

THE EBI SRS SERVER

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CAAS07f2
CAAS07f2

- Introduction
- Project
- SRS Queries
- Views
- Links
- Analysis Tools



Introduction



- **SRS**是**Sequence Retrieval System**的缩写，是目前分子生物学最重要的序列和其他数据检索工具之一。由欧洲分子生物学实验室开发，最初是为核酸序列数据库**EMBL**和蛋白质序列数据库**SwissProt**的查询开发的。通过输入关键词，你就可以对各类数据库关键词匹配查找，并输出相关信息。



国际上主要SRS数据库查询系统服务器系统的网址

- 欧洲生物信息学研究所 <http://srs.ebi.ac.uk/>
- 欧洲分子生物学实验室 <http://srs.embl.de/>
- 韩国国家基因组信息中心
<http://srs.ngic.re.kr/srs/>
- 德国癌症研究所
<http://www.dkfz-heidelberg.de/srs/>

BLAST和SRS都是序列检索 (Sequence Retrieval) 工具，但有本质差别

- **SRS**对序列数据库的查询，是指对序列、结构以及各种二次数据库中的注释信息进行关键词匹配查找。例如，选定蛋白质序列数据库**SwissProt**，输入关键词**insulin**(胰岛素)，即可找出该数据库所有胰岛素或与胰岛素有关的序列条目(**Entry**)。数据库查询有时也称数据库检索，它和互联网上通过搜索引擎 (**Search engine**) 查找需要的信息是一个概念。
- **BLAST** 是分子生物学特有的工具，它是指通过特定的序列相似性比对算法，找出核酸或蛋白质序列数据库中与检测序列具有一定程度相似性的序列。例如，给定一个胰岛素序列，通过数据库搜索，可以在蛋白质序列数据库**SwissProt**或其它选定的数据库中找出与该检测序列 (**query sequence**)具有一定相似性的序列。

SRS

[Start a Permanent Project](#)

Tips

- ★ *Want to know more about using SRS?*
- go to the [Help Center](#) for online searchable help.
- look in our [SRS@EBI FAQ](#) for answers to commonly asked questions
- ★ *Linking to SRS?*
- Please read our [Linking to SRS](#) guide for important information regarding linking to our SRS server.
- ★ [Public SRS servers worldwide](#)

Quick Text Search [Search T](#)

Find : matching :

Searches Databanks: EMBL Nucleotides

News and Announcements [Search T](#)

Important announcements:

- 13.12.07 MEDLINE and MEDLINENEW will be unavailable while Medline is updated to the 2008 release. Please use MEDLINE2008 during this update.
[Medline](#) has been updated to the 2008 release.
- 11.12.07 [EMBL](#) Release 93 is now on-line ([release notes](#), [data notes](#)).
- 06.11.07 Please Note: Saturday 10th November 2007. Some services may be affected by essential maintenance on Saturday 10th November 2007. We apologise for any inconvenience.
- 29.09.07 Please Note: Saturday 29th September 2007. Some services may be affected by essential maintenance on Saturday 29th



projects



- Project是SRS的一个强大功能，他为用户提供了数据的处理，保存，调用和交换等功能
- Project可分为**temporary project**和**permanent project**



temporary project



SRS Project Options

Save to desktop:

Open from desktop:

