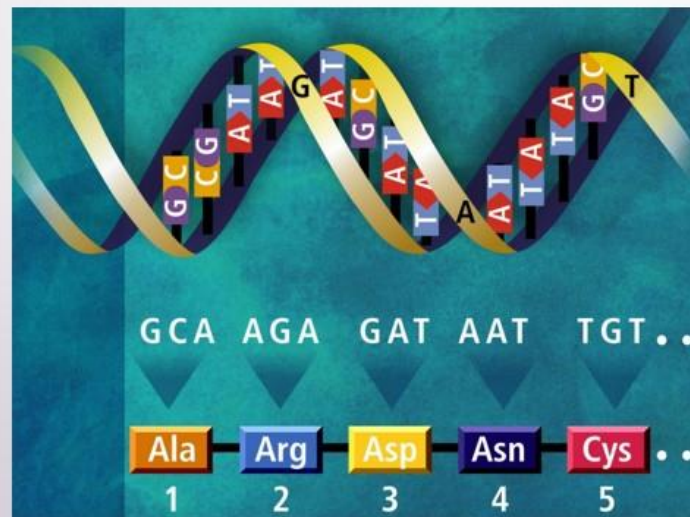


Методы экологической генетики и биоинформатики

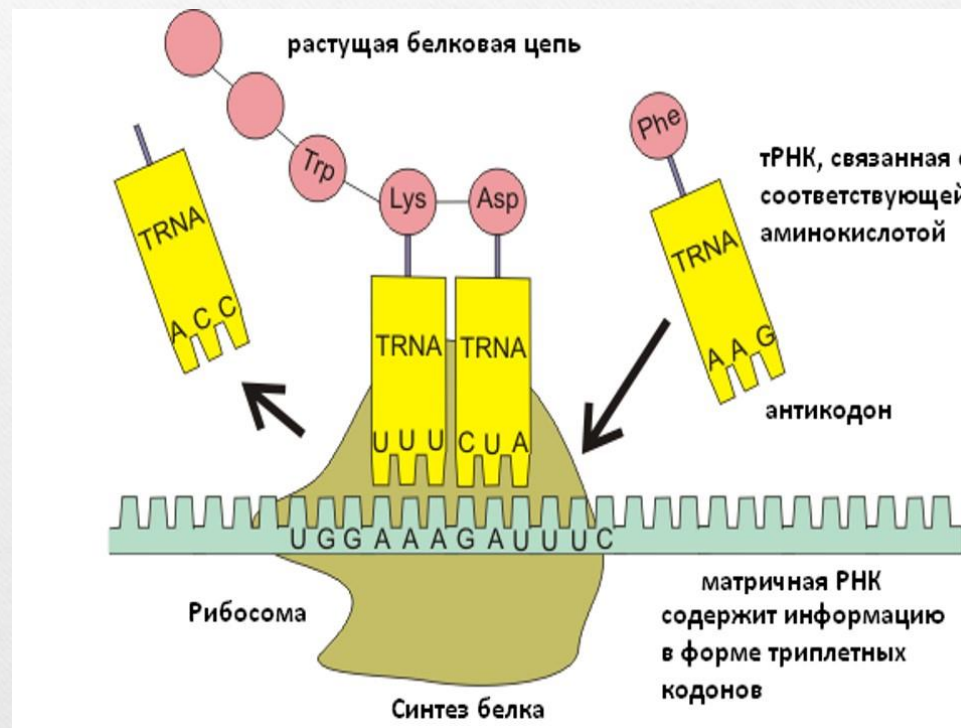
**Биоинформатика
(генетические исследования)**

ГЕНЕТИЧЕСКИЙ КОД. СПОСОБ ЗАПИСИ ГЕНЕТИЧЕСКОЙ ИНФОРМАЦИИ В ДНК



Свойства генетического кода

Триплетность генетического кода



Свойства генетического кода

Специфичность (однозначность)

- означает, что определённый кодон соответствует только одной аминокислоте

Например УЦГ соответствует аминокислоте СЕР и никакой другой

Круговое представление генетического кода

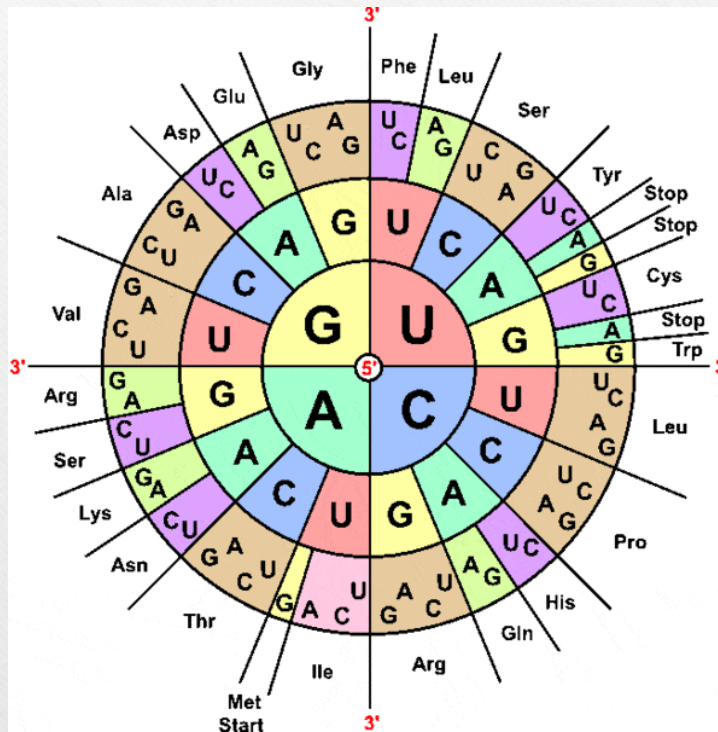
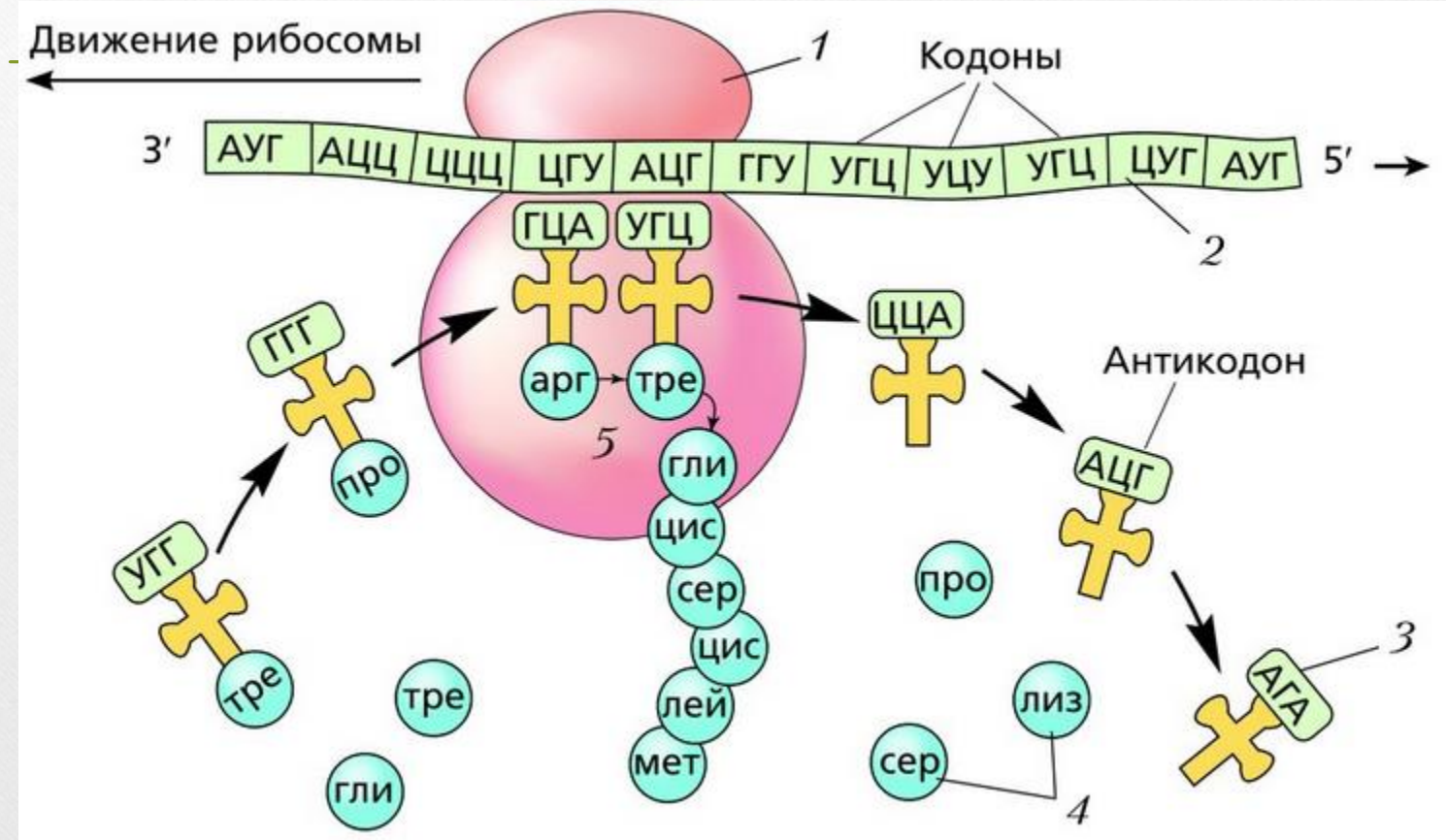


Таблица генетического кода

		Нуклеотид				
1-й	2-й				3-й	
	У	Ц	А	Г		
У	УУУ } Фенилаланин УУЦ } УУА } Лейцин УУГ }	УЦУ } УЦЦ } Серин УЦА } УЦГ }	УАУ } Тирозин УАЦ } УАА } стоп-кодона УАГ }	УГУ } Цистеин УГЦ } УГА } стоп-кодон УГГ } Триптофан	У Ц А Г	
Ц	ЦУУ } ЦУЦ } Лейцин ЦУА } ЦУГ }	ЦЦУ } ЦЦЦ } Пролин ЦЦА } ЦЦГ }	ЦАУ } Гистидин ЦАЦ } ЦАА } Глютамин ЦАГ }	ЦГУ } ЦГЦ } ЦГА } ЦГГ } Аргинин	У Ц А Г	
А	АУУ } АУЦ } Изолейцин АУА } АУГ } Метионин <i>старт-кодон</i>	АЦУ } АЦЦ } Треонин АЦА } АЦГ }	ААУ } ААЦ } Аспарагин ААА } ААГ } Лизин	АГУ } АГЦ } Серин АГА } АГГ } Аргинин	У Ц А Г	
Г	ГУУ } ГУЦ } ГУА } ГУГ } Валин	ГЦУ } ГЦЦ } ГЦА } ГЦГ } Аланин	ГАУ } ГАЦ } Аспарагиновая кислота ГАА } ГАГ } Глутаминовая кислота	ГГУ } ГГЦ } ГГА } ГГГ } Глицин	У Ц А Г	

