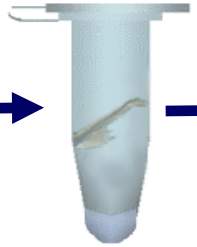
Секвенирование

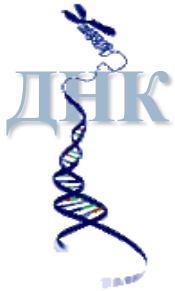
Прикладная генетика для зоологов, лекция 5

Мюге Н.С.

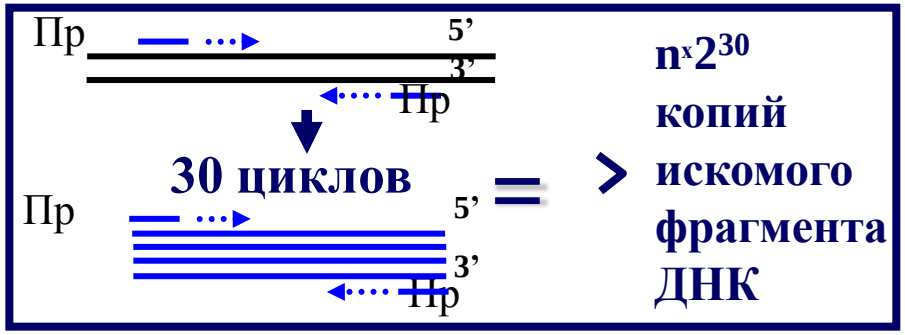
Общая схема изучения нуклеотидных последовательностей

1. Сбор материала



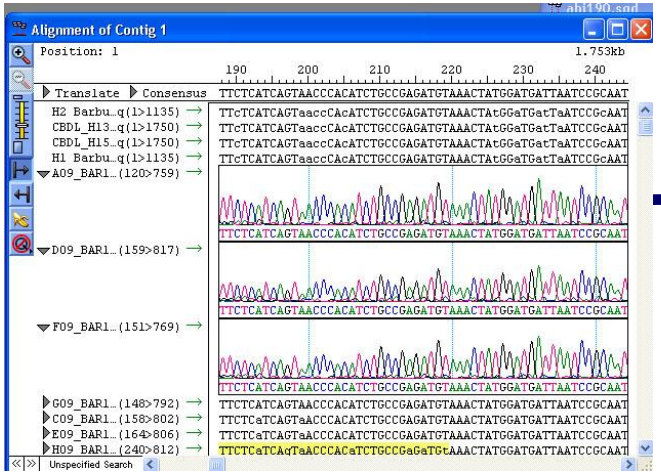


2. Выделение ДНК

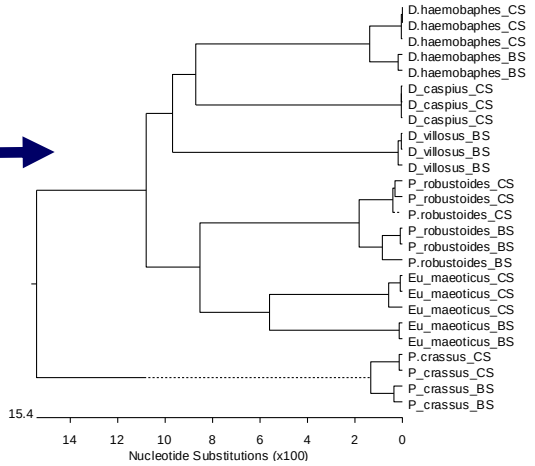


3. ПЦР-амплификация фрагмента мтДНК

4. Сиквенс пцр-фрагмента

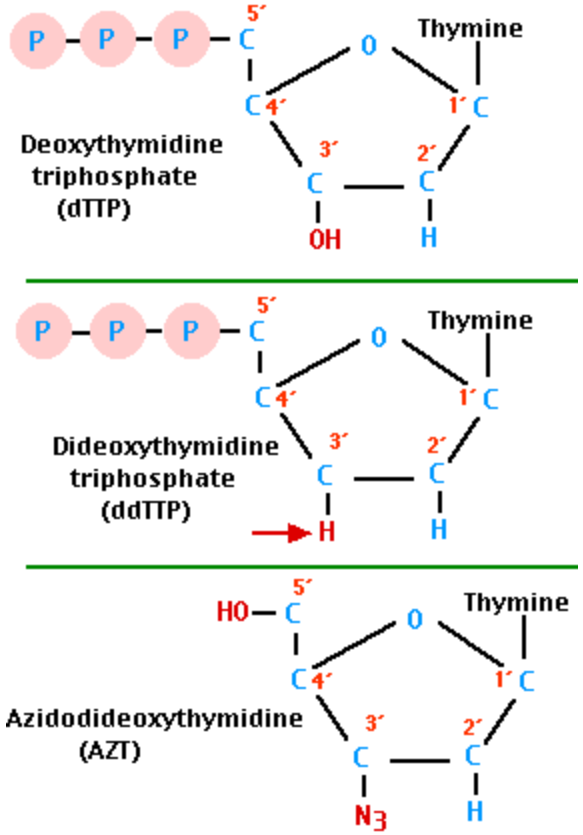


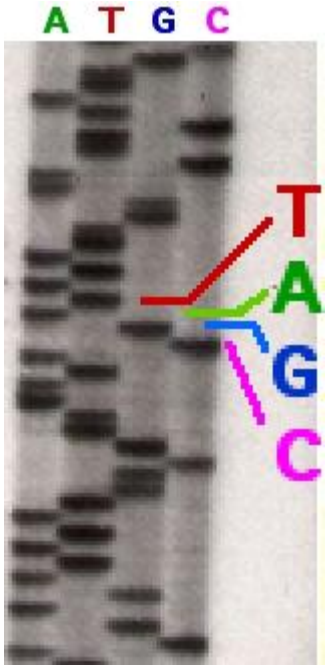
5. Стыковка и множественное выравнивание последовательностей



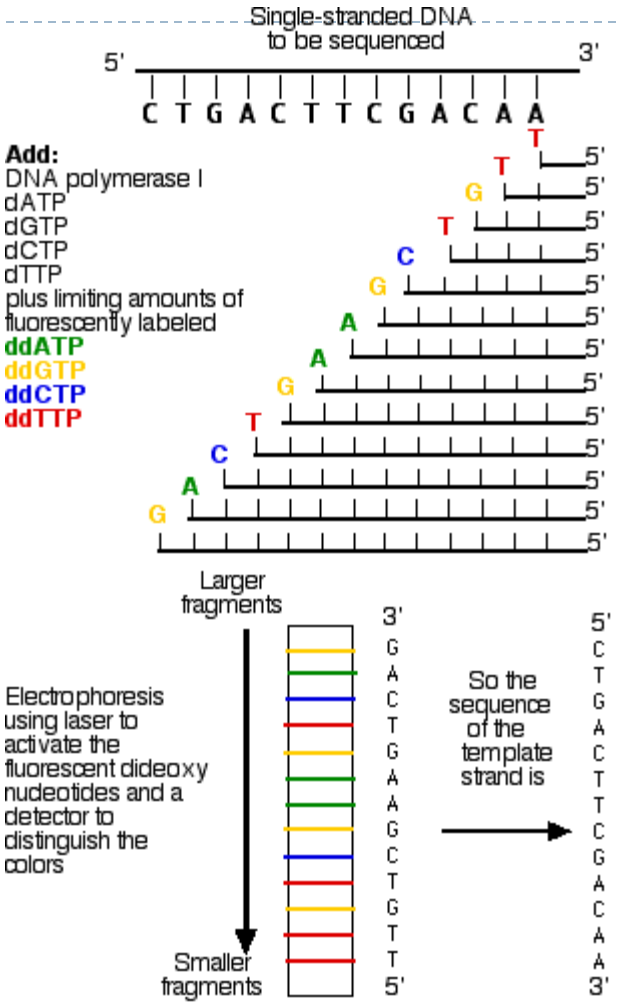
6. Филогенетическая реконструкция

Секвенирование по Сангеру (Sanger)

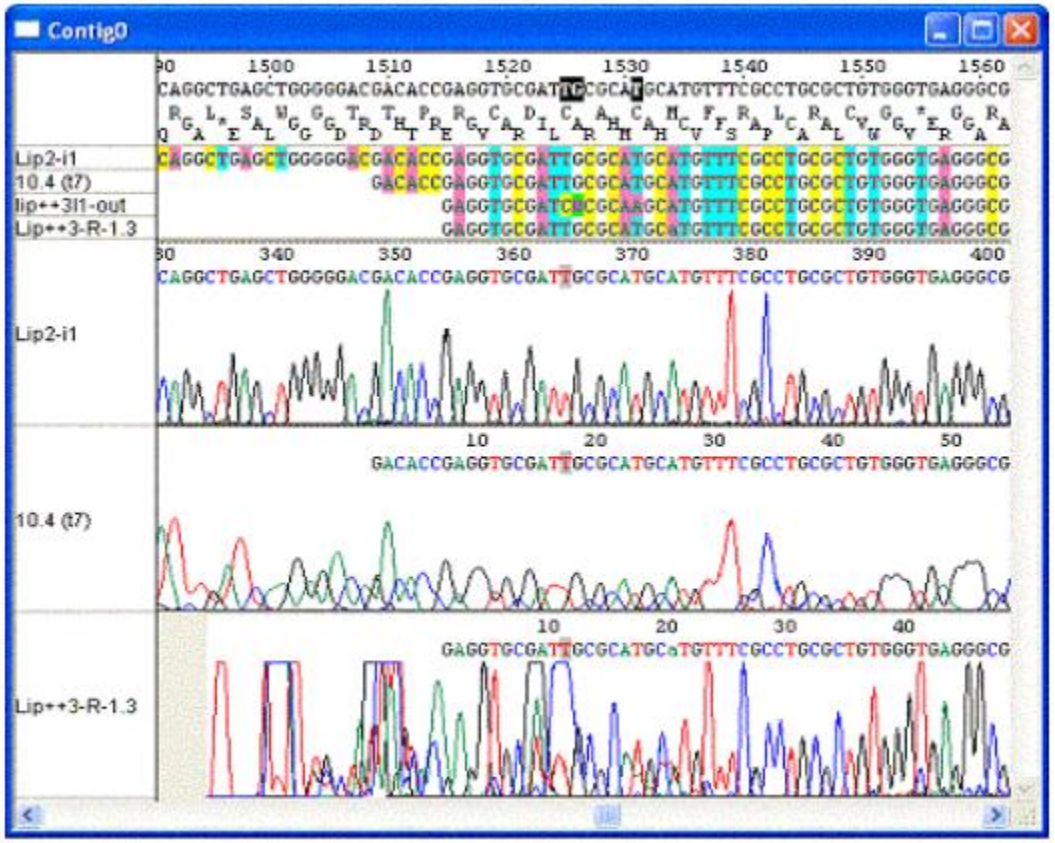




Секвенирование с флуоресцентными ddNTPs



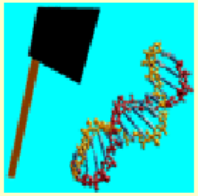
Программы для первичной обработки последовательностей Chromas и Chromas Pro.



