



Лекция № 2

Биоинформатика последовательностей Выравнивание

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Кафедра фармакологии и биоинформатики

Для студентов, обучающихся по направлению 06.03.01 «Биология»
профили Биохимия, Генетика
при изучении дисциплины «Биоинформатика»

П л а н л е к ц и и

- Парное и множественное выравнивание последовательностей.
- Методы сравнения первичной структуры белков.
- Программа Clustal.
- Система BLAST.
- Структурная биоинформатика.
- Виды вторичных структур.
- Мотивы и домены.

Биоинформатика последовательностей

- Выравнивание и определение сходства двух последовательностей
- Построение множественных выравниваний
- Распознавание генов
- Предсказание вторичной структуры белков и РНК
- Предсказание сайтов связывания белков

Формат FASTA

W. R. Pearson, D. J. Lipman – 1988

Строка-заголовок (the definition line)

> [уникальный ID] | [описание]

Последовательность белка (или ДНК) в однобуквенном коде

```
>sp|P35557|HXK4_HUMAN Hexokinase-4 OS=Homo sapiens
MLDDRARMEAAKKEKUEQILAEFQLQEEDLKKUMRRMQKEMDRGLRLETH
EEASUKMLPTYURSTPEGSEUGDFLSLDLGGTNFRUMLUKUGEGEEGQWS
UKTKHQMYSIPEDAMTGTAEMLFDYISECISDFLDKHQMKHKKLPLGFTF
SFPURHEDIDKGILLNWTKGFKASGAEGNNUUGLLRDAIKRRGDFEMDUU
AMUNDTUATMISCYEDHQCEUGMIUGTGACNACYMEEMQNVELUEGDEGR
MCUNTEWGAFGDSGELDEFLLDYDRLUDESSANPGQQLYEKLIIGGKYMGE
LURLULLRLUDENLLFHGEASEQLRTRGAFETRFUSQUESDTGDRKQIYN
ILSTLGLRPSTTDCDIURRACESUSTRAAHMCSAGLAGUINRMRESRSED
UMRITUGUDGSUYKLHPSFKERFHASURRLTPSCEITFIESEEGSGRGAA
LUSAUACKKACMLGQ
```

**Последовательность определяет функцию,
структуру и многие другие свойства
белка или ДНК**

Родственные белки имеют похожие свойства

Белки, похожие по последовательности,
похожи и по свойствам

Свойства можно предсказать, анализируя
изученные последовательности, похожие на
данную

**Гомологичные последовательности
имеют общее происхождение
(общего предка)**

Признаки гомологичности белков

Похожая аминокислотная последовательность

Сходная 3D-структура

Аналогичная функция

Средство поиска сходства

Выравнивание

«Идеальное выравнивание»

запись последовательностей одна под другой так, чтобы гомологичные фрагменты оказались друг под другом

домовой
скопидом
водомерка

лесовоз
ледоход

---лесо---воз
лед---оход---

Способы выравнивания

Цель

Максимальное количество совпадений

Расположить их друг под другом

Двигать друг относительно друга

Вставлять пробелы

Гэп (gap) – пропуск в последовательности

лесовоз

ледоход

---лесо---воз

лед---оход---

Типы выравнивания

Локальное

поиск наиболее похожих фрагментов

домовой скопид ом	домовой вод ом ерка	домов ой вод о мерка
------------------------------------	--------------------------------------	---------------------------------------

Глобальное

сравнение последовательностей целиком

лесовоз
ледоход

---лес о ---воз
лед--- о ход---

Матрица замен BLOSUM62

Ala	4																				
Arg	-1	5																			
Asn	-2	0	6																		
Asp	-2	-2	1	6																	
Cys	0	-3	-3	-3	9																
Gln	-1	1	0	0	-3	5															
Glu	-1	0	0	2	-4	2	5														
Gly	0	-2	0	-1	-3	-2	-2	6													
His	-2	0	1	-1	-3	0	0	-2	8												
Ile	-1	-3	-3	-3	-1	-3	-3	-4	-3	4											
Leu	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	4										
Lys	-1	2	0	-1	-3	1	1	-2	-1	-3	-2	5									
Met	-1	-1	-2	-3	-1	0	-2	-3	-2	1	2	-1	5								
Phe	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	6							
Pro	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	-2	-4	7						
Ser	1	-1	1	0	-1	0	0	0	-1	-2	-2	0	-1	-2	-1	4					
Thr	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5				
Trp	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	11			
Tyr	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	7		
Val	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	4	
	Ala	Arg	Asn	Asp	Cys	Gln	Glu	Gly	His	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val	

Критерии качества поиска

- ✓ Количество идентичных (похожих) аминокислот / нуклеотидов
 - для белков > 25 % при длине > 100 aa
 - для ДНК > 70 % при длине > 100 nt
- ✓ Длина выравнивания
- ✓ Вероятность наблюдать такое сходство случайным образом
 - E-value: < 10^{-6} – хорошо; > 0.001 – плохо
- ✓ Score – общая мера сходства
 - < 50 – плохо

Поиск и сравнение последовательностей

UniProt

<https://www.uniprot.org/>

225,6 млн. белков

5-HT_{2a} рецептор человека

UniProtKB | UniProtKB | Advanced | Search

BLAST Align Retrieve/ID mapping Peptide search SPARQL Help Contact

UniProt BETA The new UniProt website is here! Take me to UniProt BETA

UniProtKB - P28223 (5HT2A_HUMAN)

Display Help video BLAST Align Format Add to basket History Add a publication Feedback

Entry Publications Feature viewer Feature table

Protein **5-hydroxytryptamine receptor 2A**
Gene **HTR2A**
Organism *Homo sapiens (Human)*
Status Reviewed - Annotation score: ●●●●● - Experimental evidence at protein levelⁱ

Functionⁱ

Function
 Names & Taxonomy
 Subcellular location
 Pathology & Biotech
 PTM / Processing
 Expression
 Interaction
 Structure
 Family & Domains
 Sequences (2+)
 Similar proteins

G-protein coupled receptor for 5-hydroxytryptamine (serotonin) (PubMed:1330647, PubMed:18703043, PubMed:19057895).
Also functions as a receptor for various drugs and psychoactive substances, including mescaline, psilocybin, 1-(2,5-dimethoxy-4-iodophenyl)-2-aminopropane (DOI) and lysergic acid diethylamide (LSD) (PubMed:28129538).
Ligand binding causes a conformation change that triggers signaling via guanine nucleotide-binding proteins (G proteins) and modulates the activity of down-stream effectors (PubMed:28129538).
Beta-arrestin family members inhibit signaling via G proteins and mediate activation of alternative signaling pathways (PubMed:28129538).
Signaling activates phospholipase C and a phosphatidylinositol-calcium second messenger system that modulates the activity of phosphatidylinositol 3-kinase and promotes the release of Ca²⁺ ions from intracellular stores (PubMed:18703043, PubMed:28129538).
Affects neural activity, perception, cognition and mood (PubMed:18297054).
Plays a role in the regulation of behavior, including responses to anxiogenic situations and psychoactive substances. Plays a role in intestinal smooth muscle contraction, and may play a role in arterial vasoconstriction.

7 Publications

(Microbial infection) Acts as a receptor for human JC polyomavirus/JCPyV.

Последовательность 5-HT_{2A} Human

Sequences (2+)ⁱ

Sequence statusⁱ: Complete.

This entry describes **2** isoformsⁱ produced by **alternative splicing**. [Align](#) [Add to basket](#)

This entry has 2 described isoforms and 2 potential isoforms that are computationally mapped. [Show all](#) [Align All](#)

Isoform 1 (identifier: **P28223-1**) [UniProt] [FASTA](#) [Add to basket](#)

This isoform has been chosen as the canonicalⁱ sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.