Свойства генетического кода

Однонаправленность считывания



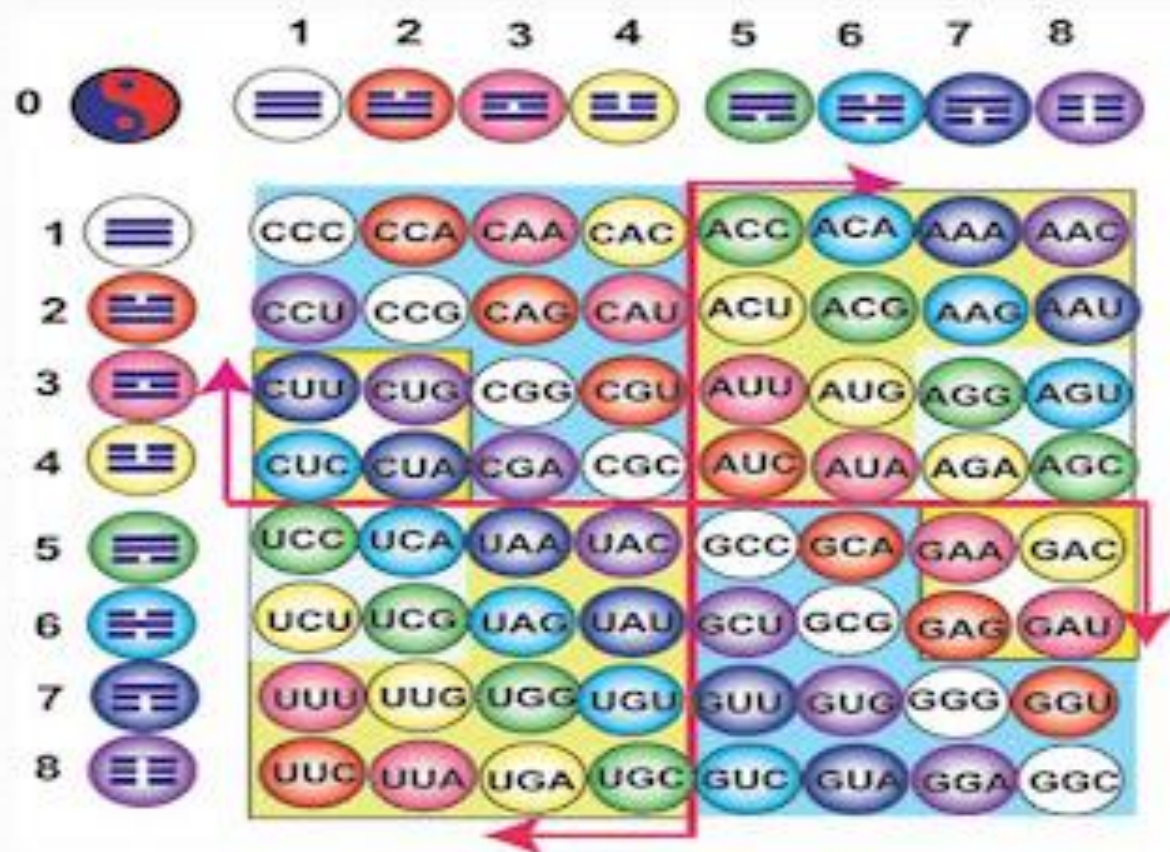
Свойства генетического кода

Однонаправленность считывания

- КОДОНЫ СЧИТЫВАЮТСЯ В ОДНОМ
направлении - от первого
нуклеотида к последующим

Генетические доказательства

Универсальность генетического кода



Один и тот же
триплет
кодирует один и
тот же тип
аминокислоты
у всех



Свойства генетического кода

Универсальность

- все свойства генетического кода характерны для всех живых организмов

Свойства генетического кода

НЕПЕРЕКРЫВАЕМОСТЬ

Каждый нуклеотид входит в состав лишь одного кодона.

ATGGTAATTCCG

кодон 1 кодон 4 кодон 7 кодон 10

кодон 2 кодон 5 кодон 8 кодон

кодон 3 кодон 6 кодон 9 ко..

Свойства генетического кода

Непрерывность

- отсутствие внутригенных знаков препинания

Неперекрываемость

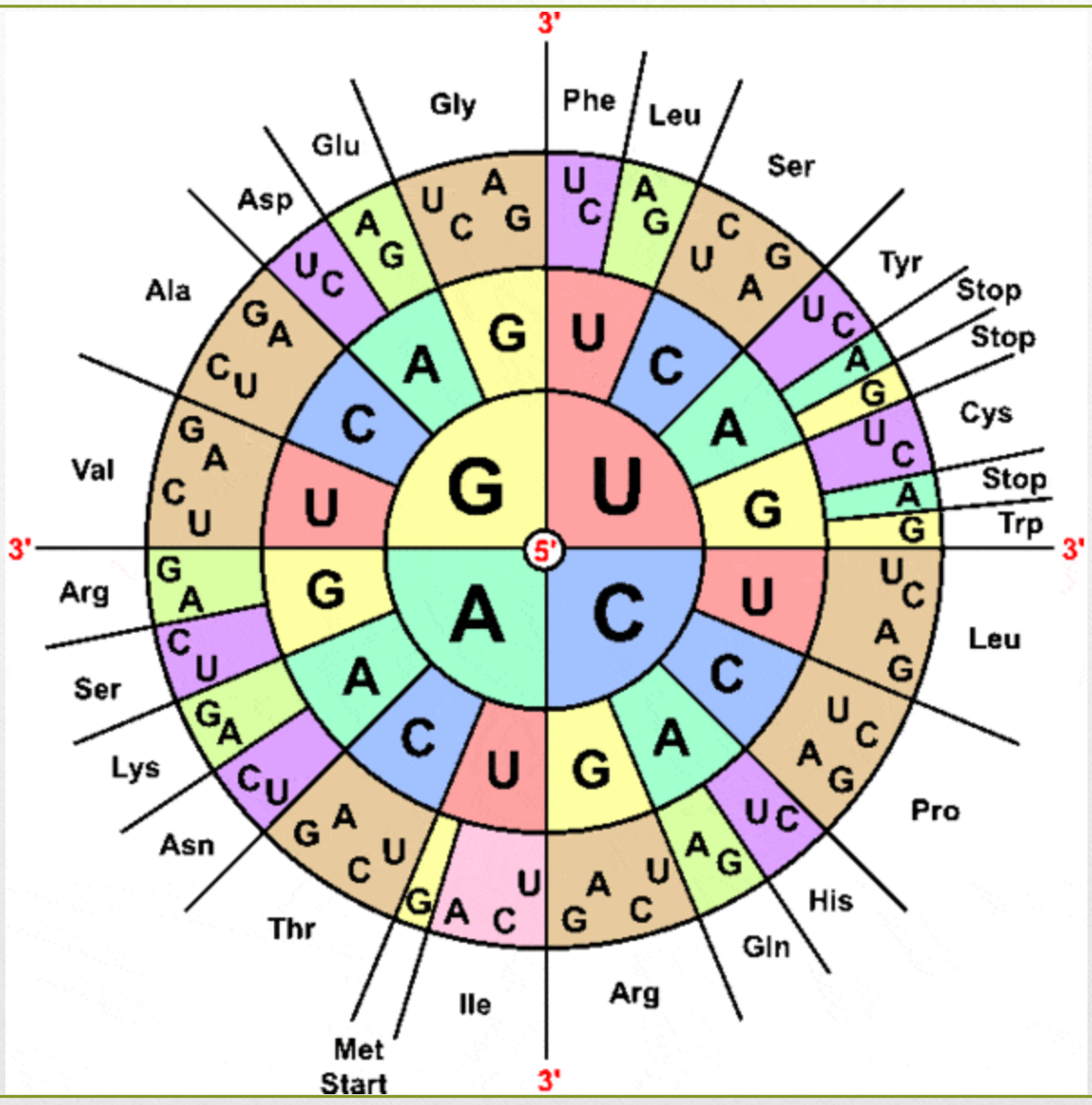
- каждый из триплетов генетического текста независим друг от друга, один нуклеотид входит в состав только одного триплета

Основные свойства генетического кода

- триплетность;
- вырожденность (избыточность);
- специфичность;
- универсальность;
- непрерывность;
- неперекрываемость;
- однонаправленность ($5' \rightarrow 3'$) считывания

Таблица генетического кода

		Нуклеотид					
1-й		2-й				3-й	
		У	Ц	А	Г		
У	УУУ	Фенилаланин	УЦУ	Тирозин	УГУ	Цистеин	У
	УУЦ		УЦЦ		УГЦ		Ц
	УУА		УЦА		УГА		А
	УУГ		УЦГ		УГГ		Г
		Лейцин	Серин	стоп-кодона	Триптофан		
Ц	ЦУУ	Лейцин	ЦЦУ	Гистидин	ЦГУ	Аргинин	У
	ЦУЦ		ЦЦЦ		ЦГЦ		Ц
	ЦУА		ЦЦА		ЦГА		А
	ЦУГ		ЦЦГ		ЦГГ		Г
		Лейцин	Пролин	Глютамин	Аргинин		
А	АУУ	Изолейцин	АЦУ	Аспарагин	АГУ	Серин	У
	АУЦ		АЦЦ		АГЦ		Ц
	АУА		АЦА		АГА		А
	АУГ		АЦГ		АГГ		Г
		Метионин старт-кодон	Треонин	Лизин	Аргинин		
Г	ГУУ	Валин	ГЦУ	Аспарагиновая кислота	ГГУ	Глицин	У
	ГУЦ		ГЦЦ		ГГЦ		Ц
	ГУА		ГЦА		ГГА		А
	ГУГ		ГЦГ		ГГГ		Г
		Валин	Аланин	Глутаминовая кислота	Глицин		



Примеры

- иРНК ucg = УЦГ = Ser (Серин)
- иРНК cac = ЦАЦ = His (Гистидин)
- иРНК acg = АЦГ = Thr (Треонин)
- иРНК ggg = ГГГ = Gly (Глицин)
- иРНК agg = АГГ = Arg (Аргинин)

Таблица аминокислот

Таблица названий и обозначений аминокислот

A	Ala	Alanine	Аланин
R	Arg	Arginine	Аргинин
N	Asn	Asparagine	Аспарагин
D	Asp	Aspartic Acid	Аспарагиновая кислота
C	Cys	Cysteine	Цистеин
Q	Gln	Glutamine	Глутамин
E	Glu	Glutamic Acid	Глутаминовая кислота
G	Gly	Glycine	Глицин
H	His	Histidine	Гистидин
I	Ile	Isoleucine	Изолейцин
L	Leu	Leucine	Лейцин
K	Lys	Lysine	Лизин
M	Met	Methionine	Метионин
F	Phe	Phenylalanine	Фенилаланин
P	Pro	Proline	Пролин
S	Ser	Serine	Серин
T	Thr	Threonine	Треонин
W	Trp	Tryptophan	Триптофан
Y	Tyr	Tyrosine	Тирозин
V	Val	Valine	Валин

Таблица названий и обозначений аминокислот

A	Ala	Alanine	Аланин
R	Arg	Arginine	Аргинин
N	Asn	Asparagine	Аспарагин
D	Asp	Aspartic Acid	Аспарагиновая кислота
C	Cys	Cysteine	Цистеин
Q	Gln	Glutamine	Глутамин
E	Glu	Glutamic Acid	Глутаминовая кислота
G	Gly	Glycine	Глицин
H	His	Histidine	Гистидин
I	Ile	Isoleucine	Изолейцин
L	Leu	Leucine	Лейцин
K	Lys	Lysine	Лизин
M	Met	Methionine	Метионин
F	Phe	Phenylalanine	Фенилаланин
P	Pro	Proline	Пролин
S	Ser	Serine	Серин
T	Thr	Threonine	Треонин
W	Trp	Tryptophan	Триптофан
Y	Tyr	Tyrosine	Тирозин
V	Val	Valine	Валин

Примеры

- иРНК ucg = Ser (Серин) = S
- иРНК cac = His (Гистидин) = H
- иРНК acg = Thr (Треонин) = T
- иРНК ggg = Gly (Глицин) = G
- иРНК agg = Arg (Аргинин) = R

