCAAkAAAAAGCGTGAAACTGGCGGTGCrAGCGTAACCGTCTGAAACGTCTGATGCGTGATArGCTTTCGTCTrGAAC
CAGCAyGCTGCTGGyCGGGCCTGGATATTyGTGATTGTGGCGCGTAAAGGCCTGGGCGAAATTGAAAACCCGGAACTG
CArTCAGCATTTTGGCAAACTGTGGAAACGTCTGGCGCGTAGCCGTCCGyACCCCGGCGGTrGACCGCGAArCAGCGC
GGkGCGTGGATAGCCAGGATGCG
```



DNA molecule: Pseudomona
Length: 413 base pairs
Molecular weight: 133038 Daltons, single stranded
Molecular weight: 267066 Daltons, double stranded
G+C content: 54.96%
A+T content: 41.65%

Bar colors correspond to the residue colors specified in the color table.

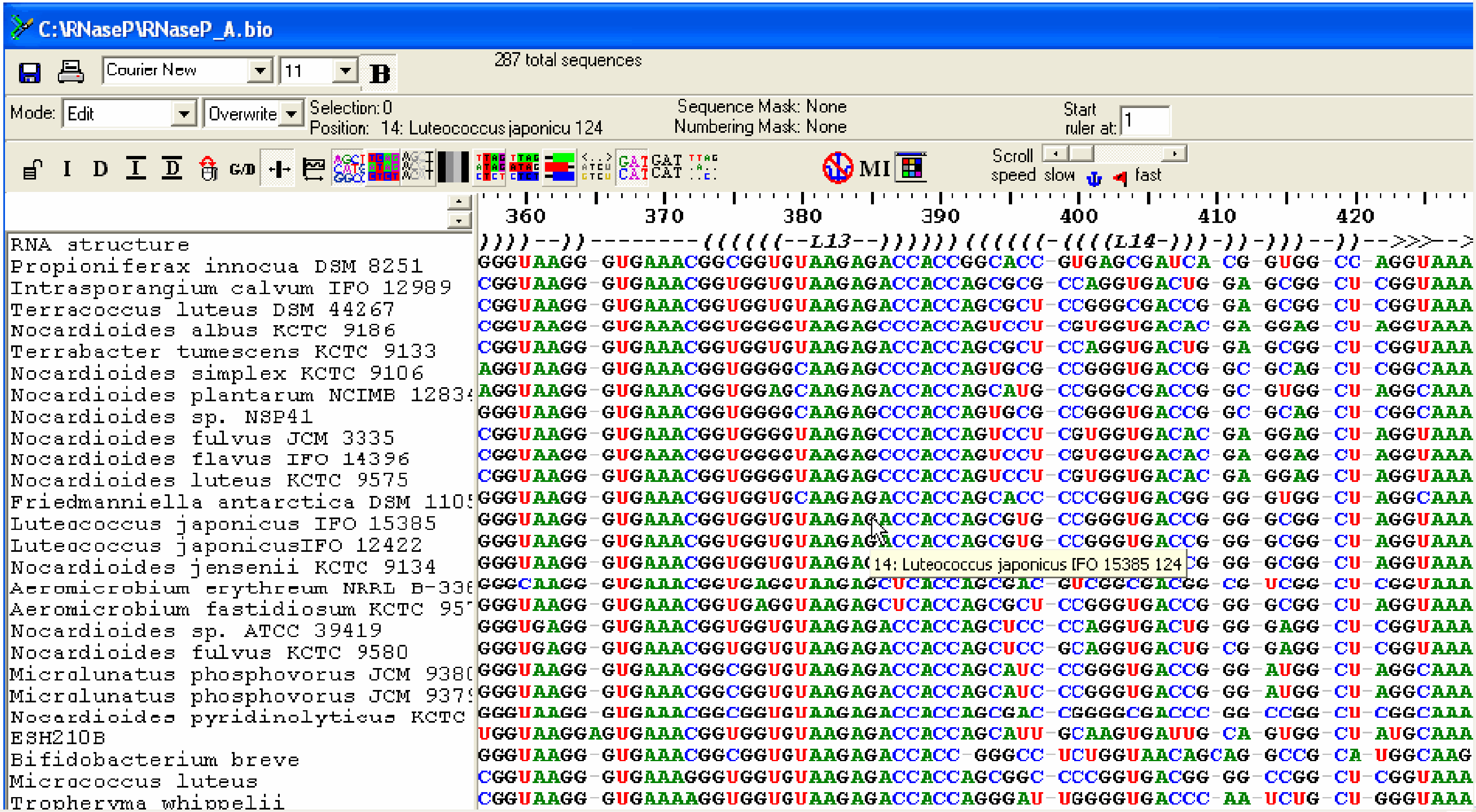
A corresponding summary is generated and displayed in the text editor:

```
DNA molecule: Pseudomona
0   Length = 413 base pairs
1   Molecular Weight = 133038 Daltons, single stranded
```

BioEdit version 7.0.0 Help Contents

Manual alignment of sequences (and button summaries)

Below is an image of the basic BioEdit alignment document window.