[« Hide](#)

Length: 471

Mass (Da): 52,603

Last modified: June 1, 1994 - v2

Checksum:ⁱ EF8AAC0BC5379DA2

BLAST [GO](#)

```
      10      20      30      40      50
MDILCEENTS LSSTTNSLMQ LNDDTRLYSN DFNSGEANTS DAFNWTVDSE
      60      70      80      90     100
NRTNLSCEGC LSPSCLSL LH LQEKNSALL TAVVIILTIA GNILVIMAVS
     110     120     130     140     150
LEKKLQ NATN YFLMSLAIAD MLLGFLVMPV SMLTILYGYR WPLPSKLC AV
     160     170     180     190     200
WIYLDVLFST ASIMHLCAIS LDRYVAIQNP IHHSRFNSRT KAFLKIIAVW
     210     220     230     240     250
TISVGISMPI PVFGLQDDSK VFKEGSCLLA DDNFVLIGSF VSFFIPLTIM
     260     270     280     290     300
VITYFLTIKS LQKEATLCVS DLGTRAKLAS FSFLPQSSLS SEKLFQRSIH
     310     320     330     340     350
REPGSYTGRR TMSISNEQK ACKVLGIVFF L FVVMWCPFF ITNIMAVICK
     360     370     380     390     400
ESCNE DVIGA LLNVFVWIGY LSSAVNPLVY TLFNKTYRSA FSRYIQCYK
     410     420     430     440     450
ENKKPLQLIL VNTIPALAYK SSQLQMGQKK NSKQDAKTTD NDCSMVALGK
     460     470
QHSEEASKDN SDGVNEKVSC V
```

FASTA 5-HT_{2A} Human

```
>sp|P28223|5HT2A_HUMAN 5-hydroxytryptamine receptor 2A OS=Homo sapiens GN=HTR2A PE=1 SV=2
MDILCEENTSLSTTNSLMQLNDDTRLYSNDNFNSGEANTSDAFNWTVDSENRTNLSCEGC
LSPSCLSLHLQEKNSALLTAVVIILTIAGNILVIMAVSLEKKLQATNYFLMSLAID
MLLGFLVMPVSMLTILYGYRWPLPSKLCVMIYLDVLFSTASIMHLCAISLDRYVAIQNP
IHHSRFNSRKAFLKIIAVWTISVGISMPIPVFGLQDDSKVFKEGSCLLADDNFVLIGSF
VSFFIPLTIMVITYFLTIKSLQKEATLCVSDLGTRAKLASFSLPQSSLSSEKLFQRSIH
REPGSYTGRRTMQSISNEQKACKVLGIVFFLFVVMWCPFFITNIMAVICKESCNEVDVIGA
LLNVFVMWIGYLS SAVNPLVYTLFNKTYRSAFSRYIQCYKENKKPLQLILVNTIPALAYK
SSQLQMGQKNSKQDAKTTDNC SMVALGKQHSEEASKDNSDGVNEKVSCV
```

Поиск с помощью BLAST

UniProtKB Advanced

BLAST Align Retrieve/ID mapping Peptide search SPARQL Help Contact

The new UniProt website is here! [Take me to UniProt BETA](#)

UniProtKB - P28223 (5HT2A_HUMAN)

Display

Entry
Publications
Feature viewer
Feature table

Protein | **5-hydroxytryptamine receptor 2A**
Gene | **HTR2A**
Organism | *Homo sapiens (Human)*
Status | Reviewed - Annotation score: - Experimental evidence at protein levelⁱ

Functionⁱ


Function
 Names & Taxonomy
 Subcellular location
 Pathology & Biotech
 PTM / Processing
 Expression
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 Structure
 Family & Domains
 Sequences (2+)
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(Microbial infection) Acts as a receptor for human JC polyomavirus/JCPyV.

Поиск с помощью BLAST

Advanced Search

[BLAST](#) [Align](#) [Retrieve/ID mapping](#) [Peptide search](#) [SPARQL](#) [Help](#) [Contact](#)

BLAST Вводим последовательность и вызываем

How to use this tool

The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences, which can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families.

1. Enter either a protein or nucleotide sequence or a UniProt identifier (e.g. P00750 or A4_HUMAN or UPI0000000001) into the form field.
2. Optionally, change the program parameters with the dropdown menus under the form.
3. Click the *Run BLAST* button.

[Help](#) [BLAST help video](#) [Other tutorials and videos](#) [Downloads](#)

```
>sp|P28223|5HT2A_HUMAN 5-hydroxytryptamine receptor 2A OS=Homo sapiens OX=9606 GN=HTR2A PE=1 SV=2
MDILCEENTSLSSSTTNSLMQLNDDTRLYSNDFNSGEANTSDAFNWTVDSENRTNLSCEGC
LSPSCLSLHLQEKNSALLTAVVILTIAGNILVIMAVSLEKKLONATNYFLMSLATAD
MLLGFVMPVSMILTILYGYRWPLPSKLCVWVYLDVLFSTASIMHLCALSDRYVAIQNP
IHHSRFNSRTKAFPKIIAVWTISVGISMPIPVFGLODDSKVFKEGSCLLADDNFVLIGSF
VSFFIPLTIMVITYFLTIKSLQKATLCVSDLCTRAKLASFSLPOSSLSSEKLFQRSIH
REPGSYTGRRTMQSISNEQKACKVLGIVFFLVVMWCFFFITNIMAVICKESCNEVDVIGA
LLNVFVWIGYLSAVNPLVYTLFNKTYRSAFSRYIQCOYKENKKPLOLILVNTIPALAYK
SSQLQMGQKNSKQDAKTTDNDCSMVALGKQHSSEASKDNSDGVNEKVSVCV
```

Target database: UniProtKB reference proteomes plus Swiss-Prot

E-Threshold: 10

Matrix: Auto

Filtering: None

Gapped: yes

Hits: 250

Run BLAST in a separate window.

Tools	Core data	Supporting data	Information
BLAST	Protein knowledgebase (UniProtKB)	Literature citations	About UniProt
Align	Sequence clusters (UniRef)	Taxonomy	Help
We'd like to inform you that we have updated our Privacy Notice to comply with Europe's new General Data Protection Regulation (GDPR) that applies since 25 May 2018.			
Peptide search	Proteomes	Subcellular locations	UniProtKB manual
		Cross-referenced databases	Tech Do not show this banner again

Поиск с помощью BLAST

UniProtKB Advanced

BLAST Align Retrieve/ID mapping Peptide search SPARQL Help Contact

BLAST Ищет ...

Job status: **RUNNING**

Running **blastp** job against **UNIPROTKB_REFPROTSWISSPROT** for 14s

Job information

Query sequence	<pre>>ep P28223 5HT2A_HUMAN 5-hydroxytryptamine receptor 2A OS=Homo sapiens OX=9606 GN=HTR2A PE=1 SV=2 MDILCEENTSLSSSTNSLMQLNDDTRLYSNDFNSEANTSDAFNWTVDSENRTNLSCEGC LSPSCLSLHLQEKNSALLTAVVVIILTIAGNILVIMAVSLEKKLQATNYFLMSLAIAID MLLGFPLVMPVSMILTILYGYRWPLPSKLCVWIIYLDVLFSTASIMHLCAISLDRYVAIQNP IHHSRFRNSRTRKFLKII LAVWTISVGI SMP I PVFGLQDSDSKVFEKGSCLLADDNFVLIGSF VSFFIPLTIMVITYFLTIKSLQKEATLCVSDLGTRAKLASFSFLPQSSLSSEKLFQRSIH REFGSYTGRRMQSISNEQKACKVLGIVFFLVVMWCPFFITNIMAVICKESCNEVDVIGA LLNVFVWIGYLSSAVNPLVYTLFNKTYRSAPFSRYIQCYKENKKPLQLILVNTIPALAYK SSQLQMGQKNSKQDARTTDNDCSMVALGKQHSSEASKDNSDGVNEKVVSCV</pre>
Job identifier	B2022021592C7BAECDB1C5C413EE0E0348724B68202E5956 (jobs are stored for 7 days)
Program	blastp
Matrix	blosum62
Threshold	10
Filtered	false
Gapped	true
Maximum number of hits reported	250

