МЕЖДУНАРОДНЫЙ УНИВЕРСИТЕТ АСТАНА

Высшая школа естественных наук

ОСНОВЫ БИОИНФОРМАТИКИ
(Практикум)

Используем сервер UniProt (Universal Protein Resource)

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АСТАНА, 2025

Белки (протеины, полипептиды) — высокомолекулярные органические вещества, состоящие из альфа-аминокислот, соединённых в цепочку пептидной связью.

Используем сервер UniProt (Universal Protein Resource) – для досту-па к базам данных EMBL, GenBank, DDBJ и др.: http://www.uniprot.org/.

RNP_HORSE

Search in
Protein Knowledgebase (UniProtKB)

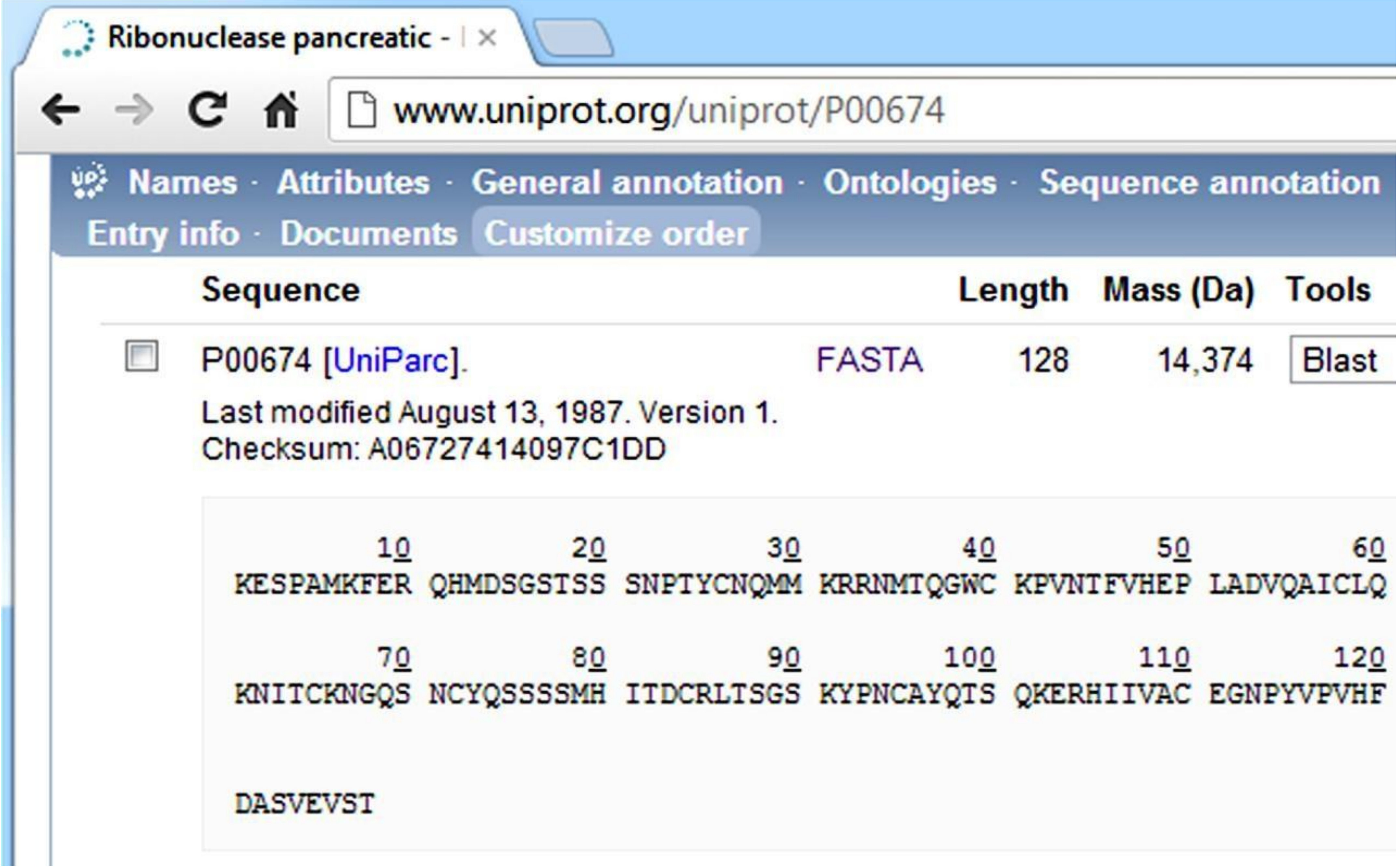
Query
RNP_HORSE

WELCOME

The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

What we provide