Contents of your temporary project

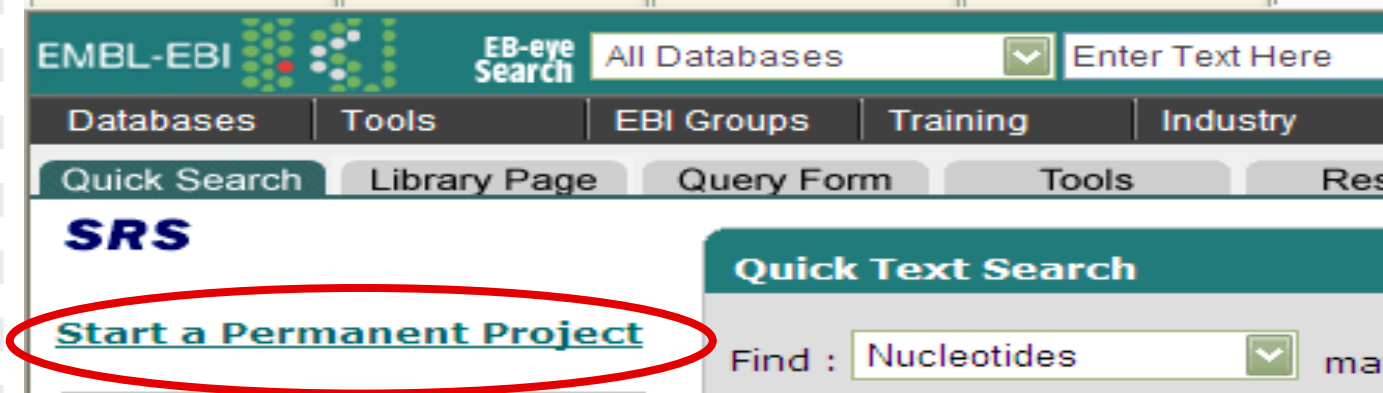
| Queries | | Views |
|---------|---------------------|-------|
| Name | Query Expression | Name |
| Q2 | [embl-AllText:cea*] | EMBL |
| Q1 | [embl-AllText:cea*] | EMBL1 |

用SRS进行搜索后，project会自动记录我们的搜索内容。我们可以在此选择保存搜索内容。但是临时project功能有限，仅有save 与open的功能



permanent project

吉祥



Explorer 用户提示

脚本提示:

Enter your SRS user name:

[http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page+srsq2+-noSess:

确定

取消

输入你的用户名

wei Options

Save to desktop:

Rename project:

Delete project:

Copy selected items to:

Other Projects

Create a project:

Open from desktop:

Switch projects:

- 保存（save）,保存当前的数据;
- 重命名（rename）,对我们的Project进行更名;
- 删除（delete）,及时删除一个不用的Project也是必要的。
- 复制 (copy), 我们也可把右边的项目例如Q1等, 拷贝到另一个Project中。
- 新建（New Project）,新建一个Project, 那么接下来的工作将会自动保存到新的Project中。
- 跳转（Switch）,此键有助于我们在不同的Project之间跳转。

吉祥

- **Project**是一个帮助我们记录我们在**SRS**上搜索，更改风格等操作的工具，通过它，可以使我们更方便进行数据的保存，尤其进行多个数据操作，能使我们将各个数据分开，有条不紊地操作，以及各个**Project**之间的数据调用等。



SRS Queries

音韻





- Quick Search
- the Standard Query Form
- the Extended Query Form




Quick Search



Quick Text Search [Search Tips](#)

Find : matching :

Searches Databanks: UniProt Proteins  **Search**

- Quick Text Search.
- Sequence Similarity / Homology Search. (**EBI SRS**中无此项)

Quick Search无需选择库,系统会根据数据的类型自动选择合适的库



the Standard Query Form & the Extended Query Form

Quick Search Library Page **Query Form** Tools Results Projects Views Databanks

Reset

Quick Search

Search Options

1. Select the **databanks** you want to search

2. Enter your **search terms** in the **Quick Search** box, or choose a **query form** from below

Standard Query Form

Extended Query Form

You can **browse** through all the **entries** in any **databanks**.

First, **select** the **databanks** you want to browse, then click:

Browse Entries

Available Databanks

Expand all

Collapse all

Show databanks tooltips

Literature, Bibliography and Reference Databases

all

MEDLINE

Taxonomy

OMIM

OMIM Morbid Map

Patent Abstracts

Karyn's Genomes

Literature, Bibliography and Reference Databases - subsections

all

MEDLINE (Updates)

MEDLINE (Main Release 2008)

MED2PUB

Gene Dictionaries and

Nucleotide sequence databases

all

EMBL

Patent DNA

EMBL (Contig)

EMBL (Annotated Cons)

EMBL (Coding Sequences)