Sequence assembly

http://www.technelysium.com.au/ChromasPro.html

proseq - Windows Internet Explorer
http://www.biology.ed.ac.uk/research/institutes/evolution/software/filatov/proseq.html
proseq | Phylogenetic programs - ... | Phylogeny Programs
Страница Сервис



Updated 6 / April / 2007

PROcessor of SEQuences (ProSeq)

(c) 1999 - 2007 by Dmitry Filatov,

ProSeq is a Windows program for sequence editing and population genetics (mol/evol) analysis.

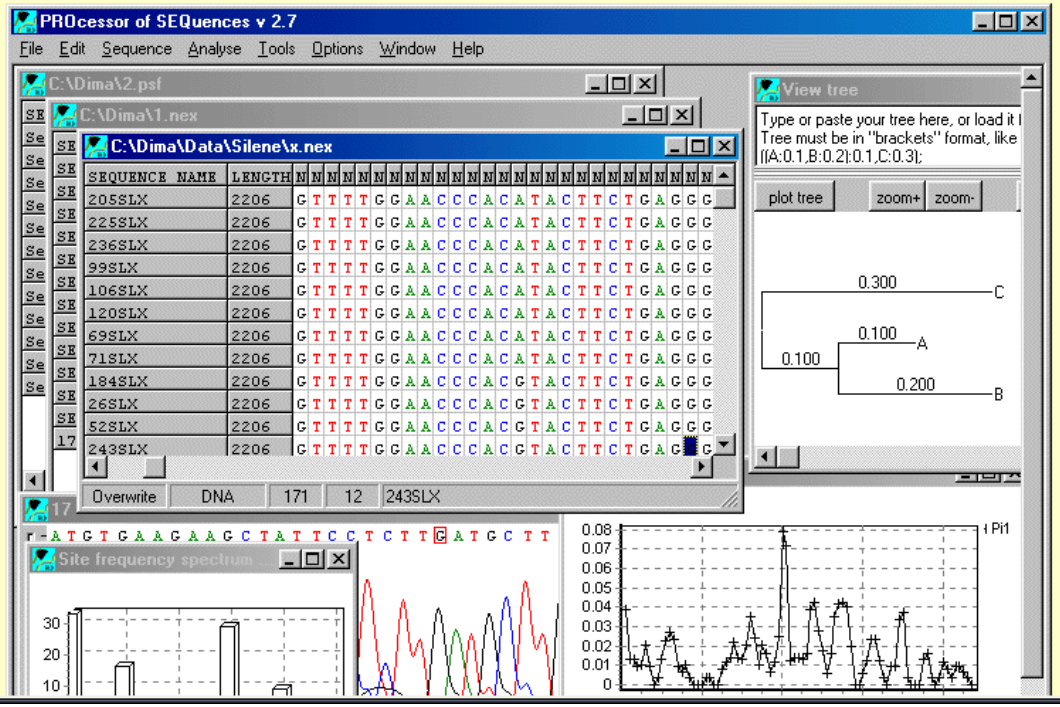
ProSeq is quite a convenient tool for sequence handling (correcting ABI chromatograms, contig assembly, hand correction of the alignments etc.) and preliminary molecular evolution analysis. However, it is recommended to check the results of the analyses by the other software since the program is under development and not all the parts of the program are thoroughly tested and completely reliable (please let me know if you found a problem!). The program have not been updated since 2002 because the new (v3) cross-platform (Windows / Linux) version is under development now. The currently distributed v2.9 is the final release of the 2.x versions. This Windows-only version will not be developed any further.

Citation:

Filatov D.A. 2002 ProSeq: A software for preparation and evolutionary analysis of DNA sequence data sets. Molecular Ecology Notes 2, 621-624

Download ProSeq2 as self extracting zip file (1.06 Mb) which includes ProSeq v 2.9, help and test files

Download new ProSeq3 (under development version) for Windows and for Linux



http://www.megasoftware.net/

MEGA - Molecular Evolutionary Genetics Analysis - Windows Internet Explorer

http://www.megasoftware.net/

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phylogenetic program - П... MEGA - Molecular Evol... Яндекс Страница Сервис

MEGA
Molecular Evolutionary Genetics Analysis

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Tamura K, Dudley J, Nei M & Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Molecular Biology and Evolution 24: 1596-1599.
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Kumar S, Tamura K & Nei M (2004) MEGA3: Integrated Software for Molecular Evolutionary Genetics Analysis and Sequence Alignment Briefings in Bioinformatics 5:150-163.
- Download PDF

MEGA update release date: February 27, 2008.

MEGA 4: Molecular Evolutionary Genetics Analysis

MEGA is an integrated tool for conducting automatic and manual sequence alignment, inferring phylogenetic trees, mining web-based databases, estimating rates of molecular evolution, and testing evolutionary hypotheses.

MEGA 4 has been tested on the following Microsoft Windows® operating systems:

Windows 95/98, NT, 2000, XP, and Vista.

New Features:

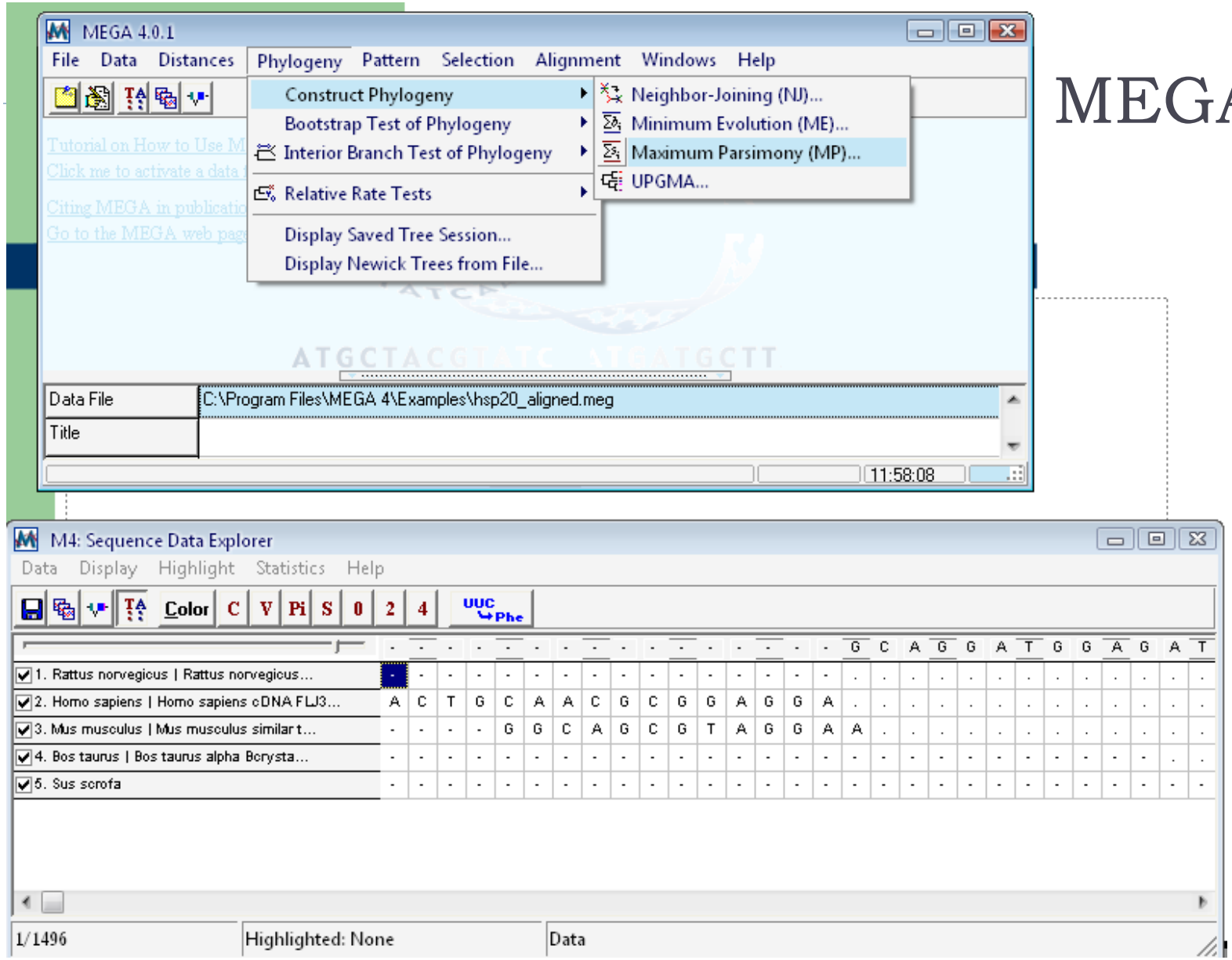
- Real-Time Caption Expert Engine
  A unique facility to generate detailed captions for different types of analyses and results. These captions are intended to provide detailed, natural language descriptions of the methods and models used in analysis. The facility aims to promote a better understanding of the underlying assumptions used in analysis, and also of the results generated.
- Maximum Composite Likelihood Method
  A method for estimating evolutionary distances between all pair of sequences simultaneously, with and without incorporating rate variation among sites and substitution