UniProtKB	Protein knowledgebase, consists of two sections: ★ Swiss-Prot, which is manually annotated and reviewed. ★ TrEMBL, which is automatically annotated and is **not** reviewed. Includes complete and reference proteome sets.

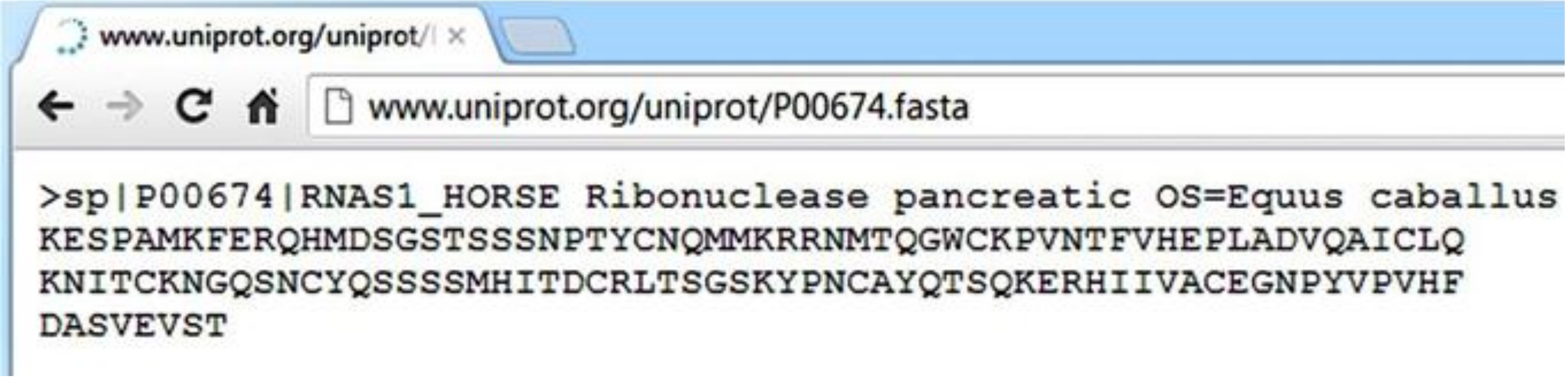


Sequence		Length	Mass (Da)	Tools
☐ P00674 [UniParc].	FASTA	128	14,374	Blast

Last modified August 13, 1987. Version 1.
Checksum: A06727414097C1DD

```
        10         20         30         40         50         60
KESPAMKFER QHMDSGSTSS SNPTYCNQMM KRRNMTQGWC KPVNTFVHEP LADVQAICLQ

        70         80         90        100        110        120
KNITCKNGQS NCYQSSSSMH ITDCRLTSGS KYPNCAYQTS QKERHIIVAC EGNPYVPVHF


DASVEVST
```