Tools	Core data	Supporting data	Information
BLAST	Protein knowledgebase (UniProtKB)	Literature citations	About UniProt
Align	Sequence clusters (UniRef)	Taxonomy	Help
Retrieve/ID mapping	Sequence archive (UniParc)	Keywords	FAQ

Поиск с помощью BLAST

UniProtKB Advanced Search

BLAST Align Retrieve/ID mapping Peptide search SPARQL Help Contact

BLAST Результат — начало списка

About BLAST Basket

Filter by:

- Reviewed (9) Swiss-Prot
- Unreviewed (241) TrEMBL
- With 3D structure (2)

Popular organisms

- Human (1)
- Mouse (1)
- Rat (1)
- Bovine (2)
- GORGO (1)

All (250)

Map to

- UniProtKB
- UniRef
- UniParc

View by

- Results table
- Taxonomy
- Text version
- XML version

Demo

Identity %

Order by: Score

Overview

Show all 250

Entry	Protein names	Match hit	Identity
P28223	5-hydroxytryptamine receptor 2A (Homo sapiens)		100.0%
A0A2I2YKA3	5-hydroxytryptamine receptor 2A (Gorilla gorilla gorilla)		100.0%
A0A2R8Z5S4	5-hydroxytryptamine receptor 2A (Pan paniscus)		99.8%
A0A2J8J9Q7	5-hydroxytryptamine receptor 2A (Pan troglodytes)		99.8%

Alignments

1 to 25 of 250 Show 25

Entry	Alignment overview	Info	Status
Query: sp P28223 SHT2A_HUMAN B20220215A084FC58F6BBA219896F365D15F2EB4402E18CT			
P28223	SHT2A_HUMAN - 5-hydroxytryptamine receptor 2A Homo sapiens (Human) - View alignment	E-value: 0.0 Score: 2,416 Ident.: 100.0%	
A0A2I2YKA3	A0A2I2YKA3_GORGO - 5-hydroxytryptamine receptor 2A - Gorilla gorilla ... - View alignment	E-value: 0.0 Score: 2,416 Ident.: 100.0%	
A0A2R8Z5S4	A0A2R8Z5S4_PANPA - 5-hydroxytryptamine receptor 2A - Pan paniscus (Py... - View alignment	E-value: 0.0 Score: 2,415	

Сравнение последовательностей

Clustal

Multiple Sequence Alignment

<http://www.clustal.org/>

Clustal



Clustal: Multiple Sequence Alignment

Multiple alignment of nucleic acid and protein sequences



Clustal Omega

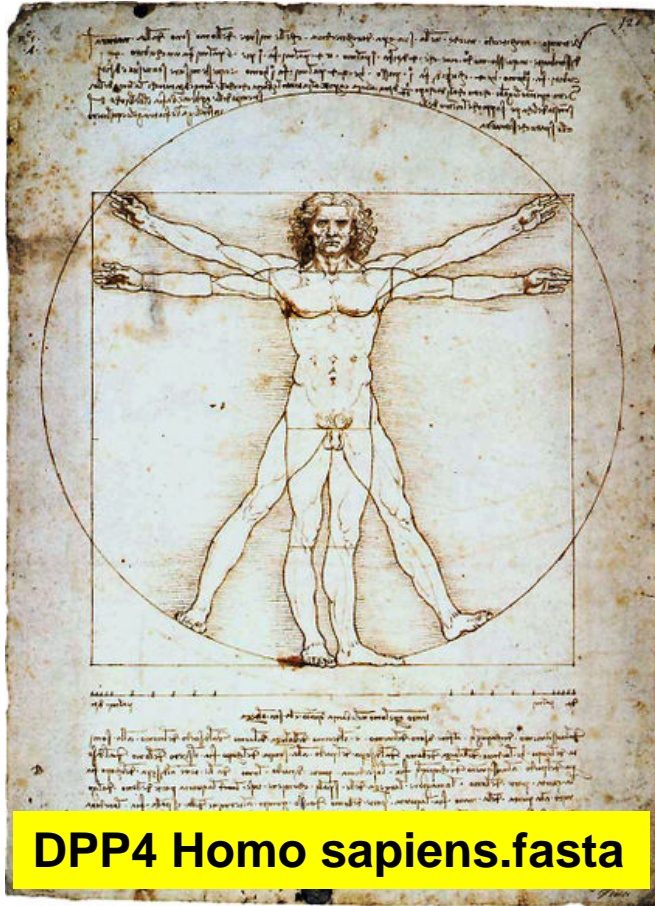
- Latest version of Clustal - fast and scalable (can align hundreds of thousands of sequences in hours), greater accuracy due to new HMM alignment engine
- Command line/web server only (GUI public beta available soon)



ClustalW/ClustalX

- "Classic Clustal"
- GUI (ClustalX), command line (ClustalW), web server versions available