Готово Интернет 100%

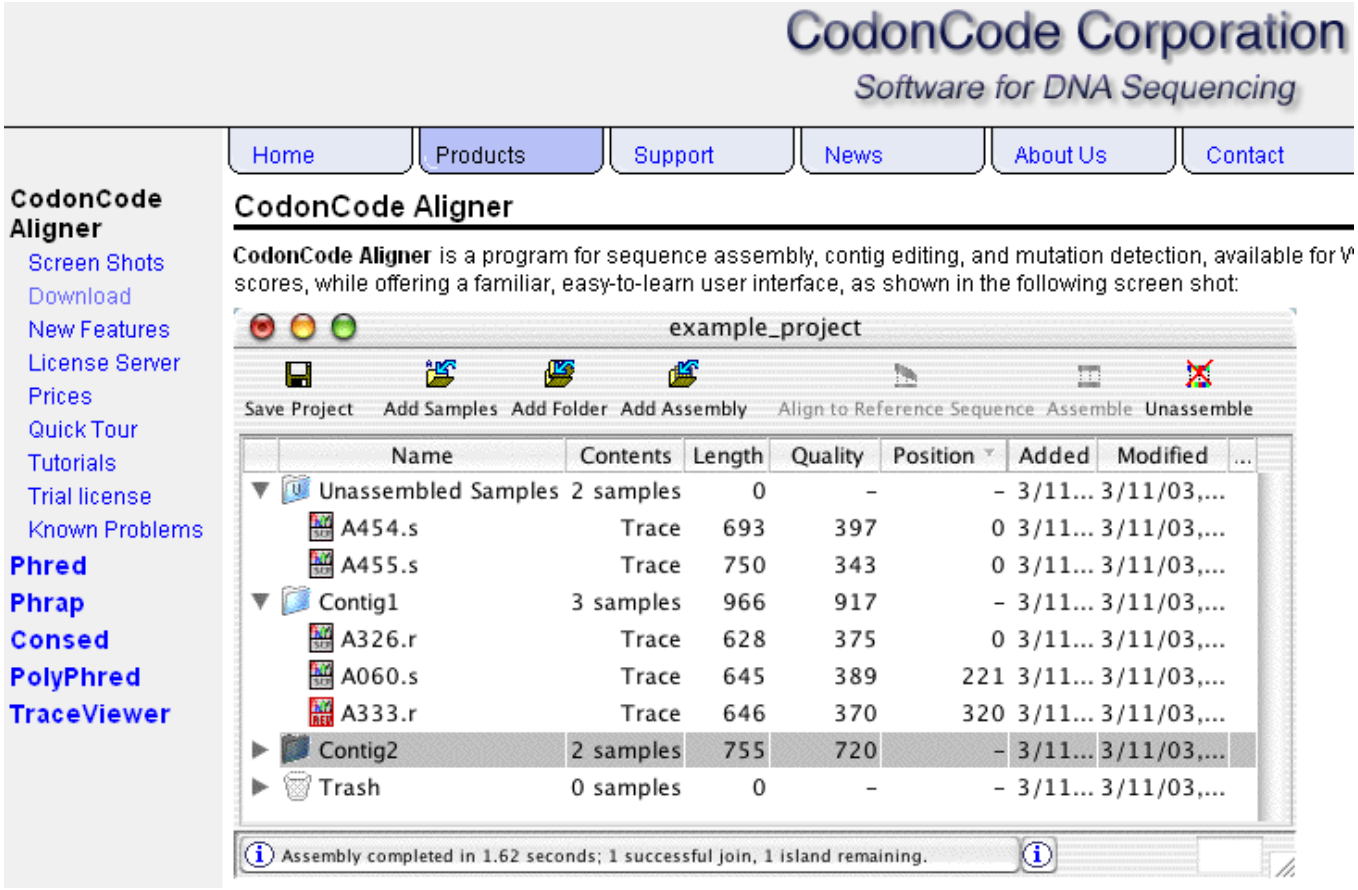
Слайд 19 из 22 Капсулы Русский (Россия)

D:\MK\... 2 Mic... 5 Inte... Adobe ... MegAlign Книга1 MEGA 4.0 11:59

MEGA4

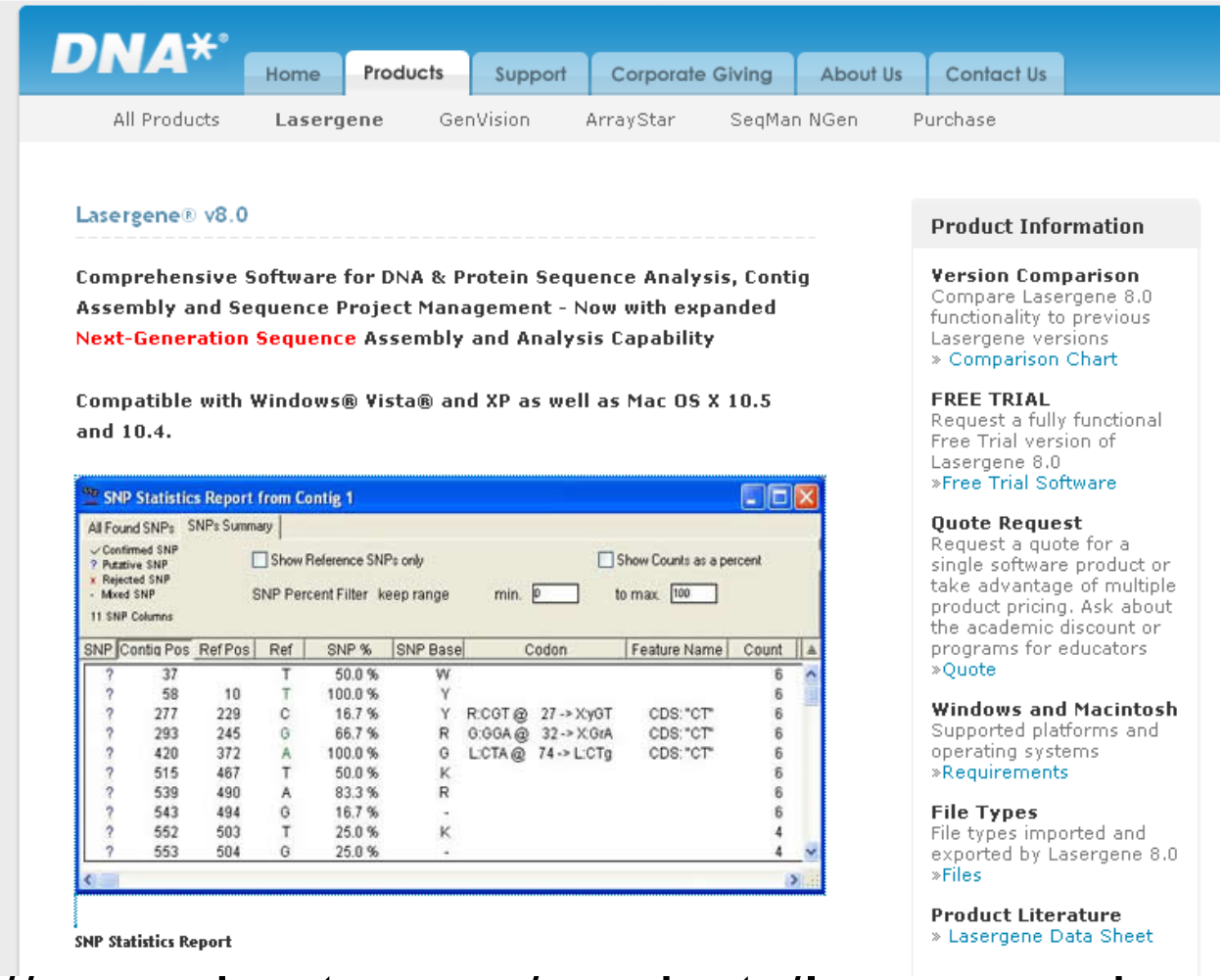

MEGA 4.0.1
File Data Distances Phylogeny Pattern Selection Alignment Windows Help
Construct Phylogeny
Bootstrap Test of Phylogeny
Interior Branch Test of Phylogeny
Relative Rate Tests
Display Saved Tree Session...
Display Newick Trees from File...
Neighbor-Joining (NJ)...
Minimum Evolution (ME)...
Maximum Parsimony (MP)...
UPGMA...
Data File
C:\Program Files\MEGA 4\Examples\hsp20_aligned.meg
Title
11:58:08
M4: Sequence Data Explorer
Data Display Highlight Statistics Help
Color C V Pi S 0 2 4
1. Rattus norvegicus | Rattus norvegicus...
2. Homo sapiens | Homo sapiens cDNA FLJ3...
3. Mus musculus | Mus musculus similar t...
4. Bos taurus | Bos taurus alpha Bcrysta...
5. Sus scrofa
1/1496
Highlighted: None
Data

Программы для первичной обработки последовательностей CodonCodeAligner.