Примеры

иРНК сас uscг сас асг gggg agg

=

Н S Н Т G R

ИЛИ

иРНК сасuscгсасасcggggagg

=

HSHTGR

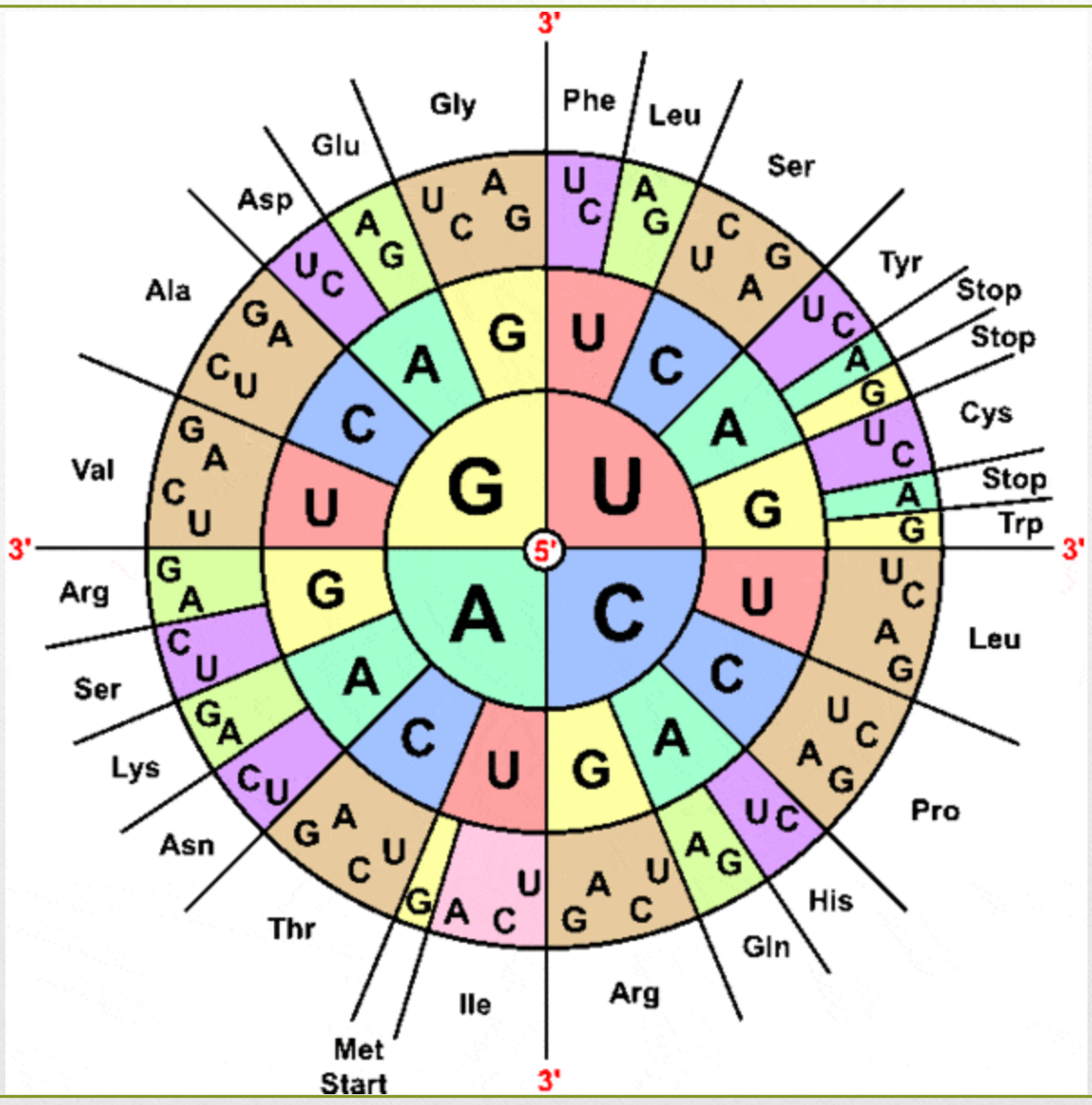
Примеры

иРНК

сга aaa aau aaa uuu gac cuc

=

???



Примеры

иРНК

сга ааа ааи ааа иии гас сис

=

ЦГА ААА ААУ ААА УУУ ГАЦ ЦУЦ

=

Таблица генетического кода

		Нуклеотид											
1-й		2-й				3-й							
		У	Ц	А	Г								
У	УУУ	Фенилаланин	УЦУ	УАУ	УГУ	У							
	УУЦ						Серин	УАЦ	УГЦ	Ц			
	УУА									Лейцин	УАА	УГА	А
	УУГ												УАГ
ЦУУ	Лейцин	ЦЦУ	ЦАУ	ЦГУ	У								
ЦУЦ						Пролин	ЦАЦ	ЦГЦ	Ц				
ЦУА									Гистидин	ЦАА	ЦГА	А	
ЦУГ												Глютамин	ЦАГ
АУУ	Изолейцин	АЦУ	ААУ	АГУ	У								
АУЦ						Треонин	ААЦ	АГЦ	Ц				
АУА									Метионин	ААА	АГА	А	
АУГ												ААГ	АГГ
Г	ГУУ	Валин	ГЦУ	ГАУ	ГГУ				У				
	ГУЦ					Аланин	ГАЦ	ГГЦ		Ц			
	ГУА									Аспарагиновая кислота	ГАА	ГГА	А
	ГУГ												Глутаминовая кислота

Таблица названий и обозначений аминокислот

A	Ala	Alanine	Аланин
R	Arg	Arginine	Аргинин
N	Asn	Asparagine	Аспарагин
D	Asp	Aspartic Acid	Аспарагиновая кислота
C	Cys	Cysteine	Цистеин
Q	Gln	Glutamine	Глутамин
E	Glu	Glutamic Acid	Глутаминовая кислота
G	Gly	Glycine	Глицин
H	His	Histidine	Гистидин
I	Ile	Isoleucine	Изолейцин
L	Leu	Leucine	Лейцин
K	Lys	Lysine	Лизин
M	Met	Methionine	Метионин
F	Phe	Phenylalanine	Фенилаланин
P	Pro	Proline	Пролин
S	Ser	Serine	Серин
T	Thr	Threonine	Треонин
W	Trp	Tryptophan	Триптофан
Y	Tyr	Tyrosine	Тирозин
V	Val	Valine	Валин