Dipeptidyl peptidase 4 — DPP-4



DPP4 Homo sapiens.fasta

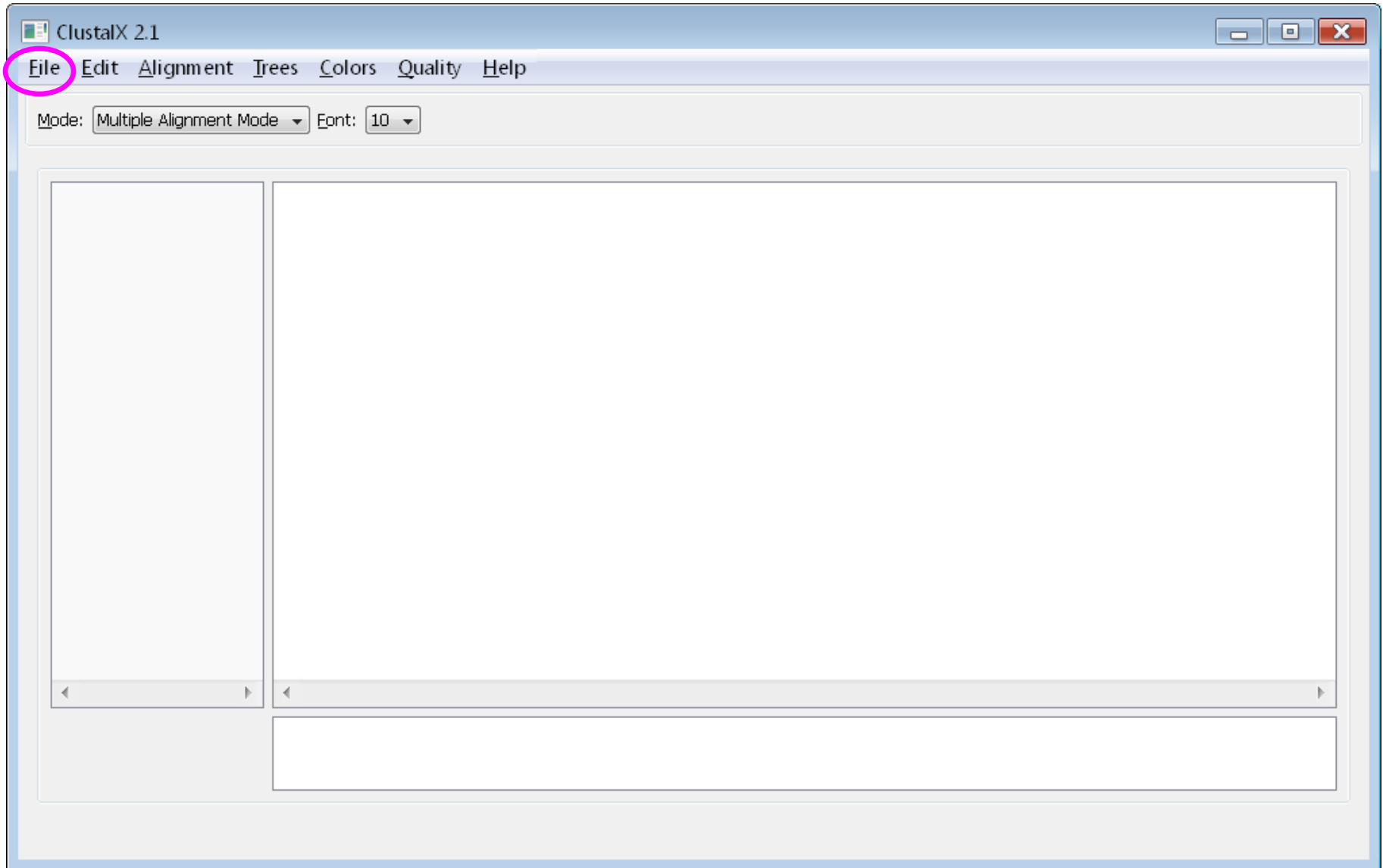


DPP4 Equus caballus.fasta

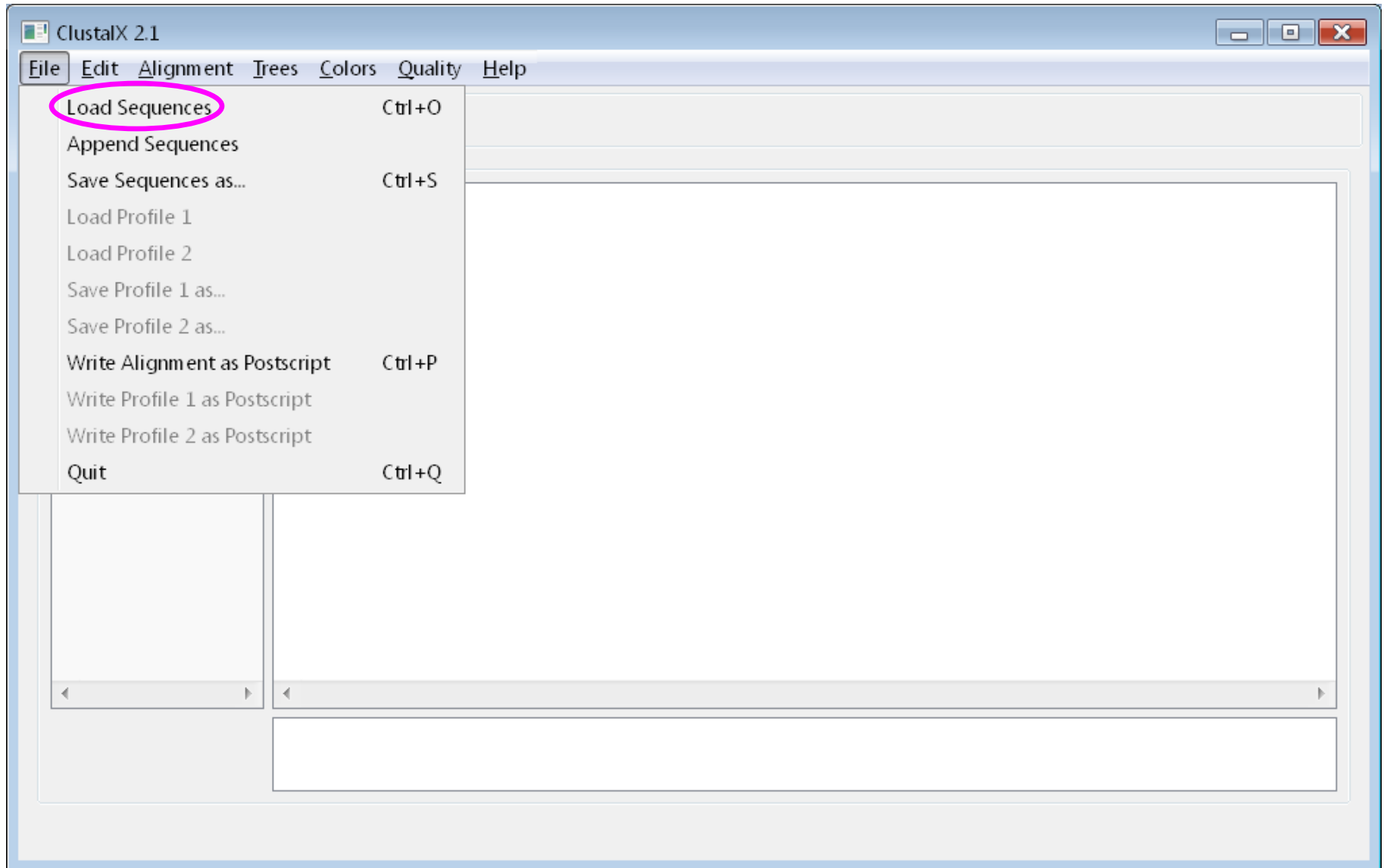


DPP4 Danio rerio.fasta

Clustal



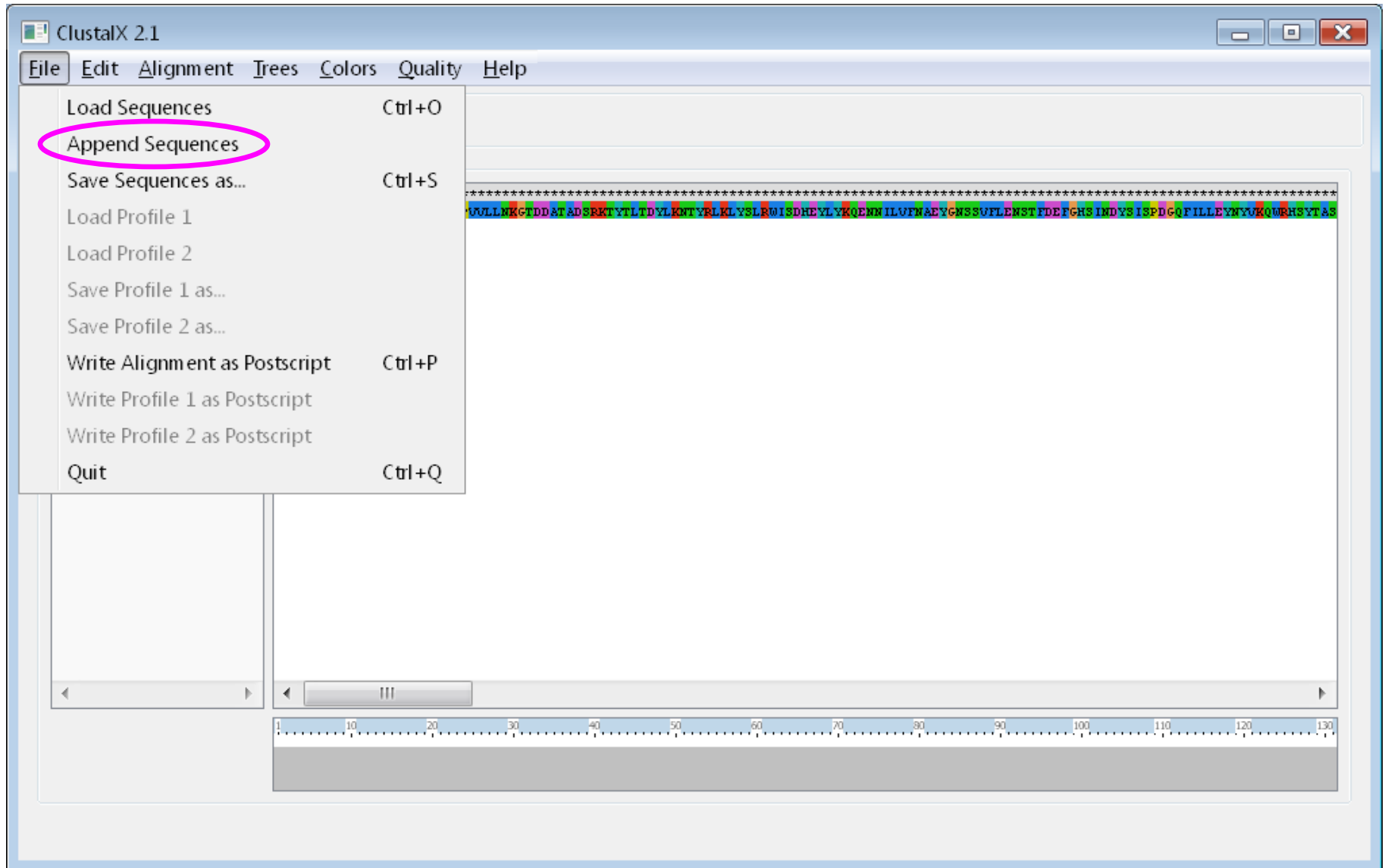
Clustal — загрузка



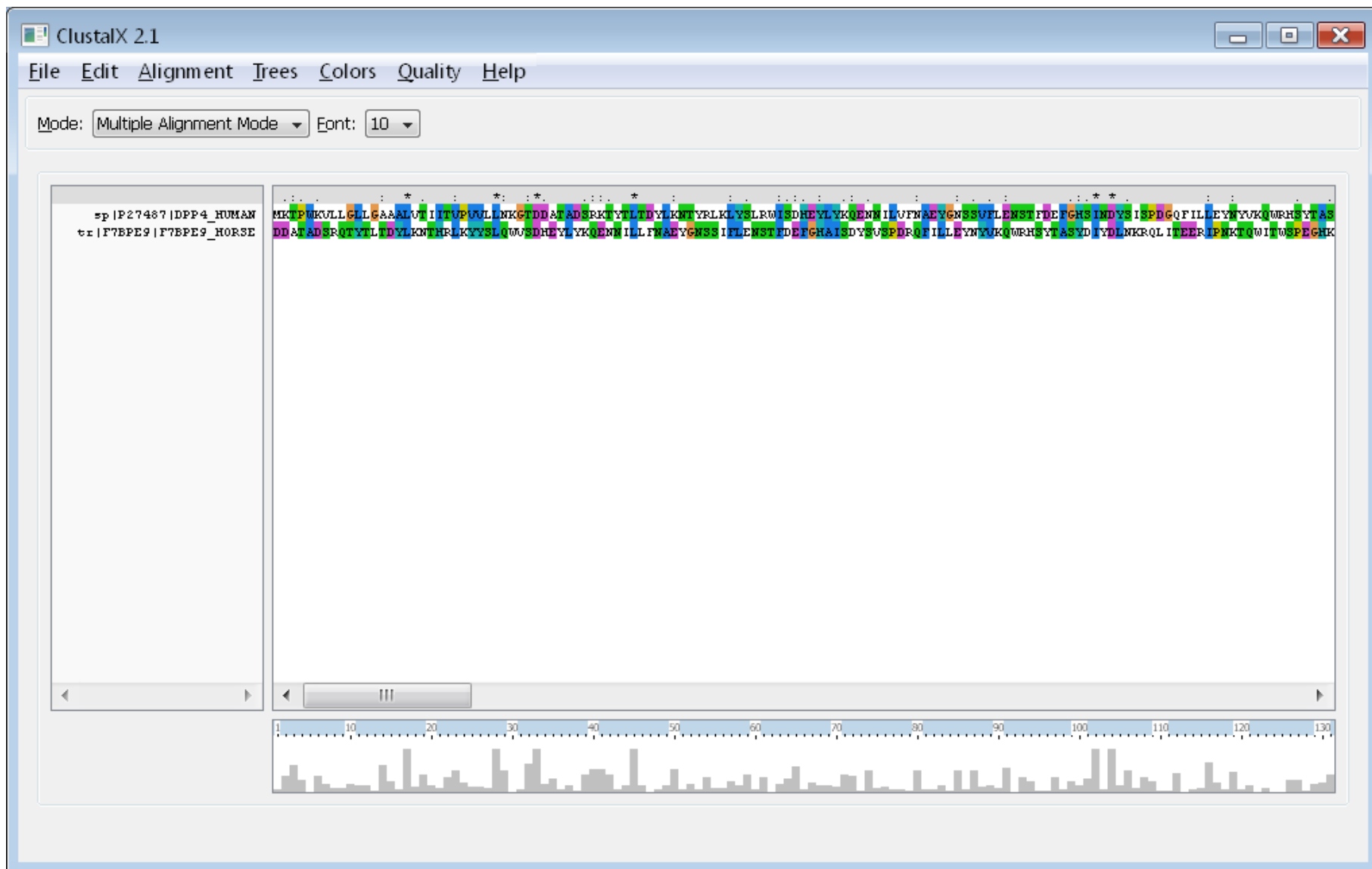
Clustal — DPP-4 Human

The screenshot displays the ClustalX 2.1 software interface. The window title is "ClustalX 2.1". The menu bar includes "File", "Edit", "Alignment", "Trees", "Colors", "Quality", and "Help". The "File" menu is circled in pink. Below the menu bar, there are two dropdown menus: "Mode: Multiple Alignment Mode" and "Font: 10". The main workspace is divided into two panes. The left pane shows a sequence identifier: "sp | P27487 | DPP4_HUMAN". The right pane displays a single line of protein sequence: "MKTPKRVLLGLLGAAALVTIITVPWVLLKGTDDATADSRRTYILTDYLNKTYRLKLYSLRQISDHEVLYKQENMILVFNAEYGNSSVFLFNSTFDEFGHSINDYSISPDCQFILLEYNVYKQQRHSYTAG". The sequence is color-coded by amino acid type. A horizontal scrollbar is located below the sequence, and a scale bar at the bottom indicates positions from 1 to 130.