Don't worry if you don't like the current view. The font, size, background color, residues colors, and title window width may all be changed. The yellow box to the lower right of the mouse arrow shows the absolute position in the current sequence. This also appears in the "Position" caption on the control bar, and the option to shut off the yellow boxes is found under
View->show sequence position by mouse arrow.



287 total sequences

Mode: Edit   Overwrite
Selection: 0
Position: 14: Luteococcus japonicu 124
Sequence Mask: None
Numbering Mask: None

```
                                   360       370       380       390       400       410       420
RNA structure                      ))))--))--------((((((--L13--))))))((((((-((((L14-)))-))-)))--))-->>>-->
Propioniferax innocua DSM 8251     GGGUAAGG-GUGAAACGGCGGUGUAAGAGACCACCGGCACC-GUGAGCGAUCA-CG-GUGG-CC-AGGUAAA
Intrasporangium calvum IFO 12989   CGGUAAGG-GUGAAACGGUGGUGUAAGAGACCACCAGCGCG-CCAGGUGACUG-GA-GCGG-CU-CGGUAAA
Terracoccus luteus DSM 44267       CGGUAAGG-GUGAAACGGUGGUGUAAGAGACCACCAGCGCU-CCGGGCGACCG-GA-GCGG-CU-CGGUAAA
Nocardioides albus KCTC 9186       CGGUAAGG-GUGAAACGGUGGGGUAAGAGCCCACCAGUCCU-CGUGGUGACAC-GA-GGAG-CU-AGGUAAA
Terrabacter tumescens KCTC 9133    CGGUAAGG-GUGAAACGGUGGUGUAAGAGACCACCAGCGCU-CCAGGUGACUG-GA-GCGG-CU-CGGUAAA
Nocardioides simplex KCTC 9106     AGGUAAGG-GUGAAACGGUGGGGCAAGAGCCCACCAGUGCG-CCGGGUGACCG-GC-GCAG-CU-CGGCAAA
Nocardioides plantarum NCIMB 1283  AGGUAAGG-GUGAAACGGUGGAGCAAGAGACCACCAGCAUG-CCGGGCGACCG-GC-GUGG-CU-AGGCAAA
Nocardioides sp. NSP41             GGGUAAGG-GUGAAACGGUGGGGCAAGAGCCCACCAGUGCG-CCGGGUGACCG-GC-GCAG-CU-CGGCAAA
Nocardioides fulvus JCM 3335       CGGUAAGG-GUGAAACGGUGGGGUAAGAGCCCACCAGUCCU-CGUGGUGACAC-GA-GGAG-CU-AGGUAAA
Nocardioides flavus IFO 14396      CGGUAAGG-GUGAAACGGUGGGGUAAGAGCCCACCAGUCCU-CGUGGUGACAC-GA-GGAG-CU-AGGUAAA