Примеры

иРНК

сга aaa aau aaa uuu gac cuc

=

R K N K F D L

Примеры

иРНК сга ааа ааи ааа ииу гас сис

=

R K N K F D L

или

иРНК сгааааааиаааиуигассис

=

RKKNKFDL

Пример с кодом ДНК

1 gggtcagact 10

11 ttgtcagaac 20

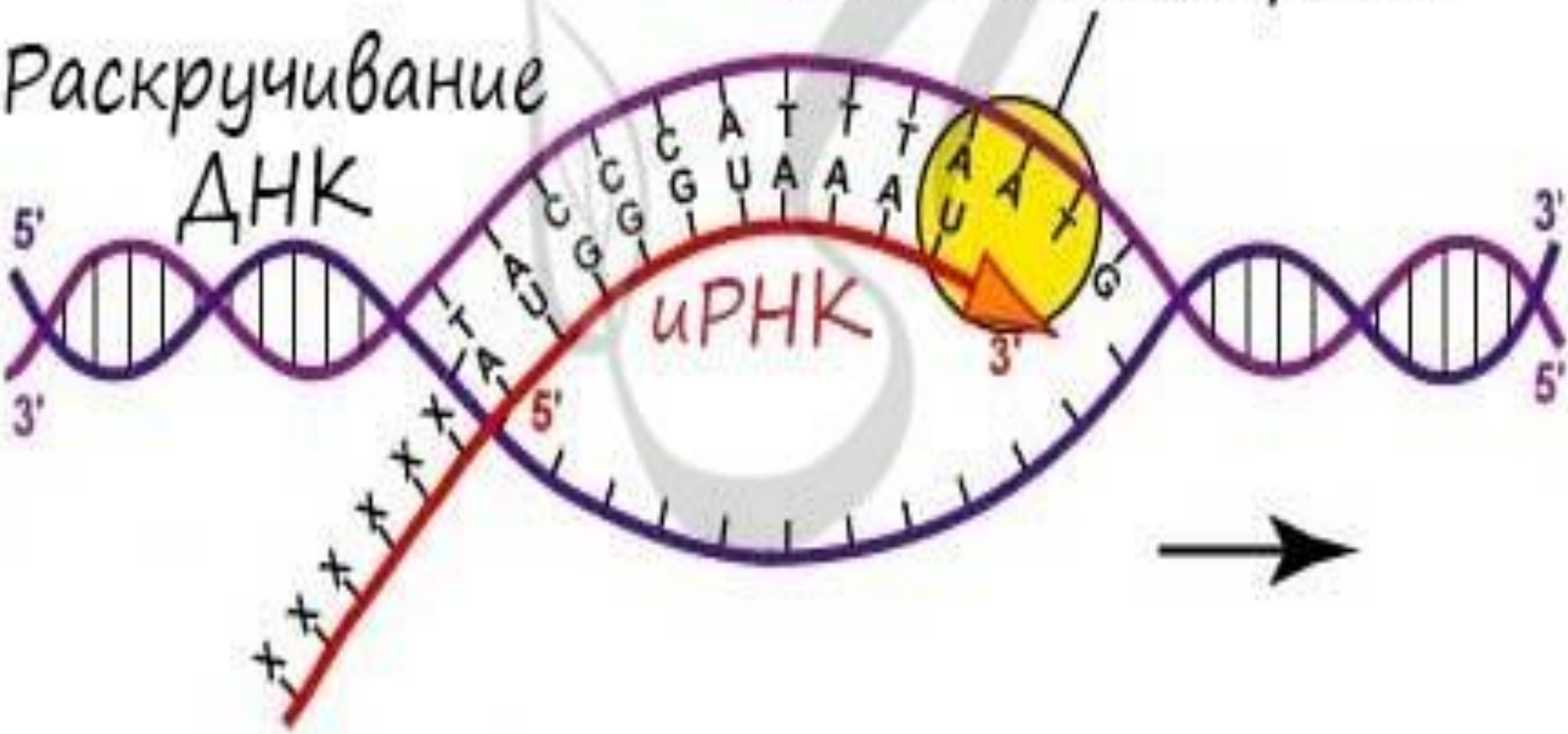
21 cagtagtcga 30

Транскрипция

синтез иРНК на матрице ДНК

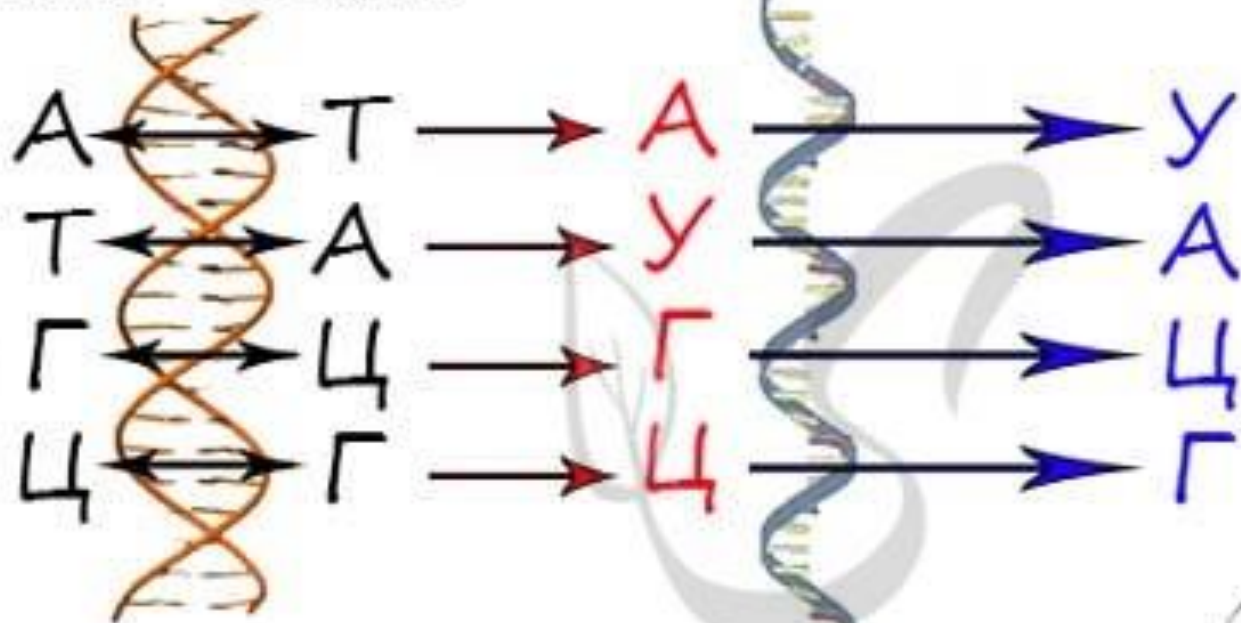
РНК полимераза

Раскручивание
ДНК



Ваш генетический словарь

1 нить 2 нить



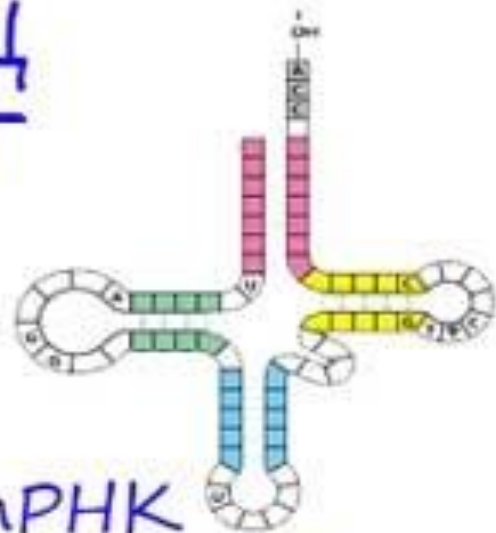
Внутри
ДНК

Между

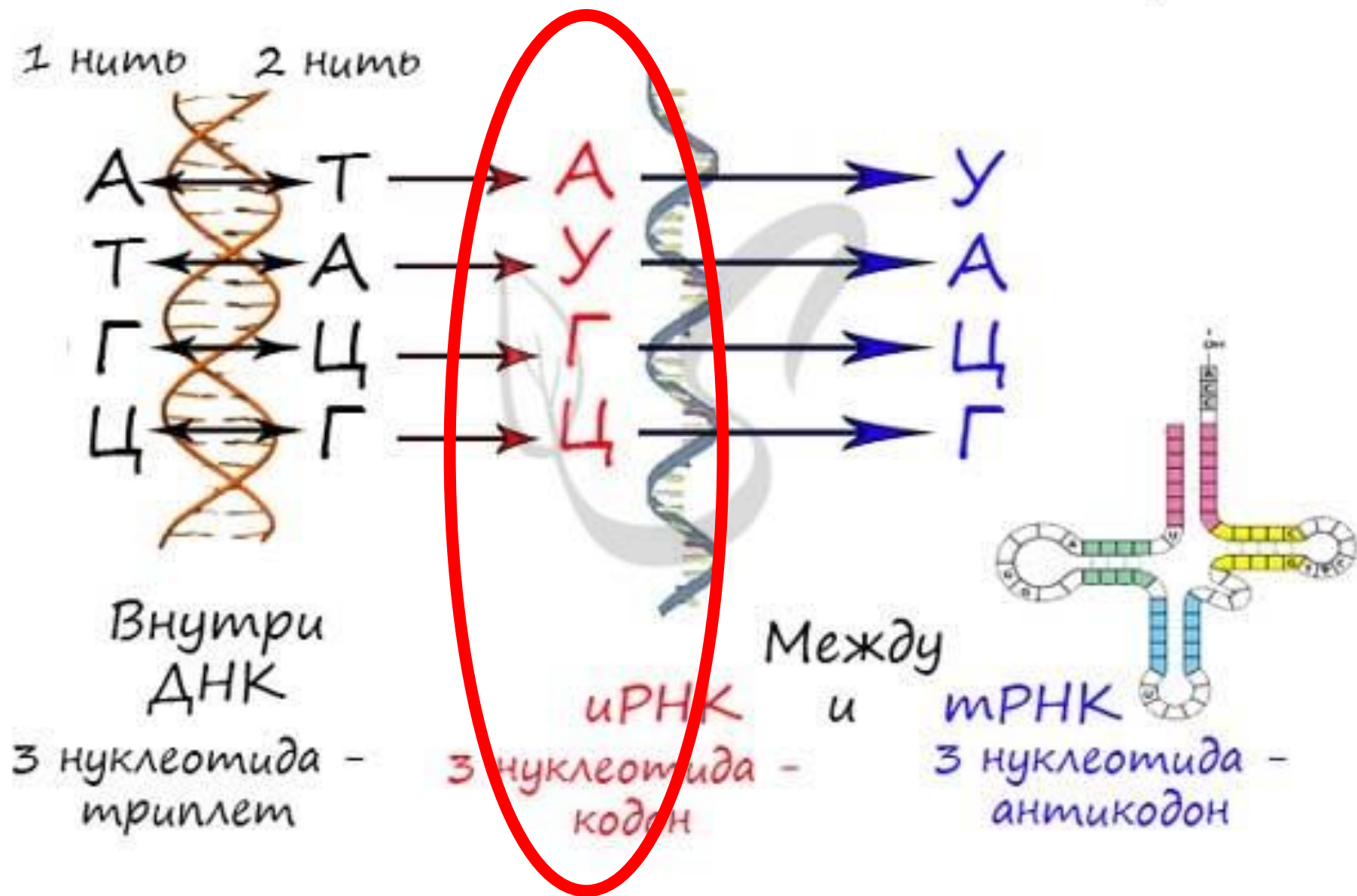
3 нуклеотида -
триплет

иРНК
3 нуклеотида -
кодон

и тРНК
3 нуклеотида -
антикодон



Ваш генетический словарь



Код ДНК

1 gggtcagact 10

11 ttgtcagaac 20

21 cagtagtcga 30

Триплетный код ДНК

ggg tca gac ttt gtc aga acc
agt agt cga

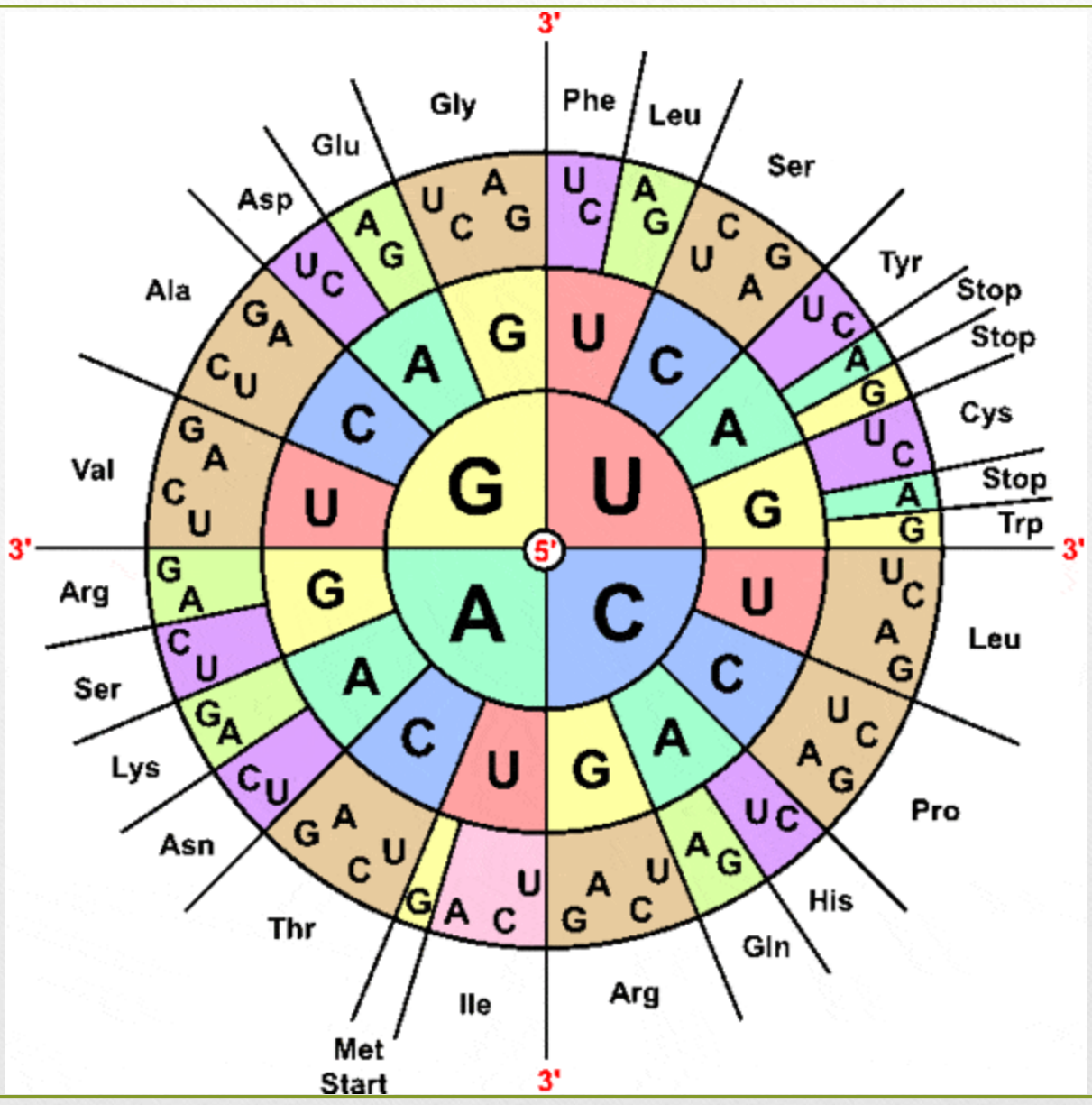
*Триплетный код ДНК
транскрипция в кодон иРНК*

ДНК ggg tca gac ttt gtc
aga acc agt agt cga

иРНК ссс agu cug aaa cag
ucu ugg uca uca gcu

Кодон иРНК

5' - ссс агу суг ааа с аг
у су угг уса уса гсу -3'



Кодон иРНК

5' - ссс агу суг ааа саг usc ugg
уса уса гси -3'

5' - ццц агу цуг ааа цаг
уцу угг уца уца гцу -3'

Таблица генетического кода

		Нуклеотид					
1-й		2-й				3-й	
		У	Ц	А	Г		
У	УУУ	Фенилаланин	УЦУ	Тирозин	УГУ	Цистеин	У
	УУЦ		УЦЦ		УГЦ		Ц
	УУА		УЦА		УГА		А
	УУГ		УЦГ		УГГ		Г
		Лейцин	Серин	стоп-кодона	Триптофан		
Ц	ЦУУ	Лейцин	ЦЦУ	Гистидин	ЦГУ	Аргинин	У
	ЦУЦ		ЦЦЦ		ЦГЦ		Ц
	ЦУА		ЦЦА		ЦГА		А
	ЦУГ		ЦЦГ		ЦГГ		Г
		Лейцин	Пролин	Глютамин	Аргинин		
А	АУУ	Изолейцин	АЦУ	Аспарагин	АГУ	Серин	У
	АУЦ		АЦЦ		АГЦ		Ц
	АУА		АЦА		АГА		А
	АУГ		АЦГ		АГГ		Г
		Метионин старт-кодон	Треонин	Лизин	Аргинин		
Г	ГУУ	Валин	ГЦУ	Аспарагиновая кислота	ГГУ	Глицин	У
	ГУЦ		ГЦЦ		ГГЦ		Ц
	ГУА		ГЦА		ГГА		А
	ГУГ		ГЦГ		ГГГ		Г
		Валин	Аланин	Глутаминовая кислота	Глицин		

Решение

Пролин Серин Лейцин
Лизин Глютамин Серин
Триптофан Серин Серин
Аланин

Таблица названий и обозначений аминокислот

A	Ala	Alanine	Аланин
R	Arg	Arginine	Аргинин
N	Asn	Asparagine	Аспарагин
D	Asp	Aspartic Acid	Аспарагиновая кислота
C	Cys	Cysteine	Цистеин
Q	Gln	Glutamine	Глутамин
E	Glu	Glutamic Acid	Глутаминовая кислота
G	Gly	Glycine	Глицин
H	His	Histidine	Гистидин
I	Ile	Isoleucine	Изолейцин
L	Leu	Leucine	Лейцин
K	Lys	Lysine	Лизин
M	Met	Methionine	Метионин
F	Phe	Phenylalanine	Фенилаланин
P	Pro	Proline	Пролин
S	Ser	Serine	Серин
T	Thr	Threonine	Треонин
W	Trp	Tryptophan	Триптофан
Y	Tyr	Tyrosine	Тирозин
V	Val	Valine	Валин