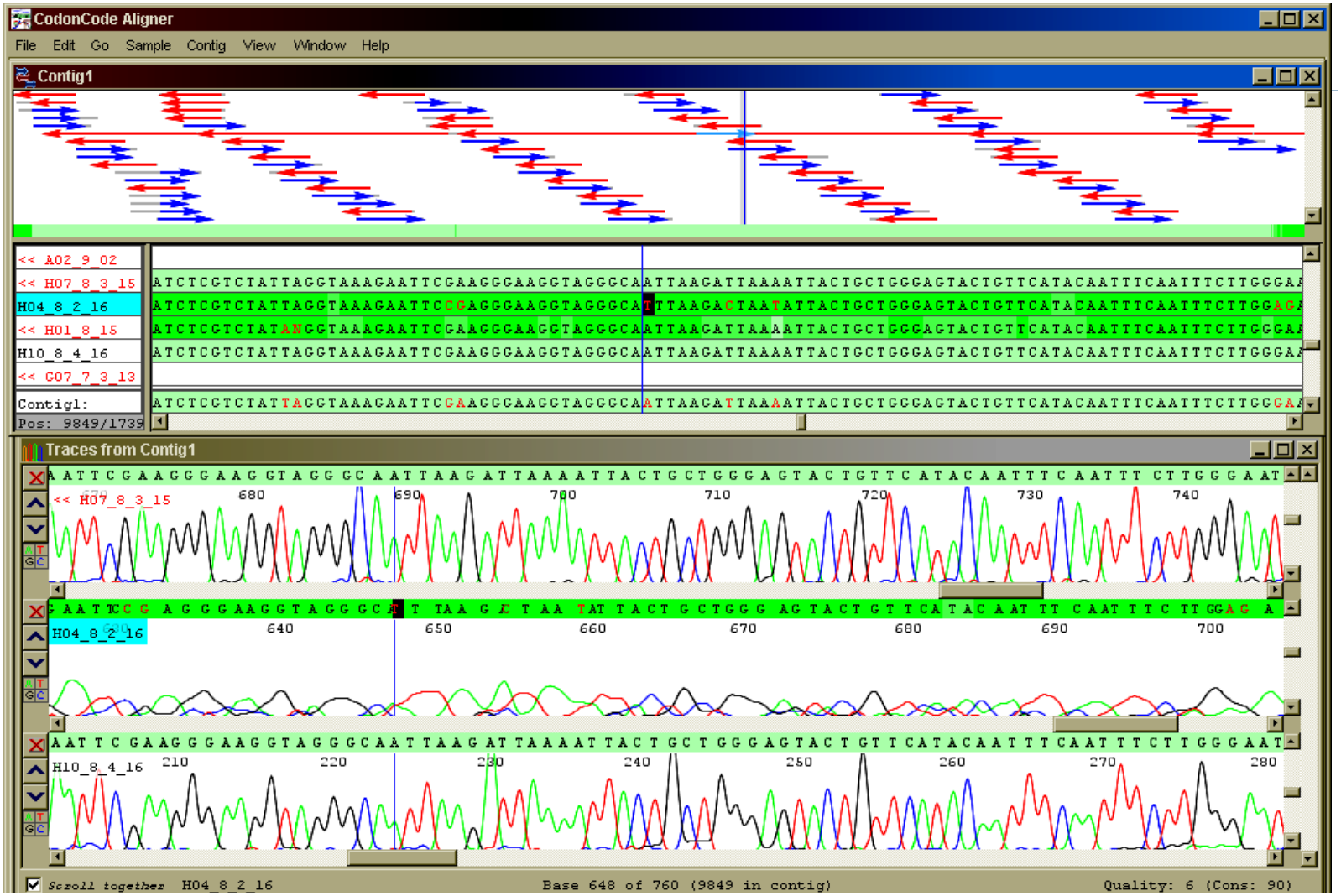
http://www.codoncode.com/aligner/

Программы для первичной обработки последовательностей LaserGene (DNASTAR)



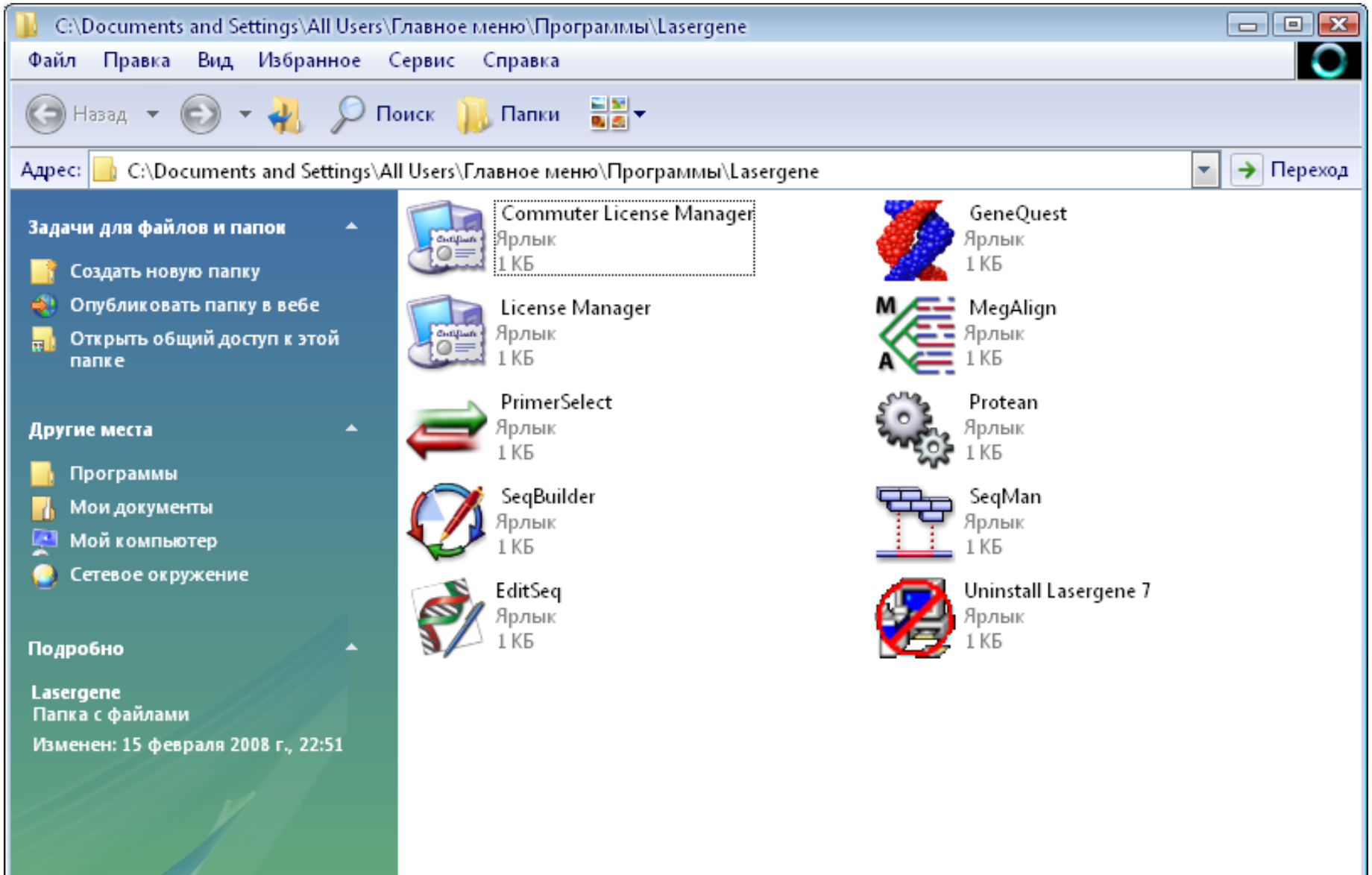
http://www.dnastar.com/products/lasergene.php

Программа Vector NTI



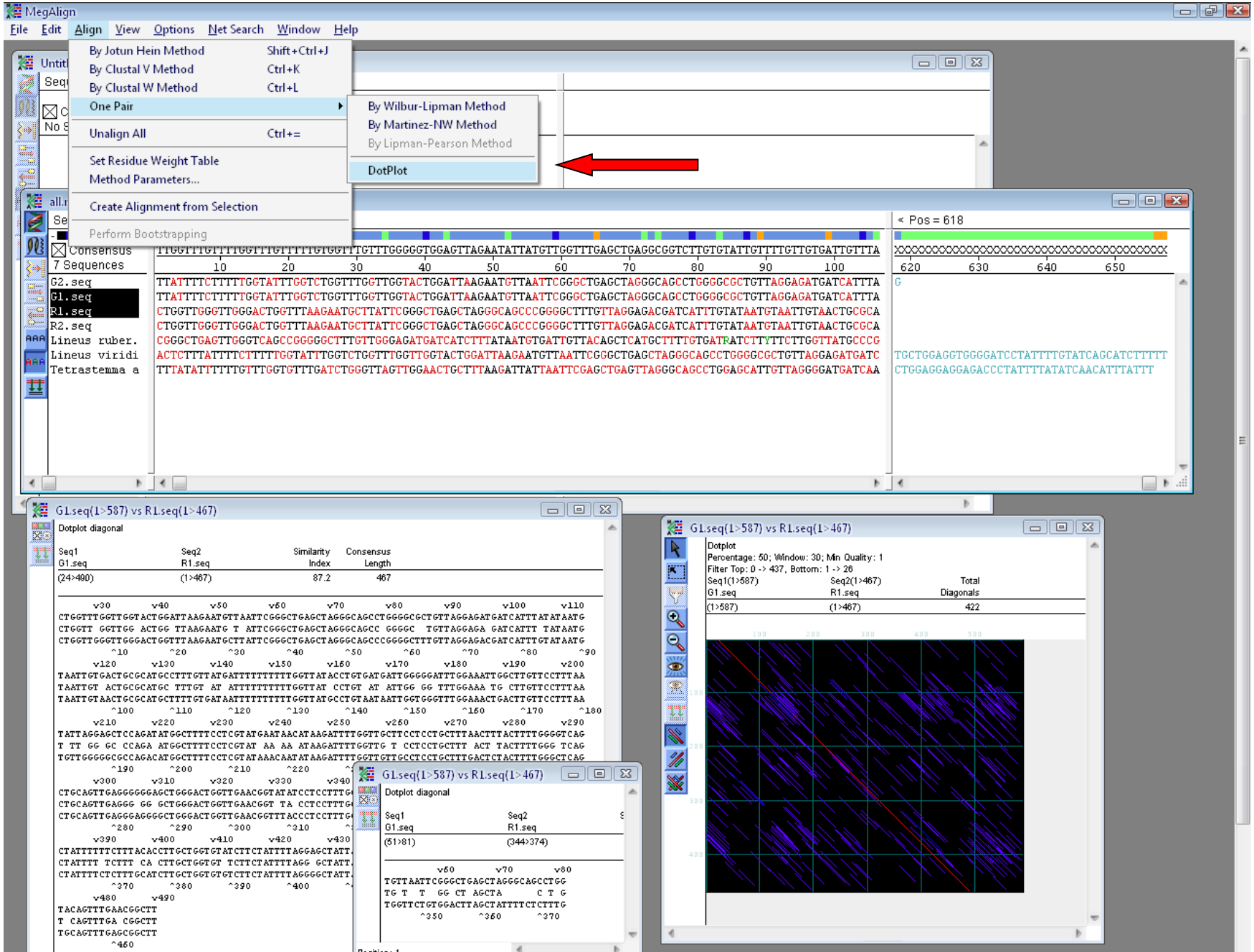
http://www.invitrogen.com/site/us/en/home/Applications/Cloning/Vector-Design-Software.html