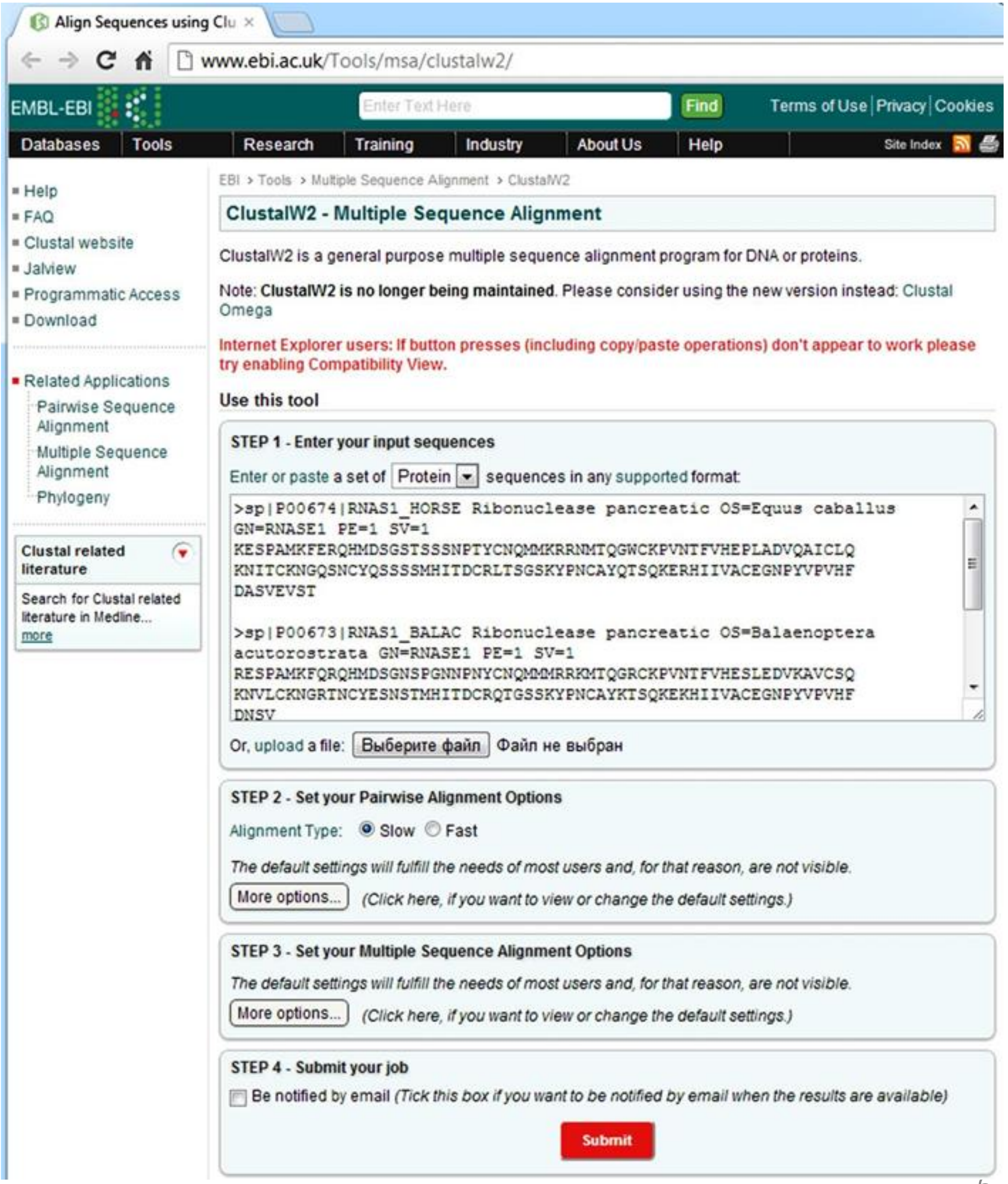
```
>sp|P00674|RNAS1_HORSE Ribonuclease pancreatic OS=Equus caballus GN=RNASE1 PE=1 SV=1
KESPAMKFERQHMDSGSTSSSNPTYCNQMMKRRNMTQGWCKPVNTFVHEPLADVQAICLQ
KNITCKNGQSNCYQSSSSMHITDCRLTSGSKYPNCAYQTSQKERHIIVACEGNPYVPVHF DASVEVST

>sp|P00673|RNAS1_BALAC Ribonuclease pancreatic OS=Balaenoptera acutorostrata GN=RNASE1 PE=1 SV=1
RESPAMKFQRQHMDSGNSPGNNPNYCNQMMMRRKMTQGRCKPVNTFVHESLEDVKAVCSQ
KNVLCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF DNSV

>sp|P00686|RNAS1_MACRU Ribonuclease pancreatic OS=Macropus rufus GN=RNASE1 PE=1 SV=1
ETPAEKFQRQHMDTEHSTASSSNYCNLMMKARDMTSGRCKPLNTFIHEPKSVVDAVCHQE
NVTCKNGRTNCYKSNSRLSITNCRQTGASKYPNCQYETSNLNKQIIVACEGQYVPVHFDA
YV
```



```
>sp|P00674|RNAS1_HORSE Ribonuclease pancreatic OS=Equus caballus
KESPAMKFERQHMDSGSTSSSNPTYCNQMMKRRNMTQGWCKPVNTFVHEPLADVQAICLQ
KNITCKNGQSNCYQSSSSMHITDCRLTSGSKYPNCAYQTSQKERHIIVACEGNPYVPVHF
DASVEVST
```

Построим для этих последовательностей множественное выравнивание с помощью программы ClustalW2

https://wwwdev.ebi.ac.uk/Tools/jdispatcher/



ClustalW2 - Multiple Sequence Alignment

ClustalW2 is a general purpose multiple sequence alignment program for DNA or proteins.