Nocardioides luteus KCTC 9575      CGGUAAGG-GUGAAACGGUGGGGUAAGAGCCCACCAGUCCU-CGUGGUGACAC-GA-GGAG-CU-AGGUAAA
Friedmanniella antarctica DSM 110  GGGUAAGG-GUGAAACGGUGGUGCAAGAGACCACCAGCACC-CCCGGUGACGG-GG-GUGG-CU-AGGCAAA
Luteococcus japonicus IFO 15385    GGGUAAGG-GUGAAACGGUGGUGUAAGAGACCACCAGCGUG-CCGGGUGACCG-GG-GCGG-CU-AGGUAAA
Luteococcus japonicusIFO 12422     GGGUAAGG-GUGAAACGGUGGUGUAAGAGACCACCAGCGUG-CCGGGUGACCG-GG-GCGG-CU-AGGUAAA
Nocardioides jensenii KCTC 9134    GGGUAAGG-GUGAAACGGUGGUGUAAGA( 14: Luteococcus japonicus IFO 15385 124 )G-GG-GCGG-CU-AGGUAAA
Aeromicrobium erythreum NRRL B-33  GGGCAAGG-GUGAAACGGUGAGGUAAGAGCUCACCAGCGAC-GUCGGCGACGG-CG-UCGG-CU-CGGUAAA
Aeromicrobium fastidiosum KCTC 95  GGGUAAGG-GUGAAACGGUGAGGUAAGAGCUCACCAGCGCU-CCGGGUGACCG-GG-GCGG-CU-AGGUAAA
Nocardioides sp. ATCC 39419        GGGUGAGG-GUGAAACGGUGGUGUAAGAGACCACCAGCUCC-CCAGGUGACUG-GG-GAGG-CU-CGGUAAA
Nocardioides fulvus KCTC 9580      GGGUGAGG-GUGAAACGGUGGUGUAAGAGACCACCAGCUCC-GCAGGUGACUG-CG-GAGG-CU-CGGUAAA
Microlunatus phosphovorus JCM 938  GGGUAAGG-GUGAAACGGCGGUGUAAGAGACCACCAGCAUC-CCGGGUGACCG-GG-AUGG-CU-AGGCAAA
Microlunatus phosphovorus JCM 937  GGGUAAGG-GUGAAACGGCGGUGUAAGAGACCACCAGCAUC-CCGGGUGACCG-GG-AUGG-CU-AGGCAAA
Nocardioides pyridinolyticus KCTC  GGGUAAGG-GUGAAACGGCGGUGUAAGAGACCACCAGCGAC-CGGGGCGACCC-GG-CCGG-CU-CGGCAAA
ESH210B                            UGGUAAGGAGUGAAACGGUGGUGUAAGAGACCACCAGCAUU-GCAAGUGAUUG-CA-GUGG-CU-AUGCAAA
Bifidobacterium breve              GGGUAAGG-GUGAAACGGCGGUGUAAGAGACCACC-GGGCC-UCUGGUAACAGCAG-GCCG-CA-UGGCAAG
Micrococcus luteus                 CGGUAAGG-GUGAAAGGGUGGUGUAAGAGACCACCAGCGGC-CCCGGUGACGG-GG-CCGG-CU-CGGUAAA
Tropheryma whippelii               CGGUAAGG-GUGAAAAGGUGGUGUAAGAGACCACCAGGGAU-UGGGGUGACCC-AA-UCUG-CU-GGGUAAA
```

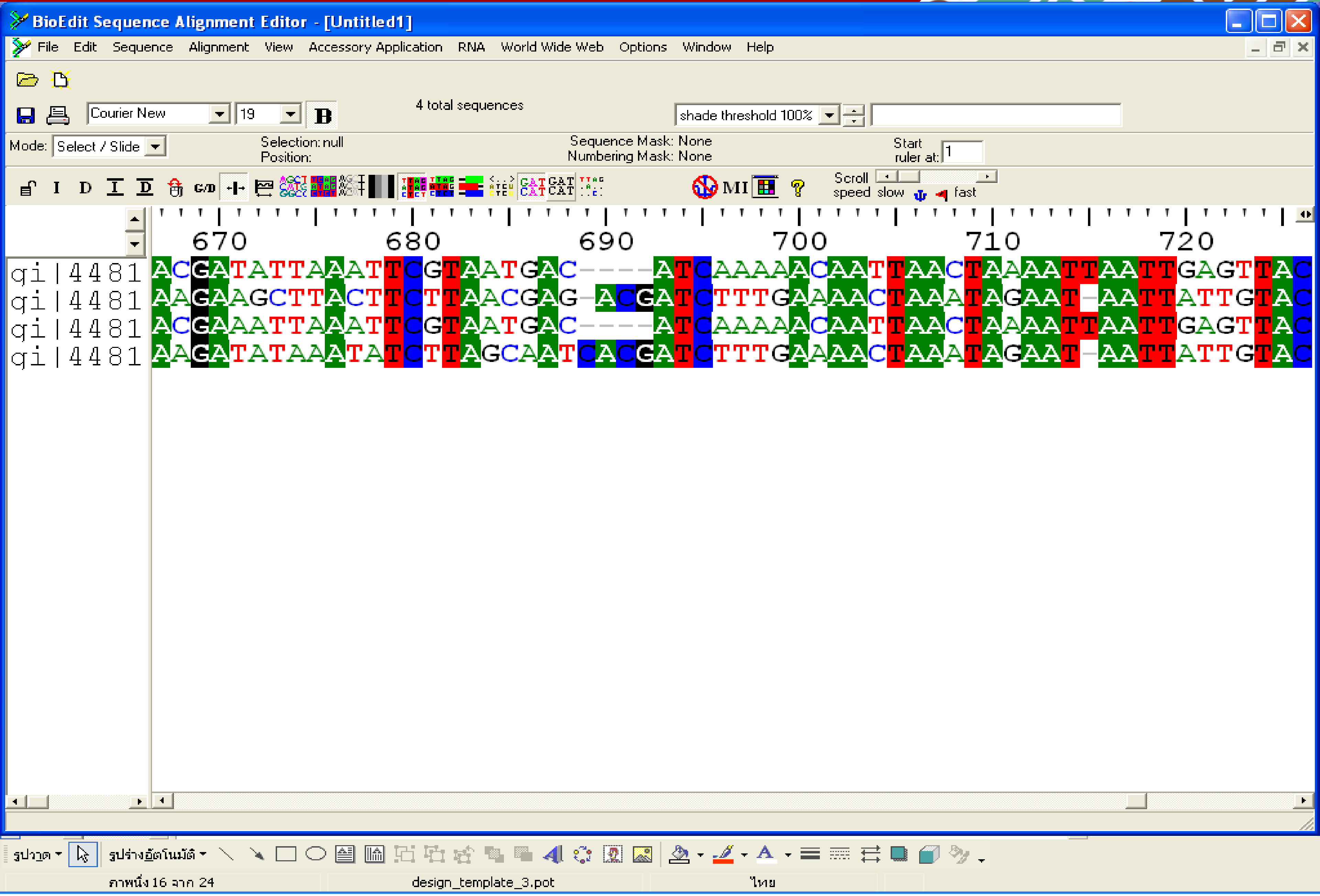