Работа с LaserGene 7.0

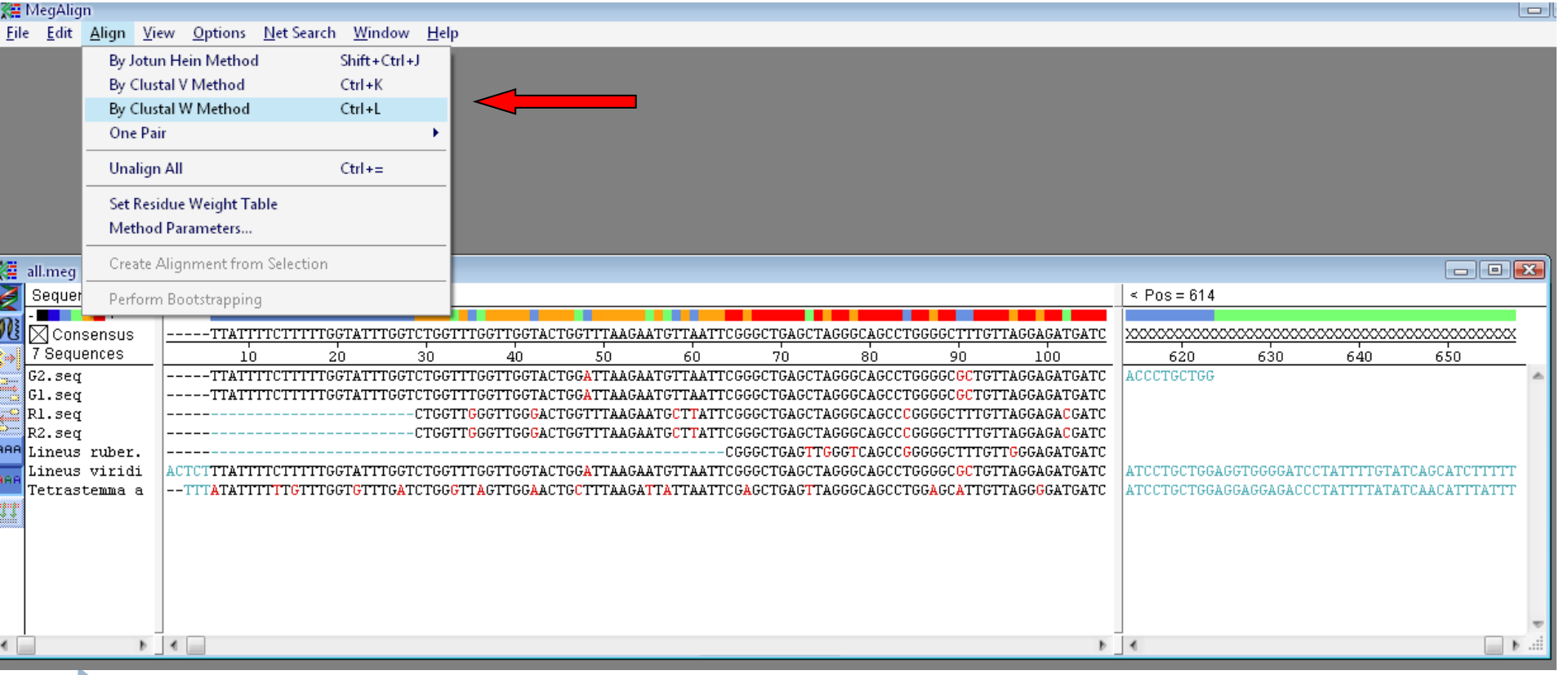


Множественное выравнивание последовательностей (программа MegAlign пакета LaserGene)

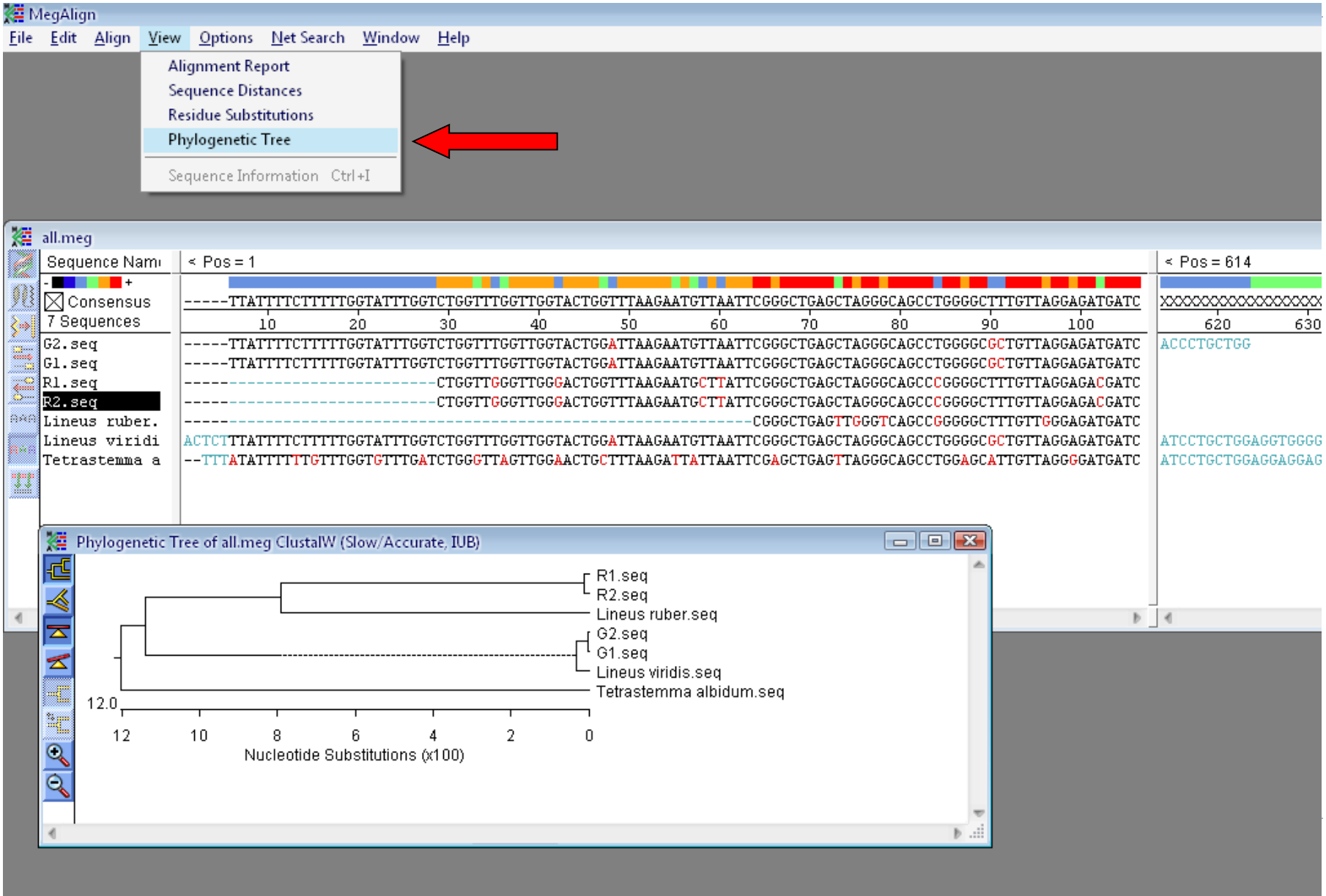
Выравнивание двух последовательностей - DotPlot



Множественное выравнивание-Clustal W



Простейшее дерево - NJ



Проверяем направление последовательностей!

Признаки «перевернутых последовательностей:

1. Большие расстояния между кластерами
2. Нелогичная группировка

Перевернуть: кликнуть на название сиквенса => поменять направление

Работа с генетическими базами данных

National Center for Biotechnology Information **GenBank** molecular sequence database	**http://www.ncbi.nlm.nih.gov**
The EMBL Nucleotide Sequence Database **(EMBL-Bank)**	**http://www.ebi.ac.uk/embl/**
DNA Data Bank of Japan (**DDBJ**)	**http://www.ddbj.nig.ac.jp/**
SwissProt (Swiss institute of bioinformatics)	**http://expasy.org/people/swissprot.html**

NCBI HomePage - Windows Internet Explorer

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

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National Library of Medicine National Institutes of Health

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Gene
Genome Project
dbGaP
GENSAT
GEO Profiles
GEO Datasets
HomoloGene
Journals
MeSH
NLM Catalog
OMIA
OMIM
PMC
PopSet
Probe

SITE MA
Alphabeti
Resource

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An introdu
NCBI

GenBan
Sequence
submissio
and softw

Literatur
databas
PubMed,
Books, ar
PubMed C

Molecula
databas
Sequence
structures
taxonomy

Genomi
biology
The human genome, whole genomes, and related resources

Tools
Data mining

Research at NCBI
People, projects, and seminars

Software

oes NCBI do?

ed in 1988 as a national resource for biology information, NCBI creates abases, conducts research in onal biology, develops software nalyzing genome data, and tes biomedical information - all for understanding of molecular s affecting human health and More...

nk® Celebrating 25 Years

hold a scientifc meeting to celebrate the 25th anniversary of GenBank.
April 7-8, 2008
uditorium, NIH Campus, Bethesda MD

click here for more information

dbGaP

aP Genome Wide Association Database

aP (database of Genotype and Phenotype) provides data from Genome Wide Association (GWA) studies. The resource is intended to help elucidate the link between genes and disease. For each study, users have access to detailed information about the phenotypic variables measured and pre-computed associations between subjects' phenotypes and genotypes. Click here to read the press release. To read more about GWA projects, see NCBI's GWA resource page

PubMed Central

An archive of biomedical and life sciences journals

- Free fulltext
- Over 1,100,000 articles from over 340 journals
- Linked to PubMed and fully searchable

Hot Spots

- Assembly Archive
- Clusters of orthologous groups
- Coffee Break, Genes & Disease, NCBI Handbook
- Electronic PCR
- Entrez Home
- Entrez Tools
- Gene expression omnibus (GEO)
- Human genome resources
- Influenza Virus Resource
- Map Viewer
- dbMHC
- Mouse genome resources
- My NCBI
- ORF finder
- Rat genome resources
- Reference

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National Library of Medicine National Institutes of Health

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An introduction to NCBI

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Sequence submission support and software

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PubMed, OMIM, Books, and PubMed Central

Molecular databases
Sequences, structures, and taxonomy

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The human genome, whole genomes, and related resources

Tools
Data mining

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People, projects, and seminars

Software

What does NCBI do?

Established in 1988 as a national resource for molecular biology information, NCBI creates public databases, conducts research in computational biology, develops software tools for analyzing genome data, and disseminates biomedical information - all for the better understanding of molecular processes affecting human health and disease. More...