EMBL ID/Accession Mapping

IMGT/LIGM-DB

IMGT/HLA

IPD-KIR

GR Gene Sets

RefSeq Genome

LiveLists

Nucleotide sequence databases - subsections

2、点击**Standard Query Form**或**Extended Query Form**

1、选择 **Databank**

the Standard Query Form



| Fields you can search | Your search terms |
|---|-------------------|
| In a single field, you can separate multiple values by: &, or ! | |
| i AllText <input type="text"/> | |
| i AllText <input type="text"/> | |
| i AllText <input type="text"/> | |
| i AllText <input type="text"/> | |

the Extended Query Form

Reset

search [EMBL \(Updates\)](#)

Search Options

Combine search terms with:

Use wildcards

Get results of type:

Result Display Options

View results using:

| Fields you can search | Your search terms | Create a view |
|--|---|--------------------------|
| In a single field, you can separate multiple values by &, , ! | | |
| AllText | <input type="text"/> | |
| AllIDs | <input type="text"/> | |
| ID | <input type="text"/> | <input type="checkbox"/> |
| Topology | <input type="checkbox"/> circular <input type="checkbox"/> linear | <input type="checkbox"/> |
| | <input type="checkbox"/> genomic dna <input type="checkbox"/> genomic rna | |
| | <input type="checkbox"/> mrna <input type="checkbox"/> other dna | |
| | <input type="checkbox"/> other rna <input type="checkbox"/> pre-rna | |
| | <input type="checkbox"/> rna <input type="checkbox"/> snorna | <input type="checkbox"/> |
| Molecule | | |



Search Terms



- Single-word search 单词条查询
- Multiple-word phrases 多词条短语
- Numbers and dates 数字和数据
- Regular expressions 规则的公式
- Wildcards 通配符





- **Single-word search**（单词条），就是只输入一个字符，无论在快速搜索，标准搜索还是扩展搜索，均可以使用，例如选择了EMBL之后，输入一个cea（SRS不区分大小写）



- 多词条比对。同样在三种搜索风格中均适用，例如输入aldehyde reductase（乙醛酸还原酶），合写成aldehydereductase时搜出来的内容每条均含aldehyde reductase，但是分写成aldehyde reductase时搜出的结果可能就只有aldehyde或reductase其中一个。
- 也可以使用逻辑符号，如**aldehyde & reductase (AND)**, **aldehyde | reductase (OR)**, **aldehyde ! reductase (BUTNOT)**.



■ Numbers and dates 数字和数据搜索。

更适合比较专业的人士，通过数字和冒号，感叹号的组合来对结果进行限定的，冒号在数字的左边时，表示结果需要小于这一数字，相反，在右边则大于这一数字。而感叹号在冒号的左边时表示没有上限，在右边表示没有下限。

但如果用的是 **Extended Query Form** 的话，就简单的多了

The screenshot displays the 'Extended Query Form' interface. It features several search criteria rows, each with a dropdown menu for the operator and input fields for values. The 'Entry Creation Date' row is set to 'between' with values '11 Mar 2002' and '9 Mar 2003'. The 'LastUpdated' row is set to 'select' with values '1 Jan YYYY' and '1 Jan YYYY'. The 'Sequence Length' row is set to 'select on' with values '>= 212' and '<= 400'. A dropdown menu is open over the 'Sequence Length' row, showing options: 'after', 'before', and 'between'. The 'before' option is highlighted. At the bottom, there is a 'View results using:' dropdown set to '* Name' and a 'Search' button.

- **规则公式搜索。** 规则搜索时不要求输入整个词条，只需输入一个词的前缀或后缀即可。这样尤其方便但我们对一个词条只记住一半时，或者同时搜索两个以上有共同词根的相关词条的情况：
 - 例如输入 `/^phos/` 将会得到以 "phos" 开头的词条的相关结果 (例如 phosphate, phosphorylase),
 - 而输入 `/ase$` 将会得到以 "ase" 结尾的词条的相关结果 (例如 kinase, phosphatase 等)。





- **通配符搜索：** 在这里通配符主要指的是相似通配符，当我们不确定一个单词，但记得词头，词尾时，可以在中间加上*或者一个？这在我们不确定单词完整拼写，或者查询几个共字头字尾的词条很有用。