Решение

Pro Ser Leu Lys Gln Ser
Trp Ser Ser Ala

=

PSLKQSWSSA

Код ДНК

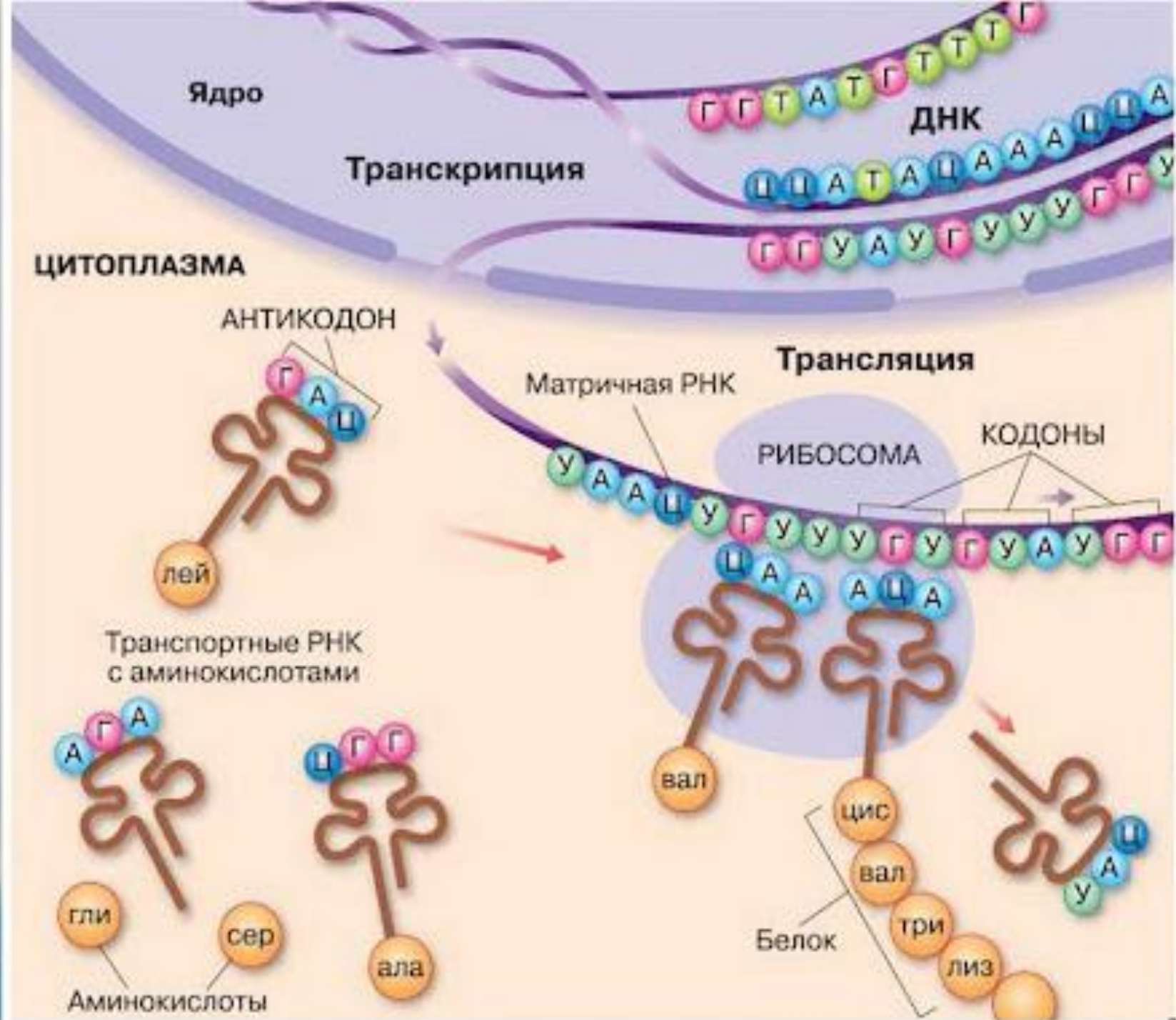
1 gggtcagact 10

11 ttgtcagaac 20

21 cagtagtcga 30

кодирует полипептидную цепь белка

PSLKQSWSSA



*Поиск гомологичных
последовательностей в базе
данных NCBI*

ncbi.nlm.nih.gov

**(National Center for
Biotechnology
Information)**

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



National Center for Biotechnology Information

All Databases

Search



UNITE

A new NIH initiative to end structural racism and achieve racial equity in the biomedical research enterprise.

LEARN MORE

NCBI Home

Resource List (A-Z)

- [All Resources](#)
- [Chemicals & Bioassays](#)
- [Data & Software](#)
- [DNA & RNA](#)
- [Domains & Structures](#)
- [Genes & Expression](#)
- [Genetics & Medicine](#)
- [Genomes & Maps](#)
- [Homology](#)
- [Literature](#)
- [Proteins](#)
- [Sequence Analysis](#)
- [Taxonomy](#)
- [Training & Tutorials](#)
- [Variation](#)

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

[About the NCBI](#) | [Mission](#) | [Organization](#) | [NCBI News & Blog](#)

Submit

Deposit data or manuscripts into NCBI databases



Download

Transfer NCBI data to your computer



Learn

Find help documents, attend a class or watch a tutorial



Develop

Use NCBI APIs and code libraries to build applications



Analyze

Identify an NCBI tool for your data analysis task



Research

Explore NCBI research and collaborative projects



Popular Resources

[PubMed](#)

[Bookshelf](#)

[PubMed Central](#)

BLAST

[Nucleotide](#)

[Genome](#)

[SNP](#)

[Gene](#)

[Protein](#)

[PubChem](#)

NCBI News & Blog

GenBank release 246.0
15 Nov 2021

GenBank release 246.0 (11/2/2021) is now available on

RefSeq Release 209 is available
12 Nov 2021

RefSeq release 209 is now available online from the FTP
A more modern BMC is on its way

Активация
требуется активи



National Center for Biotechnology Information

All Databases

Search



UNITE

A new NIH initiative to end structural racism and achieve racial equity in the biomedical research enterprise.

LEARN MORE

NCBI Home

Resource List (A-Z)

- All Resources
- Chemicals & Bioassays
- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature
- Proteins
- Sequence Analysis
- Taxonomy
- Training & Tutorials
- Variation

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

[About the NCBI](#) | [Mission](#) | [Organization](#) | [NCBI News & Blog](#)

Submit

Deposit data or manuscripts into NCBI databases



Download

Transfer NCBI data to your computer



Learn

Find help documents, attend a class or watch a tutorial



Develop

Use NCBI APIs and code libraries to build applications



Analyze

Identify an NCBI tool for your data analysis task



Research

Explore NCBI research and collaborative projects

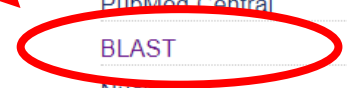
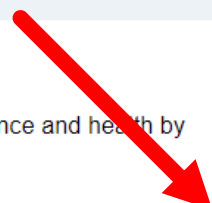


Popular Resources

- PubMed
- Bookshelf
- PubMed Central
- BLAST**
- Nucleotide
- Genome
- SNP
- Gene
- Protein
- PubChem

NCBI News & Blog

- GenBank release 246.0
15 Nov 2021
- GenBank release 246.0 (11/2/2021) is now available on
- RefSeq Release 209 is available
12 Nov 2021
- RefSeq release 209 is now available online from the FTP
- A more modern BMC is on its way



Активация
чтобы активировать



COVID-19 Information

[Public health information \(CDC\)](#) | [Research information \(NIH\)](#) | [SARS-CoV-2 data \(NCBI\)](#) | [Prevention and treatment information \(HHS\)](#) | [Español](#)

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](#)

NEWS

A new feature was added to the NCBI IgBLAST webpage
IgBLAST is now able to determine Ig isotypes


Mon, 01 Nov 2021 12:00:00 EST

[More BLAST news...](#)

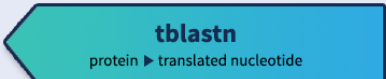
Web BLAST



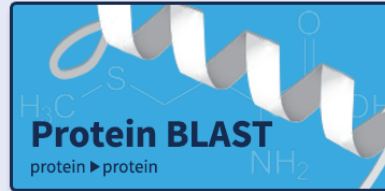
Nucleotide BLAST
nucleotide ▶ nucleotide



blastx
translated nucleotide ▶ protein



tblastn
protein ▶ translated nucleotide



Protein BLAST
protein ▶ protein

BLAST Genomes

Enter organism common name, scientific name, or tax id

Search

[Human](#)

[Mouse](#)

[Rat](#)

[Microbes](#)

Активация Windo
Чтобы активировать W



COVID-19 Information

[Public health information \(CDC\)](#) | [Research information \(NIH\)](#) | [SARS-CoV-2 data \(NCBI\)](#) | [Prevention and treatment information \(HHS\)](#) | [Español](#)

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](#)

A new feature was added to the NCBI IgBLAST webpage
IgBLAST is now able to determine Ig isotypes
Nov 01 Nov 2021 12:00:00 EST [More BLAST news...](#)


Web BLAST



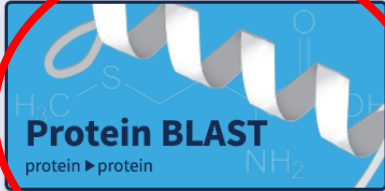
Nucleotide BLAST
nucleotide ▶ nucleotide



blastx
translated nucleotide ▶ protein



tblastn
protein ▶ translated nucleotide



Protein BLAST
protein ▶ protein

BLAST Genomes

[Human](#) [Mouse](#) [Rat](#) [Microbes](#)



Standard Protein BLAST

blastn **blastp** blastx tblastn tblastx

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

Enter Query Sequence

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

Query subrange [?](#)

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

Optional

exclude

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 [?](#)

Search database nr using Blastp (protein-protein BLAST)

Show results in a new window



Standard Protein BLAST

blastn **blastp** blastx tblastn tblastx

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

Enter Query Sequence

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

Query subrange [?](#)

From

To

Or, upload file

Выберите файл

Файл не выбран [?](#)

Job Title

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

Align two or more sequences [?](#)

Choose Search Set

Database

Non-redundant protein sequences (nr) [?](#)

Organism

Optional

Enter organism name or id—completions will be suggested

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 [?](#)

BLAST

Search database nr using Blastp (protein-protein BLAST)

Show results in a new window

Полипептидная (аминокислотная) последовательность

1 MSFPRNYQDT 10

11 NSNYANASLK 20

21 RHGADQMEIE 30

31 DNLFSSDSHP 40

41 RMGLLSRTL 50

51 PSPIIQWILP 60

Полипептидная (аминокислотная) последовательность

MSFPRNYQDTNSNYANASLKRHGADQMEIEDN
LFSSDSHPRMGLLSRTLIPSPIIQWILP

blastn

blastp

blastx

tblastn

tblastx

BLASTP programs search protein databases using a protein

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)MSFPRNYQDTNSNYANASLKRHGADQMEIEDNLFSSDSHPRMGLLSRTLIPSPI
IQWILPQuery subrange [?](#)From To

Or, upload file

Выберите файл

Файл не выбран [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#) Align two or more sequences [?](#)

Choose Search Set

Database

Non-redundant protein sequences (nr) [?](#)

Organism

Optional

 Enter organism name or id—completions will be suggested 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 [?](#)**BLAST**Search **database nr** using **Blastp** (protein-protein BLAST) Show results in a new window

blastn

blastp

blastx

tblastn

tblastx

BLASTP programs search protein databases using a protein

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)MSFPRNYQDTNSNYANASLKRHGADQMEIEDNLFSSDSHPRMGLLSRTLIPSPI
IQWILPQuery subrange [?](#)From To

Or, upload file

 Файл не выбран [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#) Align two or more sequences [?](#)

Choose Search Set

Database

 [?](#)

Organism

Optional

 exclude 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 BLAST algorithm [?](#)**BLAST**Search **database nr** using **Blastp (protein-protein BLAST)** Show results in a new window

Format Request Status

[\[Formatting options\]](#)

Job Title: Protein Sequence

Request ID	T85T33C5016
Status	Searching
Submitted at	Tue Nov 16 15:40:03 2021
Current time	Tue Nov 16 15:40:07 2021
Time since submission	00:00:03

This page will be automatically updated in 2 seconds



National Center for Biotechnology Information

8600 Rockville Pike
Bethesda MD, 20894 USA

[About us](#) [Contact us](#) [Policies](#) [FOIA](#)

Popular

[PubMed](#)
[PubMed Central](#)
[Bookshelf](#)
[PubChem](#)
[Gene](#)
[BLAST](#)
[Nucleotide](#)
[Protein](#)
[GEO](#)