GenBank® Celebrating 25 Years

NCBI will hold a scientifc meeting to celebrate the 25th anniversary of GenBank.
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Natcher Auditorium, NIH Campus, Bethesda MD

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New dbGaP

NCBI's dbGaP Genome Wide Association Database

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- Human genome resources
- Influenza Virus Resource
- Map Viewer
- dbMHC
- Mouse genome resources
- My NCBI
- ORF finder
- Rat genome resources
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http://www.ncbi.nlm.nih.gov

Entrez cross-database search - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/sites/gquery?term=Chlamys+islandica

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- Result counts displayed in gray indicate one or more terms not found

12	PubMed: biomedical literature citations and abstracts	none	Books: online books
none	PubMed Central: free, full text journal articles	none	OMIM: online Mendelian Inheritance in Man
none	Site Search: NCBI web and FTP sites	none	OMIA: online Mendelian Inheritance in Animals

10	CoreNucleotide: Core subset of nucleotide sequence records	none	dbGaP: genotype and phenotype
none	EST: Ex Go to CoreNucleotide Results Page	none	UniGene: gene-oriented clusters of transcript sequences
none	GSS: Genome Survey Sequence records	none	CDD: conserved protein domain database
5	Protein: sequence database	none	3D Domains: domains from Entrez Structure
none	Genome: whole genome sequences	none	UniSTS: markers and mapping data
none	Structure: three-dimensional macromolecular structures	none	PopSet: population study data sets
1	Taxonomy: organisms in GenBank	none	GEO Profiles: expression and molecular abundance profiles
none	SNP: single nucleotide polymorphism	none	GEO DataSets: experimental sets of GEO data
none	Gene: gene-centered information	none	Cancer Chromosomes: cytogenetic databases
none	HomoloGene: eukaryotic homology groups	none	PubChem BioAssay: bioactivity screens of chemical substances
none	GENSAT: gene expression atlas of mouse central nervous system	1	PubChem Compound: unique small molecule chemical structures
none	Probe: sequence-specific reagents	3	PubChem Substance: deposited chemical substance records
none	Genome Project: genome project information	none	Protein Clusters: a collection of related protein sequences

Chlamys islandica - CoreNucleotide Results - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/sites/entrez?db=nuccore&cmd=search&term=Chlamys%20islandica

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Found 10 nucleotide sequences. CoreNucleotide [10]

Display Summary Show 20 Sort by Send to

All: 10 Bacteria: 0 RefSeq: 0 mRNA: 1

Items 1 - 10 of 10 One page.

1: AM279651 Reports Links
Chlamys Islandica partial gst gene for glutathione transferase
gi|112292917|emb|AM279651.1|[112292917]

2: AJ304794 Reports Links
Chlamys islandica chlamysin gene for lysozyme, exons 1-4
gi|13444982|emb|AJ304794.1|[13444982]

3: BD293235 Reports Links
Chlamysin B antibacterial protein, a protein gene for and an expression system for same
gi|92140884|dbj|BD293235.1||pat|JP|2003504068|1[92140884]

4: AJ571605 Reports Links
Chlamys islandica partial mitochondrial 12S rRNA gene
gi|45433899|emb|AJ571605.1|[45433899]

5: AB102747 Reports Links
Chlamys islandica gene for ITS2, 28S rRNA, partial sequence, country:Japan: north Hokkaido (Soya strait)
gi|28375700|dbj|AB102747.1|[28375700]

6: AX074530 Reports Links
Sequence 3 from Patent WO0104328
gi|12710635|emb|AX074530.1||pat|WO|0104328|3[12710635]

7: AJ250028 Reports Links
Chlamys islandica mRNA for chlamysin
gi|6580356|emb|AJ250028.1|[6580356]

NCBI Sequence Viewer v2.0 - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nuccore&id=304466

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Range: from begin to end Reverse complemented strand Features: + Refresh