吉祥慶

- **SRS**的一般性搜索和别的数据库搜索大同小异，但是，其分类的精细程度是其他工具所不能比拟的，通过多种选择的组合，是我们搜索到的资源更加接近我们的目标，避免在很多“假阳性”数据上浪费时间。





结果与保存

- 结果的显示风格可以在设置**VIEW**时改变，也可以在得到结果后进行改变。
- 选择好目的数据后，点击保存

 ■ 可以通过**RESULT**来查看我们搜索的结果



普賢

VIEWS



Display Options

View results using:

SeqSimpleView

Sort results by:

Organism Name

- ascending
- descending

Show 30 results

per page

Printer friendly view

Apply Display Options

选择显示结果的方式

选择排列的方式

Result Display Options

View results using:

UniprotView

or

Create a view

Show 30 results

per page

Links

Use this page to set the requirements when searching for links to other entries from your existing query results.



Get to the Link Page



- **Manage your Query Results** page
- **the Query Result** page
- **the Entry** page



Find Links from the Manage your Query Results Page

MBL-EBI EB-eye Search All Databases Enter Text Here Go Reset Advanced Search Give us feedback

Databases Tools EBI Groups Training Industry About Us Help Site Index

Quick Search Library Page Query Form Tools Results Projects Views Databank

Reset

Results Options

Options are **applied** to **selected** queries only

Save results: [Save](#)

Delete results: [Delete](#)

Combine queries with: [Combine](#)

Find related info: [Link](#)

Search using a query expression: [\(Query Reference\)](#)

Result History

| Name | Type | Total No. | From | No. | Query Expression |
|-----------------------------|-------|-----------|-----------|------|---|
| <input type="checkbox"/> Q2 | query | 3191 | SWISSPROT | 3191 | [swissprot-AllText: <input type="text" value="<input type="text" value=""/> |
| <input type="checkbox"/> Q1 | query | 3191 | SWISSPROT | 3191 | [swissprot-AllText: <input type="text" value="<input type="text" value=""/> |



Find Links from the Query Result Page

The screenshot displays the EMBL-EBI EB-eye Search interface. At the top, there is a search bar with the text "All Databases" and a dropdown menu, and a text input field containing "[swissprot-AllText:oxi". Below the search bar are navigation tabs for "Databases", "Tools", "EBI Groups", "Training", "Industry", and "About Us". A "Reset" button is located on the left side of the search bar. Below the search bar, there are two main sections: "Apply Options to:" and "Result Options".

Apply Options to:

- selected results only
- unselected results only

Result Options

Launch analysis tool:
NCBI BLASTP

Show tools relevant to these results:

Link to related information:

Save results:


The search results are displayed in a table with the following entries:

| UniProtKB / Swiss-Prot | |
|--------------------------|---|
| <input type="checkbox"/> | UniProtKB/Swiss-Prot:1A11 PRUMU |
| <input type="checkbox"/> | UniProtKB/Swiss-Prot:2NPD NEUCR |
| <input type="checkbox"/> | UniProtKB/Swiss-Prot:2NPD WILMR |
| <input type="checkbox"/> | UniProtKB/Swiss-Prot:9GL ASFB7 |
| <input type="checkbox"/> | UniProtKB/Swiss-Prot:ABA2 ARATH |
| <input type="checkbox"/> | UniProtKB/Swiss-Prot:ABP1 HUMAN |
| <input type="checkbox"/> | UniProtKB/Swiss-Prot:ABP1 MOUSE |

Find Links from the Entry Page

Entry Information

Entry from:



The logo for SwissProt, featuring a stylized mountain peak in shades of blue and green, with the text 'SIB swissprot EBI' below it.