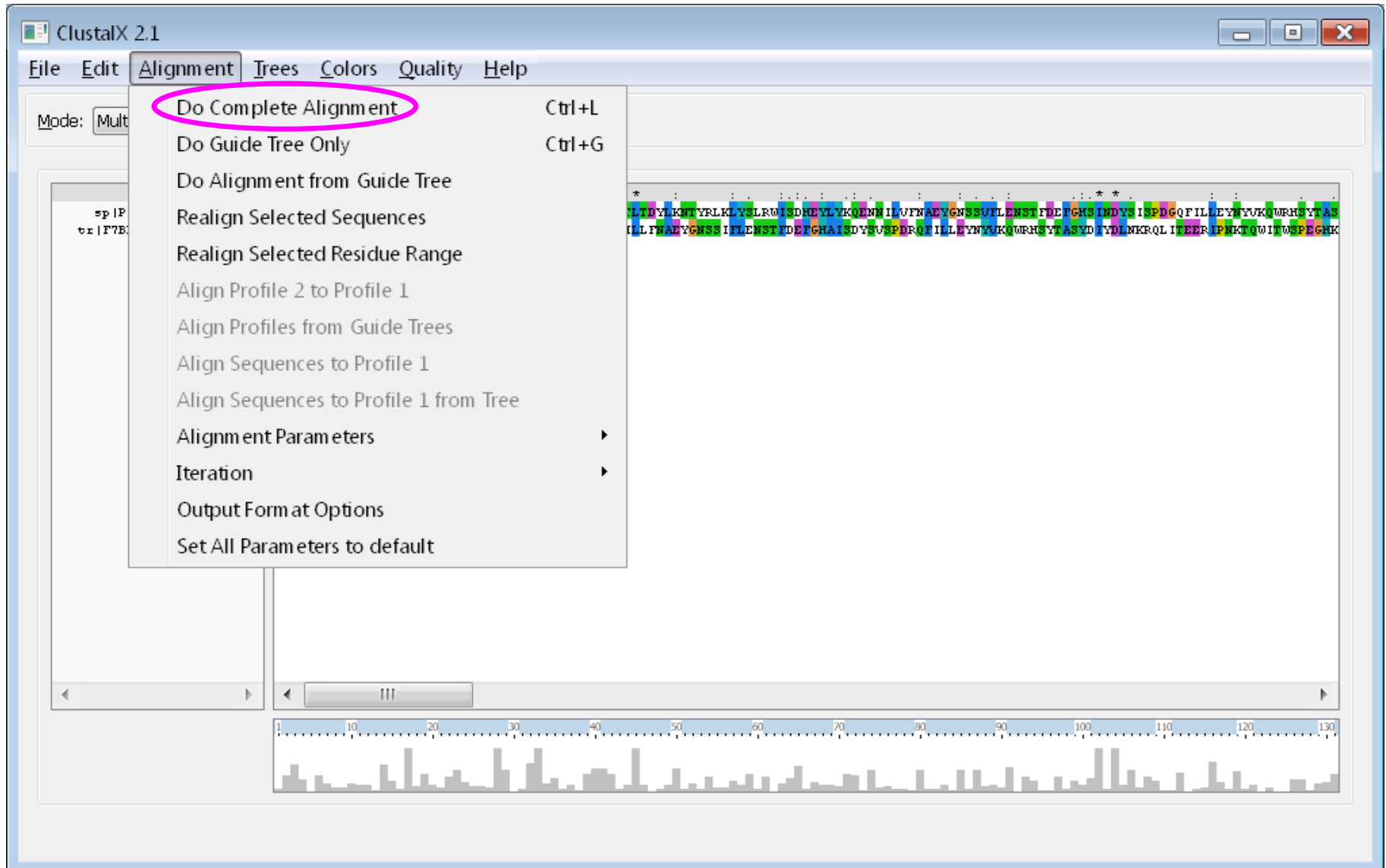
Clustal — добавление



Clustal — DPP-4 Human & Horse



Clustal — выравнивание



Clustal — результат

ClustalX 2.1

File Edit Alignment Trees Colors Quality Help

Mode: Multiple Alignment Mode Font: 10

```

>p|P27487|DPP4_HUMAN MKTPEKQLLGLLGAALVTIITVPOVLLNKGTD DATADSRKTYFLTDYLENTYRLKLYSLRNI SDHEVLYKQENN ILVFNAEYGNSSVPLENST FDEFGHSINDVSI SPDGFILLEYNYVKQQRHSYTA S
<r|F7BPE9|F7BPE9_HORSE DDATADSRQTYFLTDYLENTYRLKLYSLRNI SDHEVLYKQENN ILLFNAEYGNSSIFLENSTFDEFGHAI SDVYSVSPDRQFILLEYNVYKQQRHSYTA S

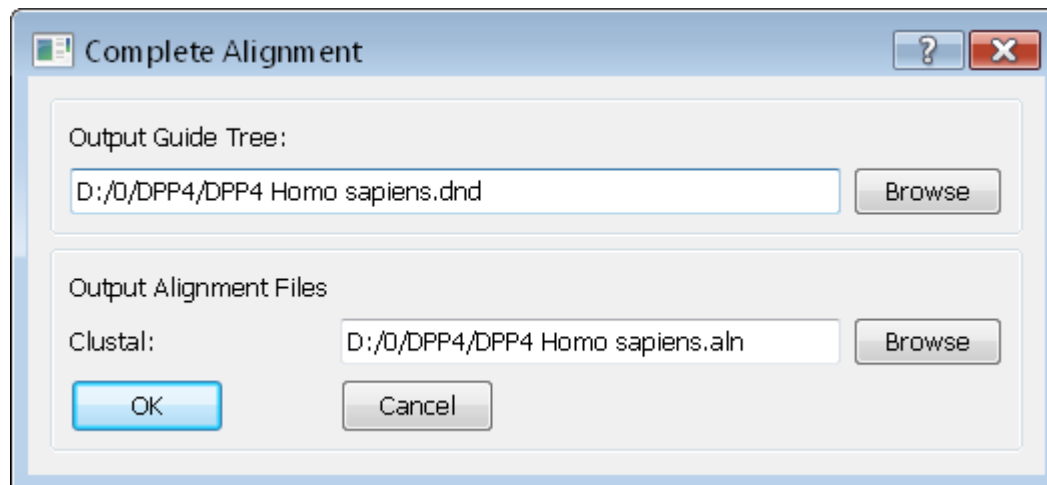
```

CLUSTAL-Alignment file created [D:/0/DPP4/DPP4 Homo sapiens.aln]

Clustal — DPP-4

Human – Horse 0.0477

Human – Danio 0.2156



Поиск и сравнение последовательностей

BLAST

Basic Local Alignment

Search Tool

<https://blast.ncbi.nlm.nih.gov/>

BLAST



U.S. National Library of Medicine
National Center for Biotechnology Information

Log in

BLAST®

[Home](#) [Recent Results](#) [Saved Strategies](#) [Help](#)

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)

ElasticBLAST is here!

NEWS

ElasticBLAST is a new cloud based tool to run your BLAST searches faster and make you more effective.

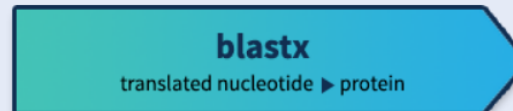
Mon, 07 Feb 2022 12:00:00 EST

[More BLAST news...](#)

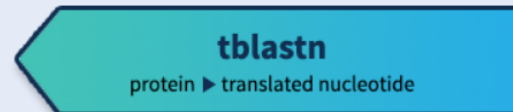
Web BLAST



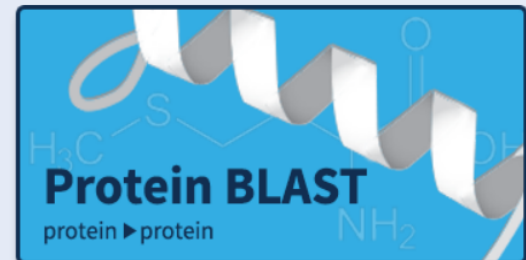
Nucleotide BLAST
nucleotide ► nucleotide



blastx
translated nucleotide ► protein



tblastn
protein ► translated nucleotide



Protein BLAST
protein ► protein

BLAST Genomes

Enter organism common name, scientific name, or tax id

Search

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[Mouse](#)

[Rat](#)

[Microbes](#)

Protein BLAST



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Standard Protein BLAST

[blastn](#)

[blastp](#)

[blastx](#)

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BLASTP programs search protein databases using a protein query. [more...](#)

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Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

Query subrange [?](#)

From

To

Or, upload file

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Job Title

Enter a descriptive title for your BLAST search [?](#)

[Align two or more sequences](#) [?](#)

Choose Search Set

Database

[?](#)

Organism

Optional

exclude [Add organism](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. [?](#)

Exclude

Optional

Models (XM/XP) Non-redundant RefSeq proteins (WP) Uncultured/environmental sample sequences

Program Selection

Algorithm

- Quick BLASTP (Accelerated protein-protein BLAST)
- blastp** (protein-protein BLAST)
- PSI-BLAST (Position-Specific Iterated BLAST)
- PHI-BLAST (Pattern Hit Initiated BLAST)
- DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm [?](#)

Protein BLAST

Загружаем и вызываем ...