1: L11232. Reports Chlamys islandica...[gi:304466] Links

Features Sequence

```
LOCUS       CMSRR18S                1815 bp    DNA     linear   INV 05-APR-2000
DEFINITION  Chlamys islandica 18S ribosomal RNA gene, complete sequence.
ACCESSION   L11232
VERSION     L11232.1  GI:304466
KEYWORDS    .
SOURCE      Chlamys islandica
  ORGANISM  Chlamys islandica
            Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
            Pectinoidea; Pectinidae; Chlamys.
REFERENCE   1  (bases 1 to 1815)
  AUTHORS   Kenchington,E.L.R.I., Naidu,K.S., Roddick,D.L., Cook,D.I. and
            Zouros,E.
  TITLE     Use of biochemical genetic markers to discriminate between adductor
            muscle of the sea scallop (Placopecten magellanicus) and the
            Iceland scallop (Chlamys islandica)
  JOURNAL   Can. J. Fish. Aquat. Sci. 50 (6), 1222-1228 (1993)
FEATURES             Location/Qualifiers
     source          1..1815
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```

Taxonomy browser (Chlamys islandica) - Windows Internet Explorer
http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=27808
Файл Правка Вид Избранное Сервис Справка
Ссылки Google bioinf biosoft conferences friends e-shoping google info library news sturgeon travel Каспий cPanel Mail Management Gmail Horde
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NCBI Taxonomy Browser

Entrez | PubMed | Nucleotide | Protein | Genome | Structure | PMC | Taxonomy | Books

Search for [ ] as complete name ☑ lock Go Clear

Display 3 levels using filter: none

Chlamys islandica

Taxonomy ID: 27808
Rank: species
Genetic code: Translation table 1 (Standard)
Mitochondrial genetic code: Translation table 5 (Invertebrate Mitochondrial)

Lineage(full)
cellular organisms; Eukaryota; Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Protostomia; Mollusca; Bivalvia; Pteriomorphia; Pectinoida; Pectinoidea; Pectinidae; Chlamys

Entrez records

Database name	Direct links
Nucleotide	10
Nucleotide Core	10
Protein	5
PubMed Central	1
Taxonomy	1

External Information Resources (NCBI LinkOut)

LinkOut	Subject	LinkOut Provider
Chlamys islandica (Muller, 1776)	taxonomy/phylogenetic	AnimalBase
Pecten islandicus Muller, 1776	taxonomy/phylogenetic	
Chlamys islandica taxonomy	taxonomy/phylogenetic	Arctos Specimen Database
Chlamys islandica	taxonomy/phylogenetic	Global Biodiversity Information Facility
Chlamys islandica (Muller, 1776)	taxonomy/phylogenetic	
Chlamys islandica (Muller, 1776)	taxonomy/phylogenetic	Integrated Taxonomic Information System
Chlamys islandica	taxonomy/phylogenetic	Ocean Biogeographic Information System
Chlamys islandica	taxonomy/phylogenetic	TreeBase

Notes:
Groups interested in participating in the LinkOut program should visit the LinkOut home page.
A list of our current non-bibliographic LinkOut providers can be found here.
To see LinkOut links in this lineage click here

Disclaimer: The NCBI taxonomy database is not an authoritative source for nomenclature or classification - please consult the relevant scientific literature for the most reliable information.

Taxonomy browser (Pectinidae) - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Undef&id=6566&lvl=3&keep=1&srchmode=1&unlock

Nucleotide | Nucleotide Core | Nucleotide EST | Nucleotide GSS | Protein | Structure | Genome Sequences
Genome Projects | Popset | SNP | 3D Domains | Domains | GEO Datasets | GEO Profiles
UniGene | UniSTS | PubMed Central | Gene | HomoloGene | MapView | LinkOut
BLAST | TRACE | Taxonomy

Lineage (full): root; cellular organisms; Eukaryota; Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Protostomia; Mollusca; Bivalvia; Pteriomorphia; Pectinoida; Pectinoidea

- **Pectinidae** (scallops) *Click on organism name to get more information.*
  - **Adamussium**
    - **Adamussium colbecki** (Antarctic scallop)
  - **Aequipecten**
    - **Aequipecten opercularis**
  - **Amusium**
    - **Amusium japonicum**
    - **Amusium pleuronectes**
  - **Anguipecten**
    - **Anguipecten picturatus**
    - **Anguipecten superbus**
  - **Annachlamys**
    - **Annachlamys macassarensis**
  - **Argopecten**
    - **Argopecten gibbus**
    - **Argopecten irradians** (bay scallop)
      - **Argopecten irradians concentricus**
      - **Argopecten irradians irradians**
    - **Argopecten purpuratus**
    - **Argopecten ventricosus**
  - **Azumapecten**
    - **Azumapecten farreri** (Farrer's scallop)
  - **Chlamys**
    - **Chlamys albidus**
    - **Chlamys distorta**
    - **Chlamys farreri**
      - **Chlamys farreri nipponensis**
    - **Chlamys glabra**
    - **Chlamys hastata**
    - **Chlamys islandica**
    - **Chlamys multistriata**
    - **Chlamys nipponensis** (Japanese scallop)
      - **Chlamys nipponensis akazara** (akazara scallop)
    - **Chlamys rosealbus**
  - **Comtopallium**

NCBI Sequence Viewer v2.0 - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nuccore&id=304466

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Send to
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File
Clipboard

Range: from begin to end everse complemented strand Features: + Refresh

1: L11232. Reports Chlamys islandica...[gi:304466] Links

Features Sequence

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LOCUS       CMSRR18S                1815 bp    DNA     linear   INV 05-APR-2000
DEFINITION  Chlamys islandica 18S ribosomal RNA gene, complete sequence.
ACCESSION   L11232
VERSION     L11232.1  GI:304466
KEYWORDS    .
SOURCE      Chlamys islandica
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            Pectinoidea; Pectinidae; Chlamys.
REFERENCE   1  (bases 1 to 1815)
  AUTHORS   Kenchington,E.L.R.I., Naidu,K.S., Roddick,D.L., Cook,D.I. and
            Zouros,E.
  TITLE     Use of biochemical genetic markers to discriminate between adductor
            muscle of the sea scallop (Placopecten magellanicus) and the
            Iceland scallop (Chlamys islandica)
  JOURNAL   Can. J. Fish. Aquat. Sci. 50 (6), 1222-1228 (1993)
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NCBI Sequence Viewer v2.0 - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=nuccore&qty=1&c_start=1&list_uids=304466&uids=&dopt=gb&dispmax=5&sendto=&fmt_mask=0&from=

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Display GenBank Show 5 File Hide: sequence all but gene, CDS and mRNA features

Range: from begin to end Reverse complemented strand Features: + Refresh

1: L11232. Reports Chlamys islandica...[gi:304466] Links

Features Sequence

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LOCUS       CMSRR18S                 1815 bp    DNA
DEFINITION  Chlamys islandica 18S ribosomal RNA gene,
ACCESSION   L11232
VERSION     L11232.1  GI:304466
KEYWORDS    .
SOURCE      Chlamys islandica
  ORGANISM  Chlamys islandica
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REFERENCE   1  (bases 1 to 1815)
  AUTHORS   Kenchington,E.L.R.I., Naidu,K.S., Roddick
            Zouros,E.
  TITLE     Use of biochemical genetic markers to dis
            muscle of the sea scallop (Placopecten ma
            Iceland scallop (Chlamys islandica)
  JOURNAL   Can. J. Fish. Aquat. Sci. 50 (6), 1222-12
FEATURES             Location/Qualifiers
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Chlamys
18s
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Имя файла: Chlamys islandica 18S.seq Сохранить

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EditSeq

File Edit Search Speech Features Goodies Net Search Window Help

Chlamys islandica 18S.seq : SEQUENCE

Position: 1 1.815kb

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DEFINITION  Chlamys islandica 18S ribosomal RNA gene, complete sequence.
ACCESSION   L11232
VERSION     L11232.1  GI:304466
KEYWORDS    .
SOURCE      Chlamys islandica
  ORGANISM  Chlamys islandica
            Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
            Pectinoidea; Pectinidae; Chlamys.
REFERENCE   1  (bases 1 to 1815)
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/organism="Chlamys islandica"
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Unspecified Search

6 Про... 6 Micr... Adobe ... Adobe P... 2 Micr... 3 Inter... EditSeq 11:44

Nucleotide BLAST: Search nucleotide databases using a nucleotide query - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi?PAGE=Nucleotides&PROGRAM=blastn&MEGABLAST=on&BLAST_PROGRAMS=megaBlast&PAGE_TYPE=BlastSear

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Enter Query Sequence

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caacctggttgatcctgccagtagtcatatgcttgtctcaaagattaagccatgcatgtctaagtacatact
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```

Query subrange

From

To

Or, upload file Обзор...

Job Title

Enter a descriptive title for your BLAST search

Choose Search Set

Database: Human genomic + transcript | Mouse genomic + transcript | Others (nr etc.)

Nucleotide collection (nr/nt)

Organism Optional: Enter organism name or id--completions will be suggested

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

Entrez Query Optional

Enter an Entrez query to limit search

Program Selection

Optimize for:

- Highly similar sequences (megablast)
- More dissimilar sequences (discontiguous megablast)
- Somewhat similar sequences (blastn)

Choose a BLAST algorithm

BLAST — Search database nr using Megablast (Optimize for highly similar sequences)

Show results in a new window

Algorithm parameters

Note: Parameter values that differ from the default are highlighted in yellow

6 Про... 6 Micr... Adobe ... Adobe P... 2 Micr... 3 Inter... EditSeq 11:45

NCBI Blast:Nucleotide sequence (1815 letters) - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi

BLAST — Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastn/ Formatting Results - WZBVGRZG014 [Reformat these Results] [Edit and Resubmit] [Sign in above to save your search strategy]

Job Title: Nucleotide sequence (1815 letters)

BLASTN 2.2.18 (Mar-02-2008)

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RID: WZBVGRZG014


Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
           6,540,652 sequences; 23,108,864,737 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs
Taxonomy reports

Query=
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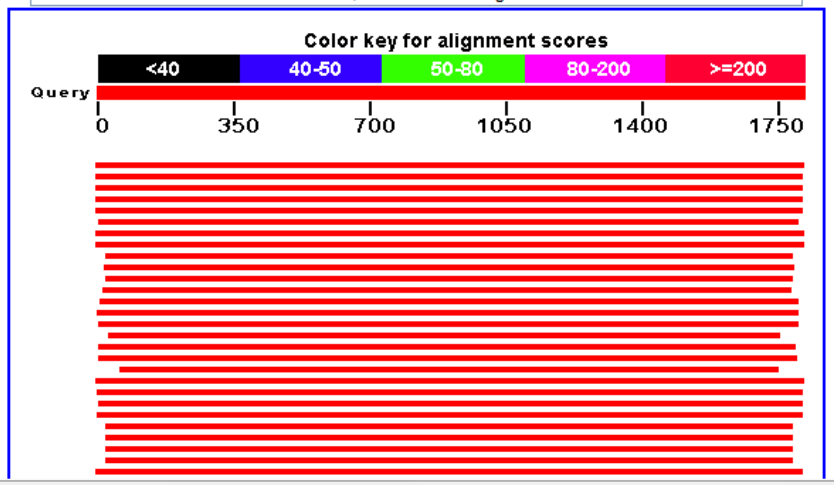
Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments



NCBI Blast:Nucleotide sequence (1815 letters) - Windows Internet Explorer
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NCBI Blast:Nucleotide sequence (1815 letters)
Страница Сервис

Distance tree of results NEW

Legend for links to other resources: U UniGene E GEO G Gene S Structure M Map Viewer