Resources

[Literature](#)
[Health](#)
[Genomes](#)
[Genes](#)
[Proteins](#)
[Chemicals](#)

Actions

[Submit](#)
[Downloa](#)
[Learn](#)
[Develop](#)
[Analyze](#)
[Research](#)

Format Request Status

[\[Formatting options\]](#)

Job Title: Protein Sequence

Request ID	T85T33C5016
Status	Searching
Submitted at	Tue Nov 16 15:40:03 2021
Current time	Tue Nov 16 15:40:07 2021
Time since submission	00:00:03

This page will be automatically updated in 2 seconds



National Center for Biotechnology Information

8600 Rockville Pike
Bethesda MD, 20894 USA

[About us](#) [Contact us](#) [Policies](#) [FOIA](#)

Popular

[PubMed](#)
[PubMed Central](#)
[Bookshelf](#)
[PubChem](#)
[Gene](#)
[BLAST](#)
[Nucleotide](#)
[Protein](#)
[GEO](#)

Resources

[Literature](#)
[Health](#)
[Genomes](#)
[Genes](#)
[Proteins](#)
[Chemicals](#)

Actions

[Submit](#)
[Downloa](#)
[Learn](#)
[Develop](#)
[Analyze](#)
[Research](#)

[Edit Search](#)

[Save Search](#)

[Search Summary](#) ▾

[How to read this report?](#)

[BLAST Help Videos](#)

[Back to Traditional Results Page](#)

Job Title	Protein Sequence
RID	T85T33C5016 Search expires on 11-18 03:40 am Download All ▾
Program	BLASTP ? Citation ▾
Database	nr See details ▾
Query ID	lcl Query_94901
Description	None
Molecule type	amino acid
Query Length	60
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](#) ▾

New [Select columns](#) ▾

Show

▾

[?](#)

select all 83 sequences selected

[GenPept](#)

[Graphics](#)

[Distance tree of results](#)

[Multiple alignment](#)

New [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	unnamed protein product [Aspergillus oryzae RIB40]	Aspergillus oryz...	128	128	100%	1e-35	100.00%	190	XP_001820068.3
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus mini...]	Aspergillus mini...	129	129	100%	9e-33	100.00%	1287	KAB8276737.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus flavus]	Aspergillus flavus	129	129	100%	1e-32	100.00%	1287	RMZ40289.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus oryzae 3.042]	Aspergillus oryz...	129	129	100%	1e-32	100.00%	1287	EIT82682.1
<input checked="" type="checkbox"/>	Cleavage/polyadenylation specificity factor, A subunit, C-terminal [Aspergillus oryzae]	Aspergillus oryzae	129	129	100%	1e-32	100.00%	1287	OOO10038.1
<input checked="" type="checkbox"/>	uncharacterized protein G4B84_003632 [Aspergillus flavus NRRL3357]	Aspergillus flavu...	129	129	100%	1e-32	100.00%	1287	XP_041143346.1
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus sergii]	Aspergillus sergii	125	125	100%	1e-31	96.67%	1287	KAE8325895.1

Windows
Чтобы активировать
компьютера.

[Edit Search](#)

[Save Search](#)

[Search Summary](#) ▾

How to read this report?

[BLAST Help Videos](#)

[Back to Traditional Results Page](#)

Job Title	Protein Sequence
RID	T85T33C5016 Search expires on 11-18 03:40 am Download All ▾
Program	BLASTP Citation ▾
Database	nr See details ▾
Query ID	lcl Query_94901
Description	None
Molecule type	amino acid
Query Length	60
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](#) ▾

[New](#) [Select columns](#) ▾

Show [?](#)

select all 83 sequences selected

[GenPept](#)

[Graphics](#)

[Distance tree of results](#)

[Multiple alignment](#)

[New](#) [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	unnamed protein product [Aspergillus oryzae RIB40]	Aspergillus oryzae	128	128	100%	1e-35	100.00%	190	XP_001820068.3
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus mini...	Aspergillus mini...	129	129	100%	9e-33	100.00%	1287	KAB8276737.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus flavus]	Aspergillus flavus	129	129	100%	1e-32	100.00%	1287	RMZ40289.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus oryzae 3.042]	Aspergillus oryzae	129	129	100%	1e-32	100.00%	1287	EIT82682.1
<input checked="" type="checkbox"/>	Cleavage/polyadenylation specificity factor, A subunit, C-terminal [Aspergillus oryzae]	Aspergillus oryzae	129	129	100%	1e-32	100.00%	1287	OOO10038.1
<input checked="" type="checkbox"/>	uncharacterized protein G4B84_003632 [Aspergillus flavus NRRL3357]	Aspergillus flavu...	129	129	100%	1e-32	100.00%	1287	XP_041143346.1
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus sergii]	Aspergillus sergii	125	125	100%	1e-31	96.67%	1287	KAE8325895.1

Windows
Чтобы активировать
компьютера.

[Edit Search](#)

[Save Search](#)

[Search Summary](#)

[How to read this report?](#)

[BLAST Help Videos](#)

[Back to Traditional Results Page](#)

Job Title	Protein Sequence
RID	T85T33C5016 Search expires on 11-18 03:40 am Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl Query_94901
Description	None
Molecule type	amino acid
Query Length	60
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](#)

[Select columns](#)

Show

100

select all 83 sequences selected

[GenPept](#)

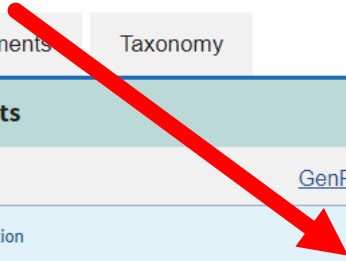
[Graphics](#)

[Distance tree of results](#)

[Multiple alignment](#)

[MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	unnamed protein product [Aspergillus oryzae RIB40]	Aspergillus oryzae	128	128	100%	1e-35	100.00%	190	XP_001820068.3
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus mini...]	Aspergillus mini...	129	129	100%	9e-33	100.00%	1287	KAB8276737.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus flavus]	Aspergillus flavus	129	129	100%	1e-32	100.00%	1287	RMZ40289.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus oryzae 3.042]	Aspergillus oryzae	129	129	100%	1e-32	100.00%	1287	EIT82682.1
<input checked="" type="checkbox"/>	Cleavage/polyadenylation specificity factor, A subunit, C-terminal [Aspergillus oryzae]	Aspergillus oryzae	129	129	100%	1e-32	100.00%	1287	OOO10038.1
<input checked="" type="checkbox"/>	uncharacterized protein G4B84_003632 [Aspergillus flavus NRRL3357]	Aspergillus flavu...	129	129	100%	1e-32	100.00%	1287	XP_041143346.1
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus sergii]	Aspergillus sergii	125	125	100%	1e-31	96.67%	1287	KAE8325895.1



Windows
Чтобы активировать
компьютера.

[< Edit Search](#)[Save Search](#)[Search Summary ▾](#)[? How to read this report?](#)[▶ BLAST Help Videos](#)[↶ Back to Traditional Results Page](#)

Job Title	Protein Sequence
RID	T85T33C5016 Search expires on 11-18 03:40 am Download All ▾
Program	BLASTP ? Citation ▾
Database	nr See details ▾
Query ID	lcl Query_94901
Description	None
Molecule type	amino acid
Query Length	60
Other reports	Distance tree of results Multiple alignment MSA viewer ?

Filter Results

Organism only top 20 will appear exclude
[+ Add organism](#)

Percent Identity

E value

Query Coverage

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

Descriptions

[Graphic Summary](#)[Alignments](#)[Taxonomy](#)

Sequences producing significant alignments

Download ▾

[New](#) Select columns ▾

Show

100 ▾

[?](#) select all 83 sequences selected[GenPept](#)[Graphics](#)[Distance tree of results](#)[Multiple alignment](#)[New](#) [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	unnamed protein product [Aspergillus oryzae RIB40]	Aspergillus oryz...	128	128	100%	1e-35	100.00%	190	XP_001820068.3
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus mini...]	Aspergillus mini...	129	129	100%	9e-33	100.00%	1287	KAB8276737.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus flavus]	Aspergillus flavus	129	129	100%	1e-32	100.00%	1287	RMZ40289.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus oryzae 3.042]	Aspergillus oryz...	129	129	100%	1e-32	100.00%	1287	EIT82682.1
<input checked="" type="checkbox"/>	Cleavage/polyadenylation specificity factor, A subunit, C-terminal [Aspergillus oryzae]	Aspergillus oryzae	129	129	100%	1e-32	100.00%	1287	OOO10038.1
<input checked="" type="checkbox"/>	uncharacterized protein G4B84_003632 [Aspergillus flavus NRRL3357]	Aspergillus flavu...	129	129	100%	1e-32	100.00%	1287	XP_041143346.1
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus sergii]	Aspergillus sergii	125	125	100%	1e-31	96.67%	287	KAE8325895.1

Win
Чтобы активировать
компьютера.

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

[? How to read this report?](#) [▶ BLAST Help Videos](#) [↶ Back to Traditional Results Page](#)

Job Title Protein Sequence
RID [T85T33C5016](#) Search expires on 11-18 03:40 am [Download Alignments](#)
Program BLASTP [?](#) [Citation](#) ▾
Database nr [See details](#) ▾
Query ID Icl|Query_94901
Description None
Molecule type amino acid
Query Length 60
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 ▾ **New** Select columns ▾ Show [?](#)

select all 83 sequences selected

[GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#) **New** [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	unnamed protein product [Aspergillus oryzae RIB40]	Aspergillus oryzae	128	128	100%	1e-35	100.00%	190	XP_001820068.3
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus mini...]	Aspergillus mini...	129	129	100%	9e-33	100.00%	1287	KAB8276737.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus flavus]	Aspergillus flavus	129	129	100%	1e-32	100.00%	1287	RMZ40289.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus oryzae 3.042]	Aspergillus oryzae	129	129	100%	1e-32	100.00%	1287	EIT82682.1
<input checked="" type="checkbox"/>	Cleavage/polyadenylation specificity factor, A subunit, C-terminal [Aspergillus oryzae]	Aspergillus oryzae	129	129	100%	1e-32	100.00%	1287	OOO10038.1
<input checked="" type="checkbox"/>	uncharacterized protein G4B84_003632 [Aspergillus flavus NRRL3357]	Aspergillus flavu...	129	129	100%	1e-32	100.00%	1287	XP_041143346.1
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus sergii]	Aspergillus sergii	125	125	100%	1e-31	96.67%	1287	KAE8325895.1

Windows
 Чтобы активировать
 компьютер.

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

[? How to read this report?](#) [BLAST Help Videos](#) [↶ Back to Traditional Results Page](#)

Job Title Protein Sequence

RID [T85T33C5016](#) Search expires on 11-18 03:40 am [Download All](#) ▾

Program BLASTP [?](#) [Citation](#) ▾

Database nr [See details](#) ▾

Query ID lcl|Query_94901

Description None

Molecule type amino acid

Query Length 60

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](#) ▾ **New** [Select columns](#) ▾ Show [?](#)

select all 83 sequences selected [GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#) **New** [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	unnamed protein product [Aspergillus oryzae RIB40]	Aspergillus oryz...	128	128	100%	1e-35	100.00%	190	XP_001820068.3
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus mini...]	Aspergillus mini...	129	129	100%	9e-33	100.00%	1287	KAB8276737.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus flavus]	Aspergillus flavus	129	129	100%	1e-32	100.00%	1287	RMZ40289.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus oryzae 3.042]	Aspergillus oryz...	129	129	100%	1e-32	100.00%	1287	EIT82682.1
<input checked="" type="checkbox"/>	Cleavage/polyadenylation specificity factor, A subunit, C-terminal [Aspergillus oryzae]	Aspergillus oryzae	129	129	100%	1e-32	100.00%	1287	OOO10038.1
<input checked="" type="checkbox"/>	uncharacterized protein G4B84_003632 [Aspergillus flavus NRRL3357]	Aspergillus flavu...	129	129	100%	1e-32	100.00%	1287	XP_041143346.1
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus sergii]	Aspergillus sergii	125	125	100%	1e-31	96.67%	1287	KAE8325895.1

Windows
Чтобы активировать
компьютера.