Entry Options

Launch analysis tool:
NCBI BLASTP

Link to related information:

Save entry:

View:

[General](#) [Description](#) [Ref](#)

General information

| | |
|-------------------|------------------------------------|
| Entry name | 1A11_PRUMU |
| Accession number | Q9MB95 |
| Integrated | 02-NOV-2001, UniProtKB/Swiss-Prot. |
| Sequence update | 01-OCT-2000, sequence version 1 |
| Annotation update | 11-SEP-2007, entry version 40 |
| UniSave | Q9MB95 |
| UniRef100 | UniRef100_Q9MB95 |
| UniParc | UPI0000124E2D |

Description and origin of the Protein

| | |
|-----------------|---|
| Description | 1-aminocyclopropane-1-carboxylate s lyase). |
| Gene name(s) | ACS1 |
| Organism source | Prunus mume (Japanese flowering ap |
| Taxonomy | Eukaryota; Viridiplantae; Streptophyt. eudicotyledons; rosids; eurosids I; Rc |
| NCBI TaxID | 102107 |

References

- [1] Mita,S., Kirita,C., Kato,M., Hyodo,H., **Expression of ACC synthase is enhan** (1999) *Physiol. Plantarum* **107**:319-32
- Position [NUCLEOTIDE SEQUENCE](#) [MR

Comments

two forms of the Link page


Link Options

Select the **databanks** you want to search for **related information**

Find **related** entries

Refine Query - **show** only **results** with **related entries**

Show only results **without** related entries



Databanks Available to Link to


[Expand all](#) [Collapse all](#)

- Literature, Bibliography and Reference Da
- Gene Dictionaries and Ontologies
- Nucleotide sequence databases
- Nucleotide related databases
- UniProt Universal Protein Resource
- Other protein sequence databases
- Protein function, structure and interaction
- Enzymes, reactions and metabolic pathwz
- Mutation and SNP databases
- Other databases
- User owned databases
- Application result databases

initiated the links from either the **Manage your Query Results** or **Query Result** pages

Link Options

Select the **databanks** you want to search for **related information**



Databanks Available to L

[Expand all](#) [Collapse](#)

- Literature, Bibliograph
- Gene Dictionaries and
- Nucleotide sequence d
- Nucleotide related da

initiated the links from either the **Entry** page

Link Options

- **Find related entries**

- This option searches for entries in the databanks you have ticked, and which have links to the current query. The result is a list of entries in the selected databanks.

- **Refine Query - show only results with related entries**

- This option searches for entries in the current query which have links to the databanks you have selected. The result is a subset of the entries with which you started.

- **Show only results without related entries**

- This option looks for entries in the current query which do not have links to the databanks you have selected. The result is a subset of the entries with which you started.

Link Options

Select the **databanks** you want to search for **related information**

Find **related** entries

Refine Query - **show only results with related entries**

Show only results without related entries

||| ➡ **Search**

Expression Linking

search for a link between two or more sets of results or between a set of results and a databank.



Search using a query expression:
[\(Query Reference\)](#)

Q1 < Q4

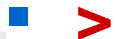
Search

Result History

| Name | Type | Total No. | From | No. | Query Expression | Comment |
|-----------------------------|--------|-----------|-------------------|----------------|------------------------------------|---------|
| <input type="checkbox"/> Q5 | query | 2505 | SWISSPROT | 2505 | <code>(([swissprot-AllText:</code> | |
| <input type="checkbox"/> Q4 | query | 227820 | EMBL SWISSPROT | 224629 3191 | <code>[libs={embl swisspro</code> | |
| <input type="checkbox"/> Q3 | select | 6 | SWISSPROT | 6 | <code>(((((([SWISSPROT-ID:1</code> | |
| <input type="checkbox"/> Q2 | query | 3191 | SWISSPROT | 3191 | <code>[swissprot-AllText:o</code> | |
| <input type="checkbox"/> Q1 | query | 3191 | SWISSPROT | 3191 | <code>[swissprot-AllText:o</code> | |



Entries in the set or databank to the left of the operator are returned if they have a link to any entries in the set or databank to the right of the operator.



Entries in the set or databank to the right of the operator are returned if they have a link to any entries in the set or databank to the left of the operator.

Linking operations.



| Operators | Example | Returns Entries in: |
|-----------|--------------|-----------------------------------|
| < | Q1 < Q2 | In Q1 that link to Q2. |
| > | Q1 > Q2 | In Q2 that link to Q1. |
| < & | Q1 < Q2 & Q3 | In Q1 that link to Q2 and Q3. |
| < | Q1 < Q2 Q3 | In Q1 that link to Q2 or Q3. |
| < ! | Q1 < Q2 ! Q3 | In Q1 that link to Q2 but not Q3. |

Expression Linking Examples

- If you have a set of EMBL entries in a query, **Q3**, which you wish to search for links with the SWISS-PROT databank, type:

Q3 < swissprot

- This will show the EMBL entries from the original query that have links to the SWISS-PROT databank.