Uniprot - Поиск в Google https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blastp Поиск

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Standard Protein BLAST

blastn blastp **blastx** tblastn tblastx

Enter Query Sequence BLASTP programs search protein databases using a protein query. [more...](#) [Reset page](#) [Bookmark](#)

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) [Query subrange](#)

```
>sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine receptor 4 OS=Homo sapiens
GX=9606 GN=HTR4 PE=1 SV=2
MDKLDANVSSSEEGFSGVEKYLITFLSTVILMALLGULLMVAVCNDRQLRKIKIVFIV
SLAFADLVSVLVMPFGAIEDVDIWIIEVFCVRLSDVLLTASIFLCCISLQRYK
ATCCQPLVIRHMTFLRDLMLGGCVIFETISFLFMAGGNNIGLIDLEKRFQNSM
STVCYENKGFIAITCSVAFLVIFFLMVLAVRIYVTAKEHARQIOMLORAGASSESE
```

From

To

Or, upload file

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database

Organism exclude

Enter organism name or id—completions will be suggested

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

Exclude Models (XM/XP) Non-redundant RefSeq proteins (WP) Uncultured/environmental sample sequences

Program Selection

Algorithm

- Quick BLASTP (Accelerated protein-protein BLAST)
- blastp (protein-protein BLAST)
- PSI-BLAST (Position-Specific Iterated BLAST)
- PHI-BLAST (Pattern Hit Initiated BLAST)
- DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

BLAST Search database nr using Blastp (protein-protein BLAST)

Show results in a new window

[+ Algorithm parameters](#)

5-HT4 Human

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Protein BLAST

Ищет ...

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Uniprot - Поиск в Google x https://www.u...Q13639.fasta x NCBI Blast...Q13639.fasta

https://blast.ncbi.nlm.nih.gov/Blast.cgi 90% Поиск

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BLAST® » blastp suite » RID-4S629D3F016 Home Recent Results Saved Strategies Help

Format Request Status

[Formatting options]

Job Title: sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine...

Request ID	4S629D3F016
Status	Searching
Submitted at	Tue Feb 18 12:00:57 2020
Current time	Tue Feb 18 12:01:04 2020
Time since submission	00:00:06

This page will be automatically updated in 2 seconds

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5-HT4 Human

Protein BLAST

Результаты — начало списка

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National Center for Biotechnology Information

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[< Edit Search](#) [Save Search](#) [Search Summary](#)

Job Title: **sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine...**

RID: 4S629D3F016

Program: BLASTP

Database: nr

Query ID: lc|Query_48713

Description: sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine receptor 4 OS ...

Molecule type: amino acid

Query Length: 388

Other reports: [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#)

Filter Results

Organism: exclude

Percent Identity: to E value: to Query Coverage: to

[Filter](#) [Reset](#)

Descriptions **Graphic Summary** Alignments Taxonomy

hover to see the title click to show alignments Show Conserved Domains

Alignment Scores: <40 40-50 50-80 80-200 >=200

100 sequences selected Putative conserved domains have been detected, click on the image below for detailed results.

Query seq. TM helix 1 TM helix 2 putative ligand binding site TM helix 3 TM helix 4 TM helix 5 TM helix 6 TM helix 7

Specific hits: 7tmA_5-HT4

Superfamilies: 7tm_GPCRs super-family

Distribution of the top 100 Blast Hits on 100 subject sequences

Query

1 70 140 210 280 350

Feedback

Protein BLAST

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BLAST » blastp suite » results for RID-4S629D3F016

Job Title: sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine...
RID: 4S629D3F016
Program: BLASTP
Database: nr
Query ID: lc|Query_48713
Description: sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine receptor 4 OS ...
Molecule type: amino acid
Query Length: 388

Filter Results

Organism: only top 20 will appear
Type common name, binomial, taxid or group name
+ Add organism

Percent Identity: [] to []
E value: [] to []
Query Coverage: [] to []

Filter Reset

Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments

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select all 100 sequences selected

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform b [Homo sapiens]	805	805	100%	0.0	100.00%	NP_000861.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform X1 [Pan troglodytes]	804	804	100%	0.0	99.74%	XP_001162339.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine 4 receptor subunit b [Homo sapiens]	803	803	100%	0.0	99.74%	CA58392.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform X2 [Pongo abelii]	802	802	100%	0.0	99.48%	XP_002816104.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform X2 [Nomascus leucogenys]	802	802	100%	0.0	99.48%	XP_003266662.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform X2 [Hylobates moloch]	798	798	100%	0.0	98.97%	XP_032014192.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform X1 [Macaca mulatta]	796	796	100%	0.0	98.45%	XP_028705660.1
<input checked="" type="checkbox"/>	PREDICTED: 5-hydroxytryptamine receptor 4 isoform X2 [Macaca fascicularis]	796	796	100%	0.0	98.45%	XP_005558258.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine (serotonin) receptor 4, isoform CRA_a [Homo sapiens]	796	796	100%	0.0	96.52%	EA061799.1
<input checked="" type="checkbox"/>	PREDICTED: 5-hydroxytryptamine receptor 4 isoform X1 [Saimiri boliviensis boliviensis]	795	795	100%	0.0	98.45%	XP_003934044.1
<input checked="" type="checkbox"/>	PREDICTED: 5-hydroxytryptamine receptor 4 isoform X3 [Chlorocebus sabaeus]	794	794	100%	0.0	98.20%	XP_008013110.1
<input checked="" type="checkbox"/>	PREDICTED: 5-hydroxytryptamine receptor 4 isoform X1 [Callithrix jacchus]	793	793	100%	0.0	98.20%	XP_008985741.1

Feedback

Protein BLAST

Детализация

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Uniprot - Поиск в Google x https://www.u...Q13639.fasta x

https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_XP_001162339

80%

Поиск

Description sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine receptor 4 OS ...

Molecule type amino acid

Query Length 388

Other reports [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#) ?

Percent Identity to **E value** to **Query Coverage** to

Filter **Reset**

Descriptions **Graphic Summary** **Alignments** Taxonomy

Alignment view **Download** ▾

1 sequences selected ?

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5-hydroxytryptamine receptor 4 isoform X1 [Pan troglodytes]

Sequence ID: [XP_001162339.1](#) Length: 388 Number of Matches: 1

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Range 1: 1 to 388 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
804 bits(2077)	0.0	Compositional matrix adjust.	387/388(99%)	388/388(100%)	0/388(0%)
Query 1	MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCNDRLRRIKTNFYIV	60			
MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCNDRLRRIKTNFYIV					
Sbjct 1	MDKLDANVSSEEGFGSVEKVVLLTFLSTVILMAILGNLLVMVAVCNDRLRRIKTNFYIV	60			
Query 61	SLAFADLLSVLVMPPFGAIELVQDIWIYGEVFCFLVRTSLDVLVLTASIFHLCCISLDRYY	120			
SLAFADLLSVLVMPPFGAIELVQDIWIYGE+FCFLVRTSLDVLVLTASIFHLCCISLDRYY					
Sbjct 61	SLAFADLLSVLVMPPFGAIELVQDIWIYGEVFCFLVRTSLDVLVLTASIFHLCCISLDRYY	120			
Query 121	AICCCQLVYRNKMTPLRIALMLGGCQWVPTFFISFLPIMQGWNNGIIDLIEKRKFNQNSN	180			
AICCCQLVYRNKMTPLRIALMLGGCQWVPTFFISFLPIMQGWNNGIIDLIEKRKFNQNSN					
Sbjct 121	AICCCQLVYRNKMTPLRIALMLGGCQWVPTFFISFLPIMQGWNNGIIDLIEKRKFNQNSN	180			
Query 181	STYCVFMVKNKPYAIFCSVVAFYIPFLLMVLAYRIVYVTAKEHAHQIQMLQRAGASSESRP	240			
STYCVFMVKNKPYAIFCSVVAFYIPFLLMVLAYRIVYVTAKEHAHQIQMLQRAGASSESRP					
Sbjct 181	STYCVFMVKNKPYAIFCSVVAFYIPFLLMVLAYRIVYVTAKEHAHQIQMLQRAGASSESRP	240			
Query 241	QSADQHS THRMRTETKAARKTLCIIMGCFCLCWAPFFVTNI VDPFIDYTVPGQVWTAFLWL	300			
QSADQHS THRMRTETKAARKTLCIIMGCFCLCWAPFFVTNI VDPFIDYTVPGQVWTAFLWL					
Sbjct 241	QSADQHS THRMRTETKAARKTLCIIMGCFCLCWAPFFVTNI VDPFIDYTVPGQVWTAFLWL	300			
Query 301	GYNSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPCSTTTINGSTHVLRD	360			
GYNSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPCSTTTINGSTHVLRD					
Sbjct 301	GYNSGLNPFLYAFLNKSFRRAFLIILCCDDERYRRPSILGQTVPCSTTTINGSTHVLRD	360			
Query 361	AVECGGQWESQCHFPATSPLVAAQPSDT 388				
AVECGGQWESQCHFPATSPLVAAQPSDT					
Sbjct 361	AVECGGQWESQCHFPATSPLVAAQPSDT 388				