Note: **ClustalW2 is no longer being maintained**. Please consider using the new version instead: Clustal Omega

Internet Explorer users: If button presses (including copy/paste operations) don't appear to work please try enabling Compatibility View.

Use this tool

STEP 1 - Enter your input sequences

Enter or paste a set of Protein sequences in any supported format:

```
>sp|P00674|RNAS1_HORSE Ribonuclease pancreatic OS=Equus caballus
GN=RNASE1 PE=1 SV=1
KESPAMKFERQHMDSGSTSSSNPTYCNQMMKRRNMTQGWCKPVNTFVHEPLADVQAICLQ
KNITCKNGQSNCYQSSSSMHITDCRLTSGSKYPNCAYQTSQKERHIIVACEGNPYVPVHF
DASVEVST

>sp|P00673|RNAS1_BALAC Ribonuclease pancreatic OS=Balaenoptera
acutorostrata GN=RNASE1 PE=1 SV=1
RESPAMKFQRQHMDSGNSPGNNPNYCNQMMMRRKMTQGRCKPVNTFVHESLEDVKAVCSQ
KNVLCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF
DNSV
```

Or, upload a file: Выберите файл Файл не выбран

STEP 2 - Set your Pairwise Alignment Options

Alignment Type: ● Slow ○ Fast

The default settings will fulfill the needs of most users and, for that reason, are not visible.

More options... *(Click here, if you want to view or change the default settings.)*

STEP 3 - Set your Multiple Sequence Alignment Options

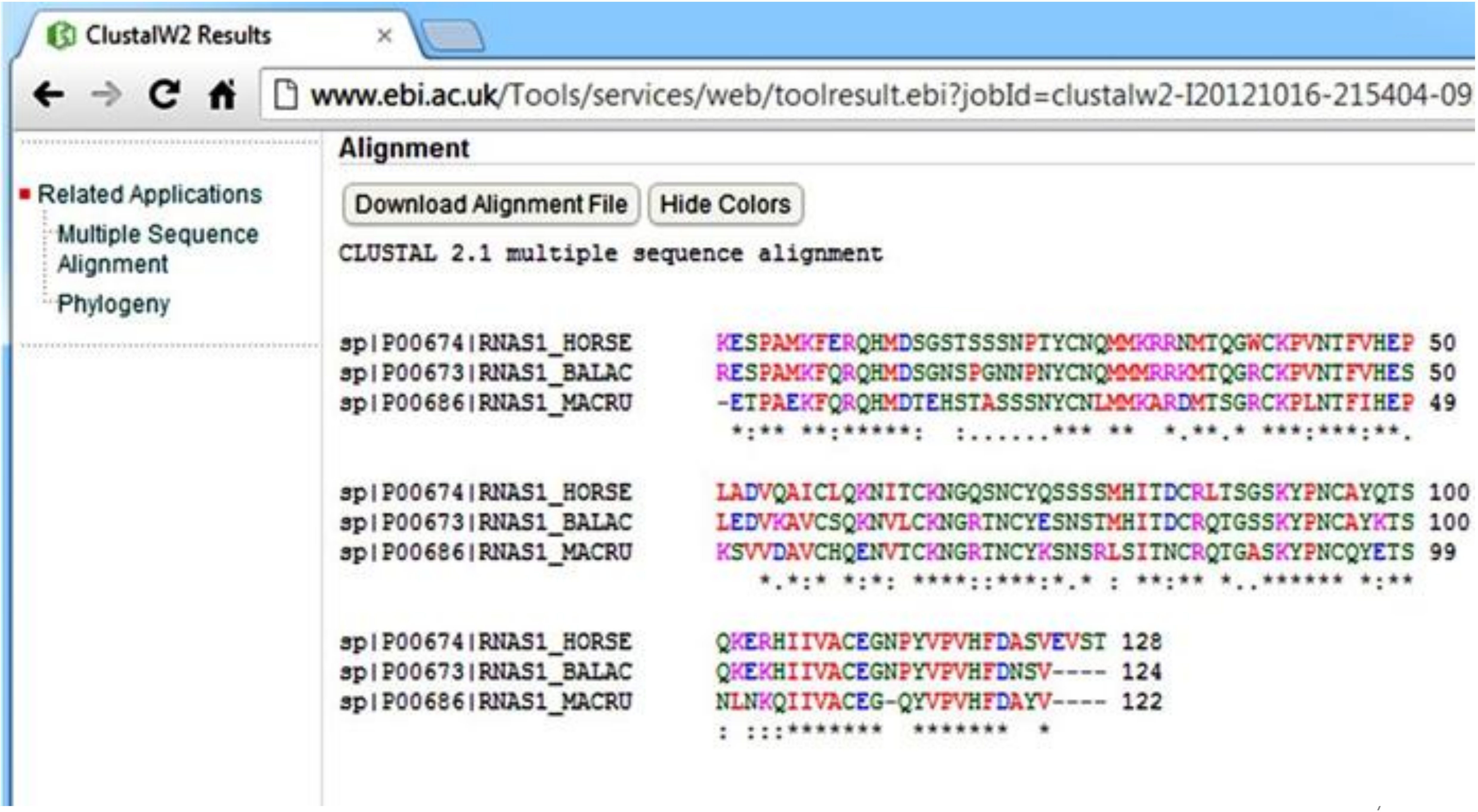
The default settings will fulfill the needs of most users and, for that reason, are not visible.