- If you would rather see the SWISS-PROT entries that the above operation returned, turn the linking operator around so that it points towards SWISS-PROT:

Q3 > swissprot

- This returns the SWISS-PROT entries that have links with the entries in **Q3**.

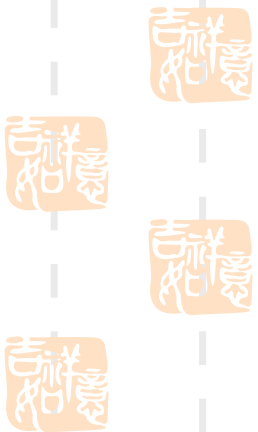
Analysis Tools

SRS analysis tools are bioinformatics programs that use a databank query as input. The output file from an analysis tool is indexed in the same way as any other databank. This enables users to store and query their analyses.



SRS与其他数据库搜索网站的一个很重要的不同之处在于：

在SRS上不仅可以搜索到我们所要查询的核酸（蛋白）的相关信息，而且可以在查找到结果的同时对这些数据进行一定的分析处理。



这项操作可以通过SRS中的分析工具来完成

在SRS首页的控制面板上可以选择键，便可进入分析工具的页面。



Tools



Quick Launch

Launch analysis tool:

AliSubSimN

Launch

Available Analysis Tools - listed by type

Expand all Collapse all

- Alignment Tools
- Display Tools
- Edit Tools
- Information Tools
- Nucleic Tools
- Protein Tools
- Sequence Tools
- Utility Search Tools

另一个是页面右侧的工具列表

一个是在页面左侧的 Quick Launch

- Packages Installation**
- [NCBI BLAST](#)
 - [OTHER](#)
 - [FASTA](#)
 - [CLUSTAL](#)
 - [HMMER](#)
 - [EMBOSS](#)

Search Descriptions

在SRS中可以通过两种途径来使用分析工具

这两种进入分析工具方式的主要区别在于：

- Quick Launch的下拉菜单中直接显示分析程序的名称；而在工具列表中则是按照程序的功能进行分类的。
- 在工具列表中可以显示与这项工具相关的其它信息。
- 因此，我们可以根据具体的情况来决定选择哪种方式进入程序。

- 进入程序后可以在输入序列的对话框中直接粘贴上**FASTA**格式的序列，或是输入文件名称。



吉祥

在SRS中的TOOLS工具的使用方法和其他的生物信息学的工具一样。而最大的不同就在于：在SRS中可以对搜索到的数据直接进行相应的处理。





吉祥

下面以CEA为例进行说明





- 在Library Page中选择Swiss-Prot,点击进入Standard Query Form。在查找区域填入CEA.点击， Search进行查找

| Fields you can search | Your search terms |
|---|---|
| In a single field, you can separate multiple values by: &, or ! | |
| |  |

 Description

 AllText

 AllText

 AllText

- 找到相关的6个结果，根据查找的目的找到相关的数据。在显示结果的页面的左侧的工具栏中可以看到**Tools**的选项，点击该键，便可进入对已选结果可以进行的相应的分析工具的页面。

Result Options

Launch analysis tool:

NCBI BLASTP **Launch**

Show tools relevant to these results: **Tools**

Link to related information: **Link**

Save results: **Save**

点击此键



Alignment Tools

- Alignment Differences
- Alignment Dot Plots
- Alignment Global
- Alignment Local
- Alignment Multiple

ClustalW Multiple protein sequence alignment - [Launch More Info...](#)

ClustalW2 Multiple protein sequence alignment - [Launch More Info...](#)

- Display Tools
- Edit Tools
- Information Tools
- Nucleic Tools
- Protein Tools
- Similarity Search Tools

对查找的结果进行Clustalw处理， 点击launch键

Reset

Job Options

Note: this tool is run by LSF batch queueing system.