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

[? How to read this report?](#) [▶ BLAST Help Videos](#) [↶ Back to Traditional Results Page](#)

Job Title Protein Sequence

RID [T85T33C5016](#) Search expires on 11-18 03:40 am [Download All](#) ▾

Program BLASTP [?](#) [Citation](#) ▾

Database nr [See details](#) ▾

Query ID lcl|Query_94901

Description None

Molecule type amino acid

Query Length 60

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

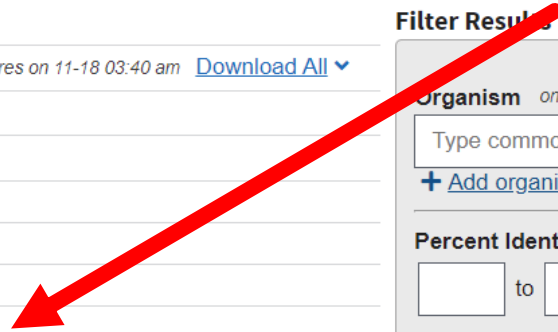
[+ Add organism](#)

Percent Identity to

E value to

Query Coverage to

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



Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments

Download ▾ **New** Select columns ▾ Show [?](#)

select all 83 sequences selected

[GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#) **New** [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	unnamed protein product [Aspergillus oryzae RIB40]	Aspergillus oryz...	128	128	100%	1e-35	100.00%	190	XP_001820068.3
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus mini...]	Aspergillus mini...	129	129	100%	9e-33	100.00%	1287	KAB8276737.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus flavus]	Aspergillus flavus	129	129	100%	1e-32	100.00%	1287	RMZ40289.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus oryzae 3.042]	Aspergillus oryz...	129	129	100%	1e-32	100.00%	1287	EIT82682.1
<input checked="" type="checkbox"/>	Cleavage/polyadenylation specificity factor, A subunit, C-terminal [Aspergillus oryzae]	Aspergillus oryzae	129	129	100%	1e-32	100.00%	1287	OOO10038.1
<input checked="" type="checkbox"/>	uncharacterized protein G4B84_003632 [Aspergillus flavus NRRL3357]	Aspergillus flavu...	129	129	100%	1e-32	100.00%	1287	XP_041143346.1
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus sergii]	Aspergillus sergii	125	125	100%	1e-31	96.67%	1287	KAE8325895.1

Windows
Чтобы активировать
компьютера.

Генетическое дерево расстояний

[Edit Search](#)

[Save Search](#)

[Search Summary](#) ▾

[How to read this report?](#)

[BLAST Help Videos](#)

[Back to Traditional Results Page](#)

Job Title	Protein Sequence
RID	T85T33C5016 Search expires on 11-18 03:40 am Download All ▾
Program	BLASTP Citation ▾
Database	nr See details ▾
Query ID	lcl Query_94901
Description	None
Molecule type	amino acid
Query Length	60
Other reports	Distance tree of results Multiple alignment MSA viewer ?

Filter Results

exclude

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

Download ▾

[New](#) Select columns ▾

Show

100 ▾

[?](#)

select all 83 sequences selected

[GenPept](#)

[Graphics](#)

[Distance tree of results](#)

[Multiple alignment](#)

[New](#) [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	unnamed protein product [Aspergillus oryzae RIB40]	Aspergillus oryz...	128	128	100%	1e-35	100.00%	190	XP_001820068.3
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus mini...]	Aspergillus mini...	129	129	100%	9e-33	100.00%	1287	KAB8276737.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus flavus]	Aspergillus flavus	129	129	100%	1e-32	100.00%	1287	RMZ40289.1
<input checked="" type="checkbox"/>	thermotolerance protein [Aspergillus oryzae 3.042]	Aspergillus oryz...	129	129	100%	1e-32	100.00%	1287	EIT82682.1
<input checked="" type="checkbox"/>	Cleavage/polyadenylation specificity factor, A subunit, C-terminal [Aspergillus oryzae]	Aspergillus oryzae	129	129	100%	1e-32	100.00%	1287	OOO10038.1
<input checked="" type="checkbox"/>	uncharacterized protein G4B84_003632 [Aspergillus flavus NRRL3357]	Aspergillus flavu...	129	129	100%	1e-32	100.00%	1287	XP_041143346.1
<input checked="" type="checkbox"/>	mono-functional DNA-alkylating methyl methanesulfonate N-term-domain-containing protein [Aspergillus sergii]	Aspergillus sergii	125	125	100%	1e-31	96.67%	1287	KAE8325895.1

Windows
Чтобы активировать
компьютера.

Blast Tree View

This tree was produced using BLAST pairwise alignments. [more...](#)[Reset Tree](#)

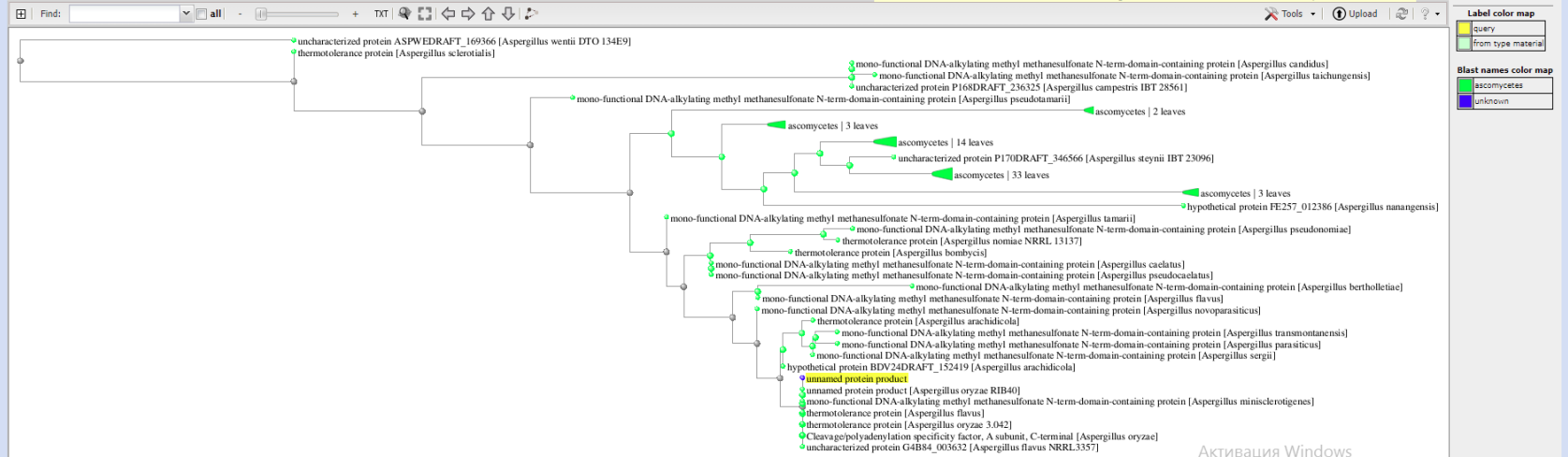
BLAST RID T85T33C5016

Query ID lcl|Query_94901

Database nr

Tree method: Fast Minimum Evolution | Max Seq Difference: 0.85 | Distance: Grishin (protein) | Sequence Label: Sequence Title (if available)

Mouse over an internal node for a subtree or alignment. Click on tree label to select sequence to download



Blast Tree View

This tree was produced using BLAST pairwise alignments. [more...](#)

[Reset Tree](#)

BLAST RID T85T33C5016

Query ID lcl|Query_94901

Database

Tree method: Fast Minimum Evolution
Max Seq Difference: 0.85
Distance: Grishin (protein)
Sequence Label: Sequence Title (if availa

Mouse over an internal node for a subtree or alignment. Click on tree label to select sequence to download

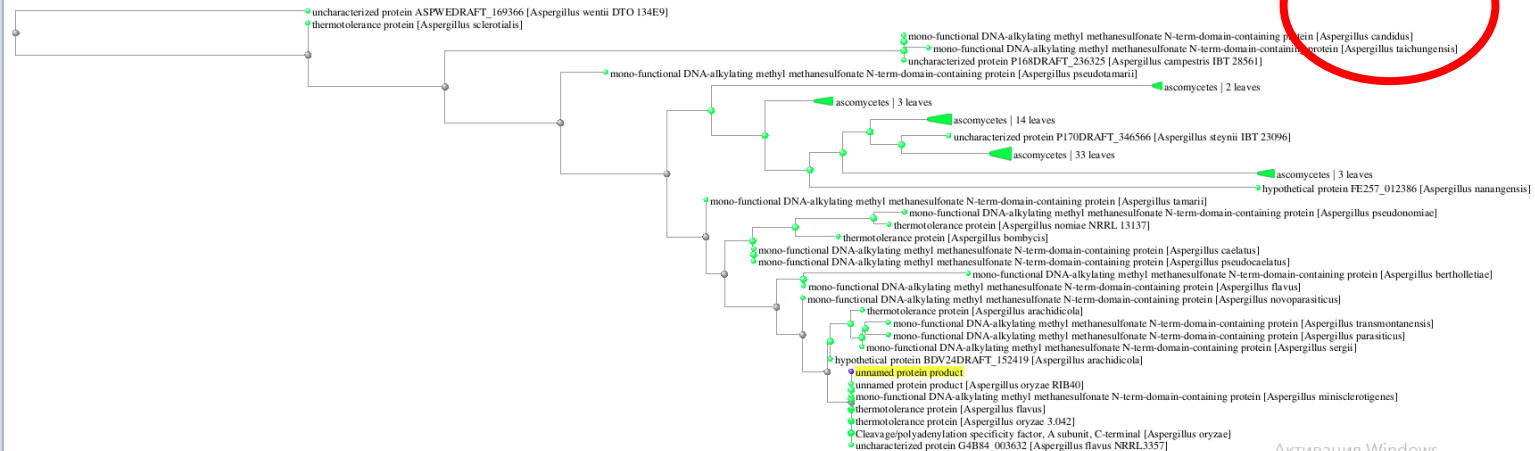
Find: all

Tools Upload

Hide legend

Label color map
query
from type material

Blast names color map
ascomycetes
unknown

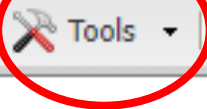


Success

Nodes 167/0 selected View port at (0.0) of 1724x515 p. 85

abase nr

or alignment. Click on tree label to select sequence to download





Upload





[Hide legend](#)

Label color map

	query
	from type material


Blast names color map

	ascomycetes
	unknown

N-term-domain-containing protein [Aspergillus candidus]
ionate N-term-domain-containing protein [Aspergillus taichungensis]
campestris IBT 28561]

ascomycetes | 2 leaves

aspergillus steynii IBT 23096]

 ascomycetes | 3 leaves

it. Click on tree label to select sequence to download

The screenshot shows a web-based phylogenetic tree viewer. At the top, there is a toolbar with icons for 'Tools', 'Upload', a refresh button, and a help button. Below the toolbar, a context menu is open, listing several actions: 'Download', 'Layout', 'Sort', 'Zoom behavior', 'Clear selection', 'Clear subtree', 'Clear rerooting', 'Expand all', and 'Edit labels'. A red arrow points from the instruction text at the top to the 'Layout' option in the menu. A red oval highlights the 'Layout' option. The background shows a partial view of a phylogenetic tree with labels such as 'in-containing protein [Asp...', '-domain-containing protein [T 28561]', '2 leaves', 'ynii IBT 23096]', 'ascomycetes', 'hypothetical prote...', and 'lus nanangensis]'. On the right side, there are color selection boxes for 'L' (yellow, light green) and 'Bla:' (green, blue).

ee label to select sequence to download

[Hide le](#)

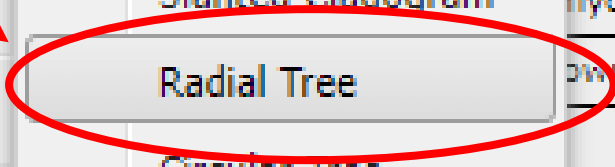
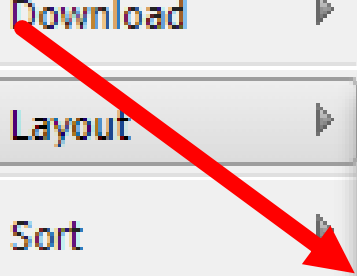
Tools | Upload | ?