Related Information

- [Gene](#) - associated gene details
- [Genome Data Viewer](#) - aligned genomic context
- [Identical Proteins](#) - Identical proteins to XP_001162339.1

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Protein BLAST

Таксономия и филогенез

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Job Title **sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine...**

RID **4S629D3F016** Search expires on 02-20 00:00 am [Download All](#)

Program **BLASTP** [Citation](#)

Database **nr** [See details](#)

Query ID **lc|Query_48713**

Description **sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine receptor 4 OS ...**

Molecule type **amino acid**

Query Length **298**

Other reports [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#)

Filter Results

Organism *only top 20 will appear* exclude

Type common name, binomial, taxid or group name

[Add organism](#)

Percent Identity to E value to Query Coverage to

[Filter](#) [Reset](#)

Descriptions **Graphic Summary** Alignments **Taxonomy**

Sequences producing significant alignments [Download](#) [Manage Columns](#) Show **100**

select all 100 sequences selected [GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#)

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform b [Homo sapiens]	805	805	100%	0.0	100.00%	NP_000861.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform X1 [Pan troglodytes]	804	804	100%	0.0	99.74%	XP_001162339.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine 4 receptor subunit b [Homo sapiens]	803	803	100%	0.0	99.74%	CAD58392.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform X2 [Pongo abelii]	802	802	100%	0.0	99.48%	XP_002816104.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform X2 [Nomascus leucogenys]	802	802	100%	0.0	99.48%	XP_003266662.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform X2 [Hylobates moloch]	798	798	100%	0.0	98.97%	XP_032014192.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine receptor 4 isoform X1 [Macaca mulatta]	796	796	100%	0.0	98.45%	XP_028705660.1
<input checked="" type="checkbox"/>	PREDICTED: 5-hydroxytryptamine receptor 4 isoform X2 [Macaca fascicularis]	796	796	100%	0.0	98.45%	XP_005558258.1
<input checked="" type="checkbox"/>	5-hydroxytryptamine (serotonin) receptor 4, isoform CRA_a [Homo sapiens]	796	796	100%	0.0	96.52%	EAW61799.1
<input checked="" type="checkbox"/>	PREDICTED: 5-hydroxytryptamine receptor 4 isoform X1 [Saimiri boliviensis boliviensis]	795	795	100%	0.0	98.45%	XP_003934044.1
<input checked="" type="checkbox"/>	PREDICTED: 5-hydroxytryptamine receptor 4 isoform X3 [Chlorocebus sabaeus]	794	794	100%	0.0	98.20%	XP_008013110.1
<input checked="" type="checkbox"/>	PREDICTED: 5-hydroxytryptamine receptor 4 isoform X1 [Callithrix jacchus]	793	793	100%	0.0	98.20%	XP_008985741.1

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Protein BLAST

Парное сравнение

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Uniprot - Поиск в Google x https://www.uniprot.org/blast/align-two

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Proteins&PROGRAM=blastp&BLAST_PROGRAMS=blastp 80% Поиск

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Align Sequences Protein BLAST

blastn blastp blastx tblastn tblastx

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Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) Query subrange

>sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine receptor 4 OS=Homo sapiens OX=9606 GN=HTR4 PE=1 SV=2
MDKLDANVSSSEEGFGSVKVVLLTFLSTVILMALLGNLLVMVAVCWDRQLRKIKNYFIV
SLAFADLLVSLVMPFGAIELVQDIWYGEVFCILVRTSLDVLITASIFHLCCISLDRY
AICCPFLVYRNMPLRIALMLGSCWVIFPFISFLPVMQSWNNIGIIDLEKRFKQNSN
STYCVFMVKFYAITCSVVFYIIPFLMLVAYFYIYVIAKEHAKIQMLQRAGASSESRP
...
Or, upload file Файл не выбран.

Job Title Enter a descriptive title for your BLAST search

Align two or more sequences

Enter Subject Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) Subject subrange

...
BLASLFFVIVASGLTFFLFSQALICFTYCRILLAAKQAVQVASTIGMASQASITLQVE
RTFRPGVESADSRRLAKHRSKALKAASLTLGILLGVEFVITWLEFFVANIVQVCCDISGG
LFDVITVLGYCNSINPILYELPMDPKRALGFLGCFRCPSRQASLASFLSITSHSGE
RFGLSQQVLELFLFPDSDSDSAGSGSSGRLTAQLILPSSATQDFELFTRAAAVNI
FNIDPAAFLRBRHRLGLFIN
...
Or, upload file Файл не выбран.

Program Selection

Algorithm blastp (protein-protein BLAST)
Choose a BLAST algorithm

BLAST Search protein sequence using Blastp (protein-protein BLAST)
 Show results in a new window

[Algorithm parameters](#)

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5-HT4 Human

5-HT6 Human

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График результатов

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https://blast.ncbi.nlm.nih.gov/Blast.cgi 80% Поиск

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Job Title sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine

RID 4S83U6WV114 [Search expires on 02-20 00:35 am](#) [Download All](#)

Program Blast 2 sequences [Citation](#)

Query ID lcl|Query_12329 (amino acid)

Query Descr sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine receptor 4 OS ...

Query Length 388

Subject ID lcl|Query_12331 (amino acid)

Subject Descr sp|P50406|5HT6R_HUMAN 5-hydroxytryptamine receptor 6 OS ...

Subject Length 440

Other reports [Multiple alignment](#) [MSA viewer](#)

Descriptions [Graphic Summary](#) [Alignments](#) **Dot Plot**

Plot of lcl|Query_12329 vs lcl|Query_12331

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Protein BLAST

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https://blast.ncbi.nlm.nih.gov/Blast.cgi 80% Поиск

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Job Title sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine
RID 4S83U6WV114 *Search expires on 02-20 00:35 am* [Download All](#) [v](#)
Program Blast 2 sequences [Citation](#) [v](#)
Query ID Icl|Query_12329 (amino acid)
Query Descr sp|Q13639|5HT4R_HUMAN 5-hydroxytryptamine receptor 4 OS ...
Query Length 388
Subject ID Icl|Query_12331 (amino acid)
Subject Descr sp|P50406|5HT6R_HUMAN 5-hydroxytryptamine receptor 6 OS ...
Subject Length 440
Other reports [Multiple alignment](#) [MSA viewer](#) [?](#)

Filter Results

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E value to
Query Coverage to
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Descriptions [Graphic Summary](#) [Alignments](#) [Dot Plot](#)

Sequences producing significant alignments [Download](#) [Manage Columns](#) [Show](#) 100 [?](#)

select all 0 sequences selected [Graphics](#) [Multiple alignment](#)

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/>	sp P50406 5HT6R_HUMAN 5-hydroxytryptamine receptor 6 OS=Homo sapiens OX=9606 GN=HTR6 PE=1 SV=1	172	172	80%	6e-54	33.84%	Query_12331

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