Name of the queue is **extsrv_interactive** -R 'msa order[p_clustalw:r15s:pg] span[hosts=1]' -L /bin/sh (batch).

ClustalW

[More Info...](#)

Job name:

Launch

Input data from entries:

```
SWISSPROT:CEAM2_MOUSE  
SWISSPROT:CEAM5_HUMAN  
SWISSPROT:CEAMA_MOUSE  
SWISSPROT:LYRIC_HUMAN  
SWISSPROT:LYRIC_MOUSE  
SWISSPROT:LYRIC_RAT
```

Parameter set options

Save current parameter set as:

General Options

Order of sequences in alignment

Algorithm for the pairwise alignments guide tree

FAST SLOW

Multiple Alignment

Use substitution matrix

Gap opening penalty:

Gap extension penalty:

Gap separation distance:

Delay Divergent sequences:

No end gap penalty

Use residue specific penalties

Tool was submitted to Queue:extsrv_interactive -R 'msa order[p_clustalw:r15s:pg] span[hosts=1]' -L /bin/sh(batch).


Tool command:

```
/ebi/extserv/bin/clustalw/clustalw -infile='./temp_clustal_1_in_tmp.s' -outorder
```

Use [Batch job status page](#) to view the [results](#)

■ 点击result 查看结果

List of Batch Jobs

| Job Name | Status | Start Date | Results from | Result Set | Queue Name |
|---|---|----------------------|--------------|------------|---|
| <input type="checkbox"/> temp_clustal_3 |  | 10-Jan-2008 15:44 | CLUSTALW | - | extsrv_interactive -R 'msa order[p_clustalw:r15s:pg] span[hosts=1]' -L /bin/sh(batch) |

! Sequence: [SWISSPROT:CEAM2_MOUSE](#) Carcinoembryonic antigen-related cell adhesion mol...

! Sequence: [SWISSPROT:CEAM5_HUMAN](#) Carcinoembryonic antigen-related cell adhesion mol...

! Sequence: [SWISSPROT:CEAMA_MOUSE](#) Carcinoembryonic antigen-related cell adhesion mol...

! Sequence: [SWISSPROT:LYRIC_HUMAN](#) Protein LYRIC (Lysine-rich CEACAM1 co-isolated pro...

! Sequence: [SWISSPROT:LYRIC_MOUSE](#) Protein LYRIC (Lysine-rich CEACAM1 co-isolated pro...

! Sequence: [SWISSPROT:LYRIC_RAT](#) Protein LYRIC (Lysine-rich CEACAM1 co-isolated pro...