Sequences producing significant alignments:
(Click headers to sort columns)

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
L11232.1	Chlamys islandica 18S ribosomal RNA gene, complete sequence	3352	3352	100%	0.0	100%	
L49051.1	Mimachlamys varia 18S ribosomal RNA, complete sequence	3317	3317	99%	0.0	99%	
L49049.1	Chlamys hastata 18S ribosomal RNA, complete sequence	3315	3315	99%	0.0	99%	
L49050.1	Crassadoma gigantea 18S ribosomal RNA, complete sequence	3278	3278	99%	0.0	99%	
L49053.1	Pecten maximus 18S ribosomal RNA, complete sequence	3267	3267	99%	0.0	99%	
AJ389649.1	Pedum spondyloideum 18S rRNA gene	3251	3251	98%	0.0	99%	
L11265.1	Argopecten irradians 18S ribosomal RNA (18S rRNA) gene, complete sequence	3247	3247	100%	0.0	98%	
X53899.1	Placopecten magellanicus gene for 18S ribosomal RNA	3245	3245	100%	0.0	98%	
DQ279939.1	Mimachlamys varia 18S ribosomal RNA gene, partial sequence	3212	3212	97%	0.0	99%	
AJ242534.1	Adamussium colbecki 18S rRNA gene	3192	3192	97%	0.0	99%	
AY070112.1	Pecten jacobaeus 18S ribosomal RNA gene, partial sequence	3190	3190	97%	0.0	99%	
AF074389.1	Argopecten gibbus 18S ribosomal RNA gene, partial sequence	3181	3181	97%	0.0	99%	
AJ389648.1	Excellichlamys spectabilis 18S rRNA gene	3168	3168	98%	0.0	98%	
AF229629.1	Spondylus sinensis 18S ribosomal RNA gene, complete sequence	3120	3120	99%	0.0	97%	
AJ389647.1	Spondylus hystrix 18S rRNA gene	3094	3094	98%	0.0	97%	
AJ310482.1	Aequipecten opercularis 18S rRNA gene	3083	3083	94%	0.0	99%	
AJ389646.1	Spondylus crassisquamatus 18S rRNA gene	3038	3038	98%	0.0	97%	
AJ389636.1	Pinna muricata 18S rRNA gene	2935	2935	98%	0.0	96%	
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AF229626.1	Plicatula australis 18S ribosomal RNA gene, complete sequence	2843	2843	98%	0.0	95%	
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AF207647.1	Glycymeris insubrica 18S ribosomal RNA gene, complete sequence	2830	2830	97%	0.0	95%	

6 Про... 6 Micr... Adobe ... Adobe P... 2 Micr... 3 Inter... EditSeq 11:47

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http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi

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NCBI Blast:Nucleotide sequence (1815 letters) Страница Сервис

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Query  1681  GAGCTCCTCGGATTGGTCCCGACACGGGGGGCAACCCTCGAGTCGGTGTGCCGAAAAGAC  1740
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>gb|L49051.1|MIYRRE  Mimachlamys varia 18S ribosomal RNA, complete sequence
Length=1815

 Score = 3317 bits (1796),  Expect = 0.0
 Identities = 1806/1811 (99%), Gaps = 0/1811 (0%)
 Strand=Plus/Plus

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NCBI Sequence Viewer v2.0 - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?cmd=Retrieve&db=Nucleotide&list_uids=1479985&dopt=GenBank&WebEnv=00F1hrRgW6ImThiLpvUm8BD0Uo

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Search Nucleotide for Go Clear

Limits Preview/Index History Clipboard Details

Display GenBank Show 5 Send to Hide: sequence all but gene, CDS and mRNA features

Range: from begin to end Reverse complemented strand Features: + Refresh

1: L49051. Reports Mimachlamys varia...[gi:1479985] Links

Features Sequence

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VERSION     L49051.1  GI:1479985
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SOURCE      Mimachlamys varia
  ORGANISM  Mimachlamys varia
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REFERENCE   1  (bases 1 to 1815)
  AUTHORS   Frischer,M., Williams,J. and Kenchington,E.
  TITLE     A molecular phylogeny of some major groups of Pectinidae inferred
            from 18S rRNA gene sequences
  JOURNAL   (in) Johnston,P.A. and Haggart,J.W. (Eds.);
            BIVALVES: AN EON OF EVOLUTION - PALEOBIOLOGICAL STUDIES HONORING
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NCBI Blast:Nucleotide sequence (1815 letters) - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi

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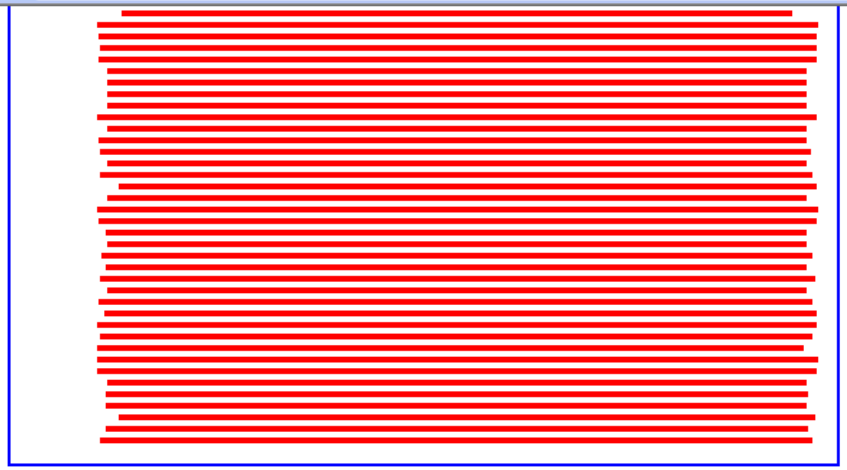
NCBI Blast:Nucleotide sequence (1815 letters) Страница Сервис



Distance tree of results NEW

Legend for links to other resources: U UniGene E GEO G Gene S Structure M Map Viewer

Sequences producing significant alignments:
(Click headers to sort columns)

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
L11232.1	Chlamys islandica 18S ribosomal RNA gene, complete sequence	3352	3352	100%	0.0	100%	
L49051.1	Mimachlamys varia 18S ribosomal RNA, complete sequence	3317	3317	99%	0.0	99%	
L49049.1	Chlamys hastata 18S ribosomal RNA, complete sequence	3315	3315	99%	0.0	99%	
L49050.1	Crassadoma gigantea 18S ribosomal RNA, complete sequence	3278	3278	99%	0.0	99%	
L49053.1	Pecten maximus 18S ribosomal RNA, complete sequence	3267	3267	99%	0.0	99%	
AJ389649.1	Pedum spondyloideum 18S rRNA gene	3251	3251	98%	0.0	99%	
L11265.1	Argopecten irradians 18S ribosomal RNA (18S rRNA) gene, complete sequence	3247	3247	100%	0.0	98%	
X53899.1	Placopecten magellanicus gene for 18S ribosomal RNA	3245	3245	100%	0.0	98%	
DQ279939.1	Mimachlamys varia 18S ribosomal RNA gene, partial sequence	3212	3212	97%	0.0	99%	
AJ242534.1	Adamussium colbecki 18S rRNA gene	3192	3192	97%	0.0	99%	
AY070112.1	Pecten jacobaeus 18S ribosomal RNA gene, partial sequence	3190	3190	97%	0.0	99%	
AF074389.1	Argopecten gibbus 18S ribosomal RNA gene, partial sequence	3181	3181	97%	0.0	99%	
AJ389648.1	Excellichlamys spectabilis 18S rRNA gene	3168	3168	98%	0.0	98%	
AF229629.1	Spondylus sinensis 18S ribosomal RNA gene, complete sequence	3120	3120	99%	0.0	97%	
AJ389647.1	Spondylus hystrix 18S rRNA gene	3094	3094	98%	0.0	97%	
AJ310482.1	Aequipecten opercularis 18S rRNA gene	3083	3083	94%	0.0	99%	
AJ389646.1	Spondylus crassisquamatus 18S rRNA gene	3038	3038	98%	0.0	97%	

Blast Tree View Widget - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/blast/treeview/blast_tree_view.cgi?request=page&rid=WZBVGRZG014&queryID=lcl|10446&distmode=on

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NCBI Blast:Nucleotide seq... Blast Tree View Widget Страница Сервис

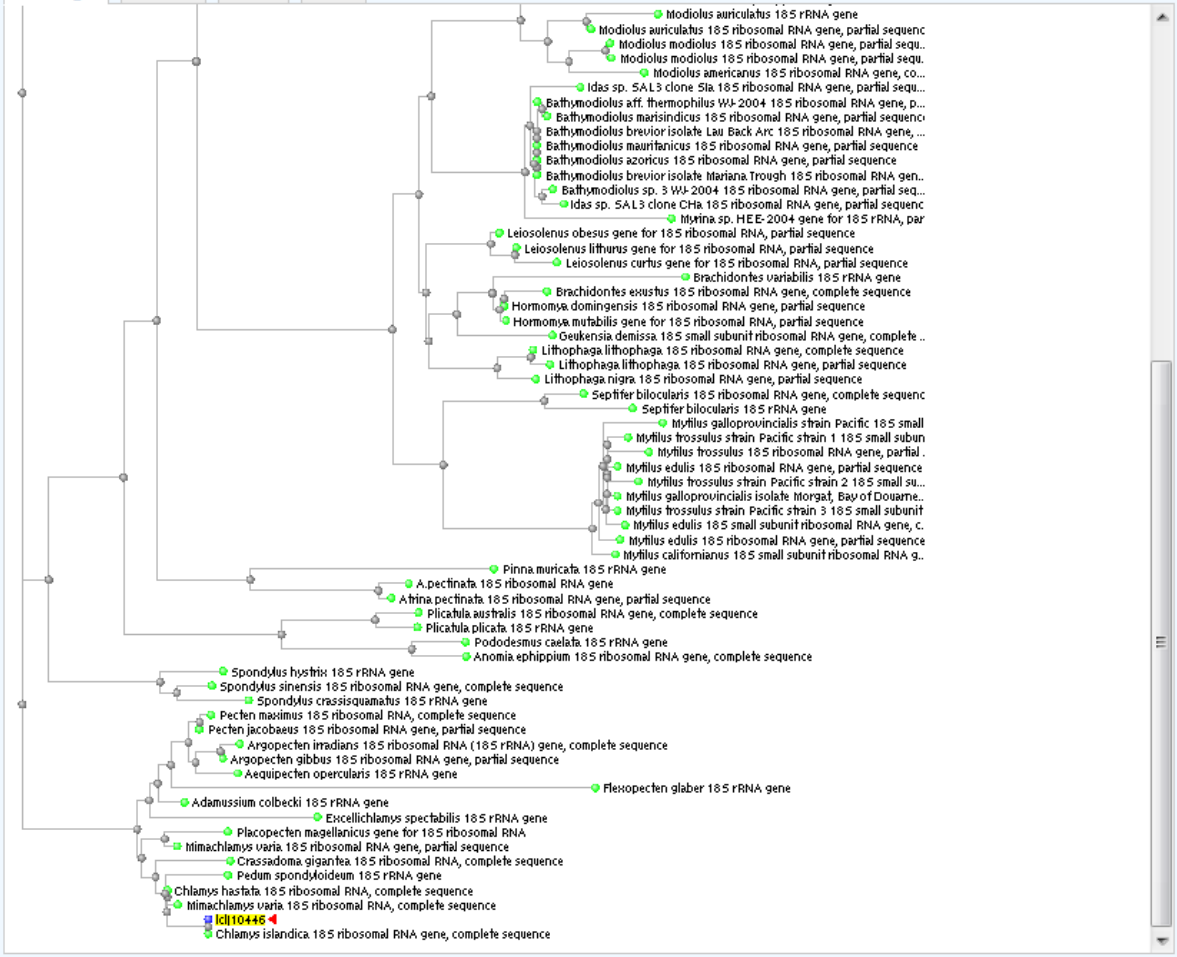
Tree view for rid: WZBVGRZG014, query ID: lcl|10446, database: nr

This tree was produced using BLAST pairwise alignments. more...

Tree method: Fast Minimum Evolution | Sequence Label: Sequence Title (if available) | Max Seq Difference: 0.75 | Reset | Hide Color Map

rectangle slanted radial force ☑ Show distance

Mouse over an internal node for a subtree or alignment



Blast names color map
unknown
bivalves
brachiopods
segmented worms

Программа для построения «сети наименьших расстояний» (minimum spanning network)

TCS: Phylogenetic network estimation using statistical parsimony

© 2000-2005 Mark Clement, Jacob Derington, Steve Woolley and David Posada

Current version is 1.21

TCS is a Java computer program to estimate gene genealogies including multifurcations and/or reticulations (i.e. networks). The network estimation implemented in TCS is also known as Statistical Parsimony, which is described in Templeton, A. R., K. A. Crandall and C. F. Sing. 1992. A cladistic analysis of phenotypic associations with haplotypes inferred from restriction endonuclease mapping and DN sequence data. III. Cladogram estimation. Genetics 132:619-633. For a review on networks and instraspecific genealogies you may read Posada D and Crandall KA. 2001. Trends in Ecology and Evolution 1 (1): 37-45

Operative systems
A jar file is provided that should run in any OS (macintosh, windows, unix-like) with a java virtual machine installed.

Citation
Clement M, Posada D and Crandall K. 2000. TCS: a computer program to estimate gene genealogies. Molecular Ecology 9(10): 1657-1660

http://darwin.uvigo.es/software/tcs.html

Формат файла GenBank

Chlamys islandica 18S.gb - WordPad

Файл Правка Вид Вставка Формат Справка

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VERSION     L11232.1  GI:304466
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SOURCE      Chlamys islandica
  ORGANISM  Chlamys islandica
            Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
            Pectinoidea; Pectinidae; Chlamys.
REFERENCE   1  (bases 1 to 1815)
  AUTHORS   Kenchington,E.L.R.I., Naidu,K.S., Roddick,D.L., Cook,D.I. and
            Zouros,E.
  TITLE     Use of biochemical genetic markers to discriminate between adductor
            muscle of the sea scallop (Placopecten magellanicus) and the
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  JOURNAL   Can. J. Fish. Aquat. Sci. 50 (6), 1222-1228 (1993)
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Формат файла Fasta (.fas .fasta)

sequences.fasta - WordPad

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example1.nex - AkelPad

Файл Правка Вид Настройки Справка

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example.phy - AkelPad

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Seq9    ATGATATTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAG
Seq10    ATGATATTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq11    ATGATATTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq12    ATGATATTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq13    ATGATATTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq14    ATGATATTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq15    ATGATATTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq16    CTGATTTTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq17    ATGATATTTGTCCTCATGGAAGGACATATTTTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq18    ATGATATTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq19    ATGATATTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq20    ATGATATTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq21    CTGATTTTTGTCCTCATGGAAGGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq22    ATGATATTTGTCCTCATGGAAGGACATATTTTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq23    ATGATATTTGTCCTCATGGAACGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq24    ATGATATTTGTCCTCATGGAACGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq25    ATGATATTTGTCCTCATGGAACGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq26    ATGATATTTGTCCTCATGGAACGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq27    ATGATATTTGTCCTCATGGAACGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq28    ATGATATTTGTCCTCATGGAACGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
Seq29    ATGATATTTGTCCTCATGGAACGACATATCCTATGAAAGCTGTTGCTATAACTATTAAAAGGAGGGTGATTCCAATATTTCAAGTTTCTTTAAGTATAAAAC
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