Label color	
	query
	from type n

- Download ▶
- Layout ▶
- Sort ▶
- Zoom behavior ▶
- Clear selection
- Clear subtree
- Clear rerooting
- Expand all
- Edit labels

- Rectangle Cladogram
- Slanted Cladogram
- Radial Tree
- Circular tree
- Force Layout
- Use distance
- Midpoint root

nes c
mycete
own
[*Aspergillus nanantingensis*]



Blast Tree View

This tree was produced using BLAST pairwise alignments. [more...](#)

[Reset Tree](#)

BLAST RID **T85T33C5016**

Query ID **lcl|Query_94901**

Database **nr**

Tree method **Fast Minimum Evolution** | Max Seq Difference **0.85** | Distance **Grishin (protein)** | Sequence Label **Sequence Title (if availa**

Mouse over an internal node for a subtree or alignment. Click on tree label to select sequence to download

[Hide legend](#)

Find: all

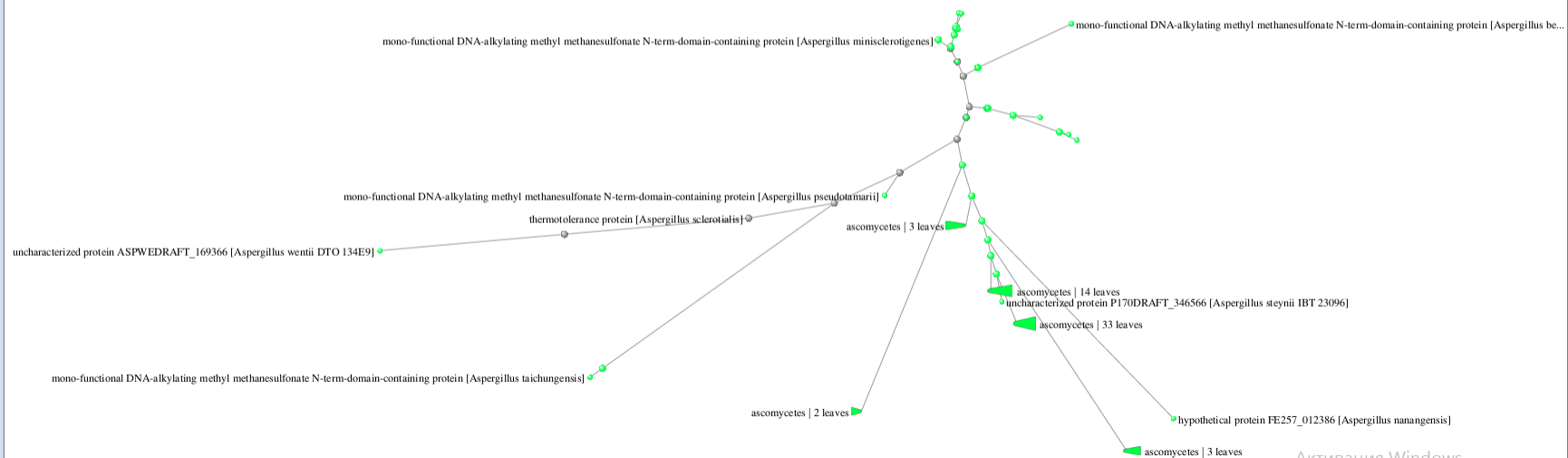
Tools | Upload | ?

Label color map

query
from type material

Blast names color map

ascomycetes
unknown



Blast Tree View

This tree was produced using BLAST pairwise alignments. [more...](#)

[Reset Tree](#)

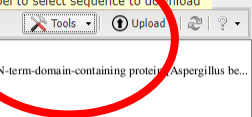
BLAST RID [T85T33C5016](#)

Query ID [Icl|Query_94901](#)

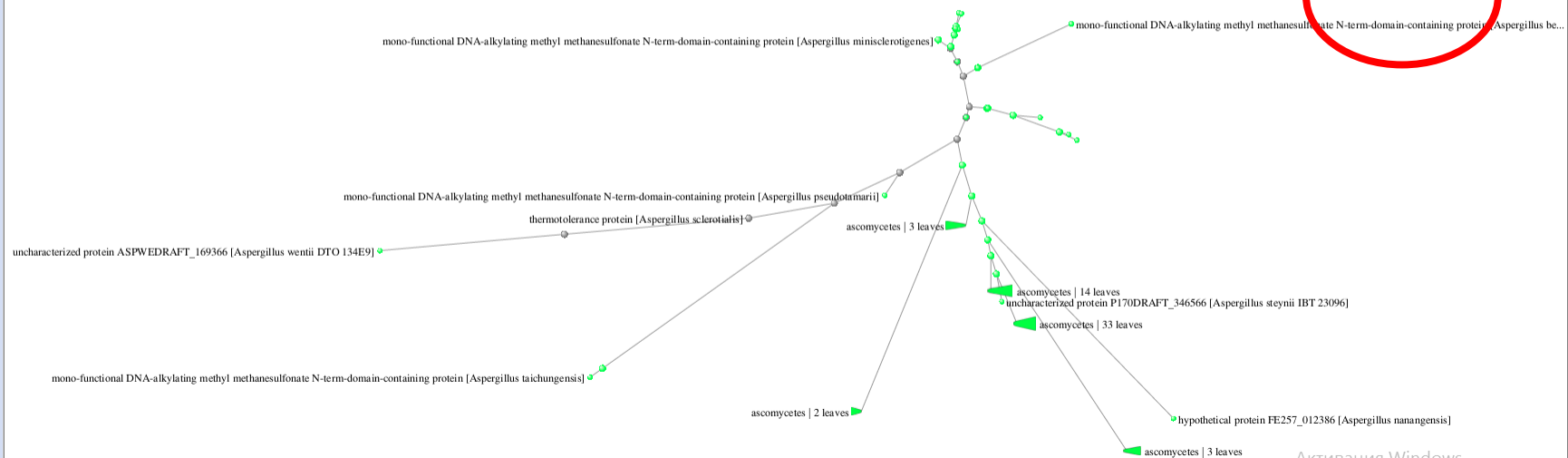
Database [...](#)

Tree method: [Fast Minimum Evolution](#)
Max Seq Difference: [0.85](#)
Distance: [Grishin \(protein\)](#)
Sequence Label: [Sequence Title \(if availa](#)

Mouse over an internal node for a subtree or alignment. Click on tree label to select sequence to download



Find: all



Hide legend

Label color map

- query
- from type material

Blast names color map

- ascomycetes
- unknown

nr

ment. Click on tree label to select sequence to download

[Hide](#)



Tools ▾

Upload



methyl methanesulfonate N-term-domain-containing protein [Aspergillus be...

Label color

<input type="checkbox"/>	query
<input type="checkbox"/>	from type

Blast names

<input type="checkbox"/>	ascomyce
<input type="checkbox"/>	unknown

Click on tree label to select sequence to download

[Hide legend](#)

Tools | Upload | ?

- Download
- Layout
- Sort
- Zoom behavior
- Clear selection
- Clear subtree
- Clear rerooting
- Expand all
- Edit labels

- ASN text file
- ASN binary file
- Newick file
- NEXUS file
- PDF file

Label color map

query
from type materi
t names color
ascomycetes
unknown

anesulfonate N-ter

Click on tree label to select sequence to download

[Hide legend](#)

Tools | Upload | ?

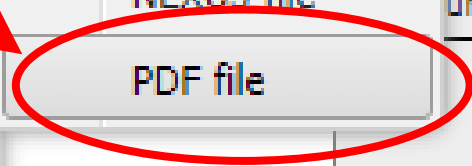
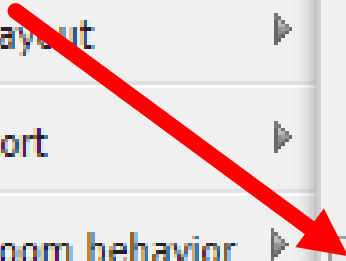
- Download
- Layout
- Sort
- Zoom behavior
- Clear selection
- Clear subtree
- Clear rerooting
- Expand all
- Edit labels

- ASN text file
- ASN binary file
- Newick file
- NEXUS file
- PDF file

Label color map

query
from type materi
t names color i
ascomycetes
unknown

anesulfonate N-ter



Download PDF-file

Export tree as PDF file

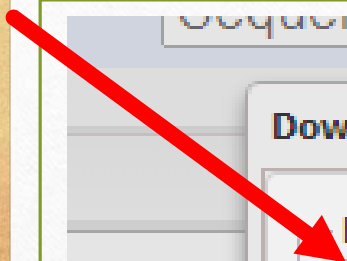
Create PDF-file

Create PDF-file before downloading.

View

Save

Cancel



te N-term-d

i-domain-co

[Aspergillu

r an internal n

mk

unconformity surface | of the surface

Sequence Label

Sequence Title (if available) 

Download PDF-file

Export tree as PDF file

Create PDF-file

<https://go.usa.gov/xE8PK>

View

Save

Cancel

Sequence Label

Sequence Title (if available) 

Download PDF-file

Export tree as PDF file

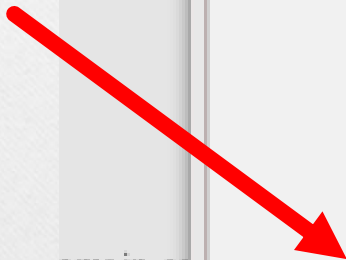
Create PDF-file

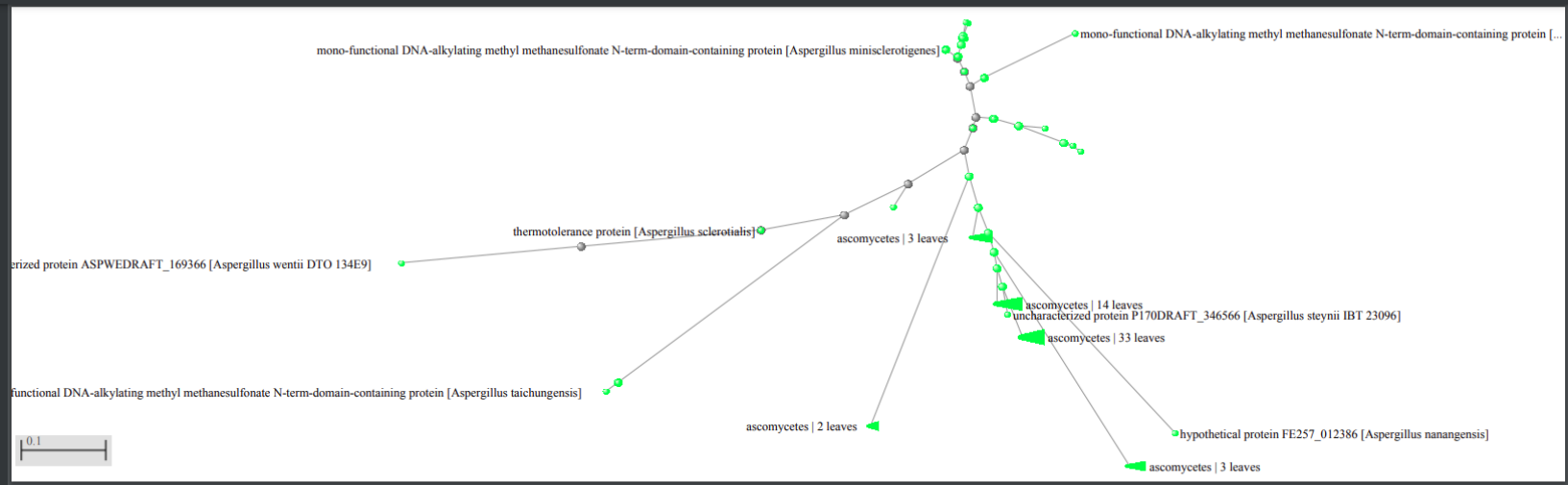
<https://go.usa.gov/xs8PK>

View

Save

Cancel





Sequence Label

Sequence Title (if available) 

Download PDF-file

Export tree as PDF file

Create PDF-file

<https://go.usa.gov/xs8PK>

View

Save

Cancel





СПАСИБО ЗА ВНИМАНИЕ!