More options... *(Click here, if you want to view or change the default settings.)*

STEP 4 - Submit your job

☐ Be notified by email *(Tick this box if you want to be notified by email when the results are available)*

Submit



Alignment

```
CLUSTAL 2.1 multiple sequence alignment


sp|P00674|RNAS1_HORSE      KESPAMKFERQHMDSGSTSSSNPTYCNQMMKRRNMTQGWCKPVNTFVHEP 50
sp|P00673|RNAS1_BALAC      RESPAMKFQRQHMDSGNSPGNNPNYCNQMMMRRKMTQGRCKPVNTFVHES 50
sp|P00686|RNAS1_MACRU      -ETPAEKFQRQHMDTEHSTASSSNYCNLMMKARDMTSGRCKPLNTFIHEP 49
                            *:** **:*****:  :......*** **  *.**.* ***:***:**.

sp|P00674|RNAS1_HORSE      LADVQAICLQKNITCKNGQSNCYQSSSSMHITDCRLTSGSKYPNCAYQTS 100
sp|P00673|RNAS1_BALAC      LEDVKAVCSQKNVLCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTS 100
sp|P00686|RNAS1_MACRU      KSVVDAVCHQENVTCKNGRTNCYKSNSRLSITNCRQTGASKYPNCQYETS 99
                              *.*:* *:*: ****::***:*.* : **:** *..****** *:**

sp|P00674|RNAS1_HORSE      QKERHIIVACEGNPYVPVHFDASVEVST 128
sp|P00673|RNAS1_BALAC      QKEKHIIVACEGNPYVPVHFDNSV---- 124
sp|P00686|RNAS1_MACRU      NLNKQIIVACEG-QYVPVHFDAYV---- 122
                           : :::*******  *******  *
```

Ссылки:

https://www.ncbi.nlm.nih.gov/
http://www.uniprot.org/
https://lifemap-ncbi.univ-lyon1.fr/

https://ru.wikipedia.org/wiki/%D0%9F%D0%BE%D0%BB%D1%8B%D0%BD%D1%8C

https://ru.wikipedia.org/wiki/%D0%9E%D0%B4%D1%83%D0%B2%D0%B0%D0%BD%D1%87%D0%B8%D0%BA

https://xn--80abvyzg.xn--p1ai/%D0%B1%D0%B8%D0%BE%D0%B8%D0%BD%D1%84%D0%BE%D1%80%D0%BC%D0%B0%D1%82%D0%B8%D0%BA%D0%B0/#11