4 total sequences

Selection: 0
Position:

Sequence Mask: None
Numbering Mask: None

Start ruler at: 1

```
                 10        20        30        40        5
gi|44815|GATCACCTCCTTTCTATGGAGATATTTACATTACTGACTATTTAATTCTA
gi|44814|AGCTAAAACTAAAAAAATAACACCATTAGTTAAAGAGACTAATTTATTAA
gi|44813|GATCACCTCCTTTCTATGGAGATATTTATATTACTGACTATTTAATTCTA
gi|44812|TTTAAATAATAGTTAAACTTAAAAAGAAAATTGCTAGAATTAAATAATTA
```



Courier New 19 B

4 total sequences

shade threshold 100%

Mode: Select / Slide

Selection: null
Position:

Sequence Mask: None
Numbering Mask: None

Start ruler at: 1

```
            670       680       690       700       710       720
gi|4481 ACGATATTAAATTCGTAATGAC----ATCAAAAACAATTAACTAAAATTAATTGAGTTAC
gi|4481 AAGAAGCTTACTTCTTAACGAG-ACGATCTTTGAAAACTAAATAGAAT-AATTATTGTAC
gi|4481 ACGAAATTAAATTCGTAATGAC----ATCAAAAACAATTAACTAAAATTAATTGAGTTAC
gi|4481 AAGATATAAATATCTTAGCAATCACGATCTTTGAAAACTAAATAGAAT-AATTATTGTAC
```

ภาพนิ่ง 16 จาก 24 design_template_3.pot ไทย

รวม Hot Keys A-Z สำหรับ MS Office

*CTRL+ A = Select All เลือกทั้งหมด ★
*CTRL+ B = Bold ตัวหนา ★
*CTRL+ C = Copy คัดลอก
CTRL+ D = Font format กำหนดรูปแบบอักษร
CTRL+ E = Center ตรงกลาง
*CTRL+ F = Find ค้นหา ★
CTRL+ G = Goto ไปที่
CTRL+ H = Replace แทนที่
*CTRL+ I = Italic ตัวเอียง ★
CTRL+ J = Justify จัดชิดขอบ
CTRL+ K = Insert Hyper Link แทรกการเชื่อมโยงหลายมิติ
CTRL+ L = Left จัดชิดซ้าย
CTRL+ M = Indent เพิ่มระยะเยื้อง
CTRL+ N = New สร้างแฟ้มใหม่
CTRL+ O = Open เปิดแฟ้มใหม่
CTRL+ P = Print พิมพ์ ★
CTRL+ Q = Reset Paragraph ตั้งค่าย่อหน้าใหม่
CTRL+ R = Right จัดชิดขวา
*CTRL+ S = Save จัดเก็บ (บันทึก) ★
CTRL+ T = Tab (ตั้งระยะแท็บ)
*CTRL+ U = Underline ขีดเส้นใต้ ★
*CTRL+ V = Paste วาง ★
*CTRL+ W = Close ปิดแฟ้ม ★
*CTRL+ X = Cut ตัด ★
*CTRL+ Y = Redo or Repeat ทำซ้ำ ★
*CTRL+ Z = Undo ยกเลิกการกระทำครั้งล่าสุด ★