CLUSTAL W (1.83) multiple sequence alignment

```
CEAM2_MOUSE      -----MELASAPHLKGGQVPWFGLLLTASLLASWSPPTTAQVTVMAFPLHAAE
CEAM5_HUMAN      -----MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTAKLTIESTPFNVAE
CEAMA_MOUSE      -----MELASAPHLKGGQVPWVGLLLTASLLTYWSPATTAQVTVEAVPPNVTA
LYRIC_HUMAN      MAARSWQDELAQQAEEGSARLREMLSVGLGFLRTELGLDLGLEPKRYPGWVILVGTGALG
LYRIC_MOUSE      MAARSWQDELAQQAEEGSARLRELLSVGLGFLRTELGLDLGLEPKRYPGWVILVGTGALG
LYRIC_RAT        MAARSWQDELAQQAEEGSARLRELLSVGLGFLRTELGLDLGLEPKRYPGWVILVGTGALG
```

```
                *  **  :.      : *  *  *      ..      :      .
```

```
CEAM2_MOUSE      GNNVILVVYNNMMKGVSAFVSHKGGSTTSTNAEIVRFVTGTNKTIKGPVHSGRETLYSNGSL
CEAM5_HUMAN      GKEVLLLVHNLFPQHLLFGYSWYKGERVDGNRQIIIGYVIGTQQATPGPAYSGREIIYPNASL
CEAMA_MOUSE      DNNVLLLVHNLFPQTLRVFYWYKGNNGAGHNEIGRFVTSINRSKMGLAHSGRETIYSNGSL
LYRIC_HUMAN      LLLLFLLGYGWAAACAGARKKRRSPPRKREEAAAVPAAAPDDLALLKNLRSEEQKKKNRK
LYRIC_MOUSE      LLLLFLLGYGWAAACAGARKKRRSPPRKREEAAP-PTPAPDDLAQLKNLRSEEQKKKNRK
LYRIC_RAT        LLLLFLLGYGWAAACAGARKKRRSPPRKREEVTP-PTPAPEDPAQLKNLRSEEQKKKNRK
```

```
                :*: :.      : .      . :      *      :
```

```
CEAM2_MOUSE      LIQRVTMKDTGVYTIEMTDQNYRRRVLTG----QFHVHKLKLLKSNITSNNSNPVEGDDSV
CEAM5_HUMAN      LIQNIIQNNTGFTLHVIKSDLVNEEATG----QFRVYPELPKPSISSNNSKPVEDKDAV
CEAMA_MOUSE      FFQSVTKNDEGVYTYLMLDQNFETIPISVR----FHVHPSLLP-----SLSPPTTGQVTV
LYRIC_HUMAN      KLSEKPKPNGRTVEVAEGEAVRTPQSVTAKQPPEIDKKNEKSCKNKKKSKSDAKAVQNSS
LYRIC_MOUSE      KLPEKPKPNGRTVEVPEDEVVRNPRSITAKQAPETDKKNEKSCKNKKKSKSDAKAVQNSS
LYRIC_RAT        KLPEKPKPNGRTVEIPEDEVVRTPRSITAKQPPEIDKKNEKSCKNKKKSKSDAKAVQNSS
```

```
                :      :      :      .      :      . *      .      :
```

吉祥如意

- 由此可以看出，SRS可以方便快捷的查找出相关数据的同时，并可以对得到的数据作出准确地分析。这样就不会像以前在其它数据库查出结果后再将结果进行分析那么繁琐了。



SRS在UNIX下的命令行

- SRS不仅可以在Windows下使用，而且也可以在Unix环境中操作。
- 使用getz可以通过命令行进行数据库的查询。

例如：从SWISS-PROT 数据库中检索 azuri

结果列表

```
getz "[swissprot-des:azurin]"
```



SRS命令行



| Option | Default | Function |
|----------------------|---------|--|
| -help | | Help with getz. |
| -e | FALSE | Prints the entire entry. |
| -t | FALSE | Copy the complete text (annotation) part of the entry.. |
| -d | FALSE | Copy the data (e.g. sequence) part of the entry. |
| -i | FALSE | Print the tokens that would be generated for indexing. |
| -f <string> | "" | Include fields in entry list. |
| -vf <string> | "" | List of fields that will be placed into a table view. |
| -w | FALSE | Appends a wildcard to each search word. |
| -lb <n> | 0 | Number of first entry in set to be viewed. |
| -ll <n> | 0 | Number of entries to be viewed in one go. |
| -lv | FALSE | List all values that match the query. |
| -lvf | FALSE | List all values that match the query, plus the number of entries for each match. |
| -lmin <n> | 0 | List only values that occur at least the specified number of times. Use together with -lv. |
| -c | FALSE | Report the number of entries that were found, but not the entries themselves. |
| -info | FALSE | Prints info about the specified databank. |
| -libs | FALSE | Prints a list of all active databanks. |
| -view <string> | "" | Name of view to be used when displaying entries. |
| -rs <string> | "" | String of one or more characters to separate records in view. |
| -cs <string> | "" | String of one or more characters to separate columns in view. |
| -sf <string> | "" | Format of sequence output file. |
| -af <string> | "" | Format of sequence alignment output file. |
| -html | FALSE | Select HTML format for output. |
| -ascii | TRUE | Select ASCII format for output. |
| -off | FALSE | Accesses the off-line version of a databank. |
| -id <string> | "" | The user ID, or filename associated with a WWW session. |
| -sort <string> | "" | The name of the field on which to sort the query. |
| -sortDir <string> | "" | Ascending (0) or descending sort. |

THANK YOU

FOR YOUR ATTENTIONS

