

DTU



Tools to understand genetic variations

Bioinformatics, MPM

Virtual Ribosome 2: Translate from DNA >> Protein

VirtualRibosome - 2.0

A comprehensive tool for translating DNA sequences to the corresponding peptide sequences.

The Virtual Ribosome is a comprehensive tool for translating DNA sequences to the corresponding peptide sequences.

Besides being a strong translation tool in it's own right (with an integrated ORF finder, support for all translation tables defined by the NCBI taxonomy group, and a number of options regarding START and STOP codons), the Virtual Ribosome can work directly on files containing annotation of gene structure. This makes it easy to map various aspect of Intron/Exon structure onto the translated sequence.

Submission Instructions Output format Abstract

Submission

Paste in DNA sequences in FASTA, GenBank or TAB format

Upload DNA sequences in FASTA, GenBank or TAB format

No file selected.

View [example DNA files](#)

Instructions: Basic usage - Paste in or upload one or more DNA sequences in FASTA (sequence only), GenBank (CDS sections are processed) or TAB (sequence and intron/exon annotation) format and hit submit. The Virtual Ribosome will then translate the DNA sequences using the standard genetic code (by default). Options can be customized in the section below.

Options

Amino acid side chain properties

TWENTY-ONE PROTEINOGENIC α -AMINO ACIDS

Side chain charge at physiological pH 7.4

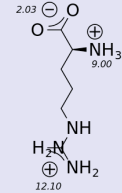
pK_a values shown italicized

⊕ Positive
⊖ Negative

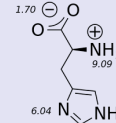
A. Amino Acids with Electrically Charged Side Chains

Positive

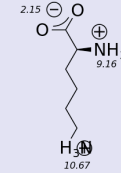
Arginine
Arg **R**



Histidine
His **H**

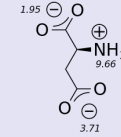


Lysine
Lys **K**

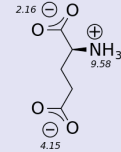


Negative

Aspartic Acid
Asp **D**

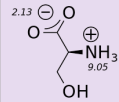


Glutamic Acid
Glu **E**

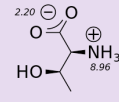


B. Amino Acids with Polar Uncharged Side Chains

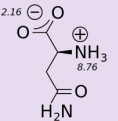
Serine
Ser **S**



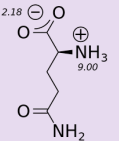
Threonine
Thr **T**



Asparagine
Asn **N**

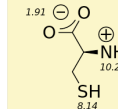


Glutamine
Gln **Q**

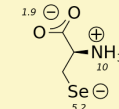


C. Special Cases

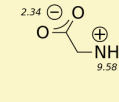
Cysteine
Cys **C**



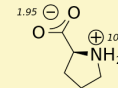
Selenocysteine
Sec **U**



Glycine
Gly **G**

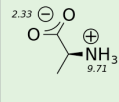


Proline
Pro **P**

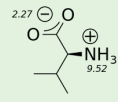


D. Amino Acids with Hydrophobic Side Chains

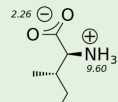
Alanine
Ala **A**



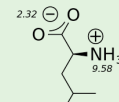
Valine
Val **V**



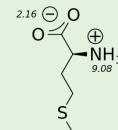
Isoleucine
Ile **I**



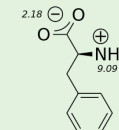
Leucine
Leu **L**



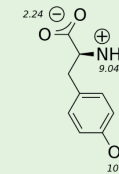
Methionine
Met **M**



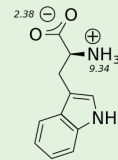
Phenylalanine
Phe **F**



Tyrosine
Tyr **Y**



Tryptophan
Trp **W**



Amino acid transitions: BLOSUM 62

	C	S	T	A	G	P	D	E	Q	N	H	R	K	M	I	L	V	W	Y	F		
C	9																				C	
S	-1	4																				S
T	-1	1	5																			T
A	0	1	0	4																		A
G	-3	0	-2	0	6																	G
P	-3	-1	-1	-1	-2	7																P
D	-3	0	-1	-2	-1	-1	6															D
E	-4	0	-1	-1	-2	-1	2	5														E
Q	-3	0	-1	-1	-2	-1	0	2	5													Q
N	-3	1	0	-2	0	-2	1	0	0	6												N
H	-3	-1	-2	-2	-2	-2	-1	0	0	1	8											H
R	-3	-1	-1	-1	-2	-2	-2	0	1	0	0	5										R
K	-3	0	-1	-1	-2	-1	-1	1	1	0	-1	2	5									K
M	-1	-1	-1	-1	-3	-2	-3	-2	0	-2	-2	-1	-1	5								M
I	-1	-2	-1	-1	-4	-3	-3	-3	-3	-3	-3	-3	-3	1	4							I
L	-1	-2	-1	-1	-4	-3	-4	-3	-2	-3	-3	-2	-2	2	2	4						L
V	-1	-2	0	0	-3	-2	-3	-2	-2	-3	-3	-3	-2	1	3	1	4					V
W	-2	-3	-2	-3	-2	-4	-4	-3	-2	-4	-2	-3	-3	-1	-3	-2	-3	11				W
Y	-2	-2	-2	-2	-3	-3	-3	-2	-1	-2	2	-2	-2	-1	-1	-1	-1	2	7			Y
F	-2	-2	-2	-2	-3	-4	-3	-3	-3	-3	-1	-3	-3	0	0	0	-1	1	3	6		F
	C	S	T	A	G	P	D	E	Q	N	H	R	K	M	I	L	V	W	Y	F		

Variant Effect Predictor

e!Ensembl BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

VEP

Web Tools

- Web Tools
 - BLAST/BLAT
 - Variant Effect Predictor**
 - Linkage Disequilibrium Calculator
 - Variant Recoder
 - File Chameleon
 - Assembly Converter
 - ID History Converter
 - VCF to PED Converter
 - Data Slicer

Configure this page

Custom tracks

Export data

Share this page

Bookmark this page

Variant Effect Predictor ?

New job

Species: Homo_sapiens ×

Assembly: GRCh38.p14
[Change species](#)
If you are looking for VEP for Human GRCh37, please go to [GRCh37 website](#).

Name for this job (optional):

Input data:

Either paste data:

Examples: [Ensembl default](#), [VCF](#), [Variant identifiers](#), [HGVS notations](#), [SPDI](#)

Or upload file: No file selected.

Or provide file URL:

Transcript database to use:

- Ensembl/GENCODE transcripts
- Ensembl/GENCODE basic transcripts
- RefSeq transcripts
- Ensembl/GENCODE and RefSeq transcripts

PDB: Protein Structure DataBase

The screenshot displays the RCSB PDB website interface. At the top, a dark blue navigation bar contains links for Deposit, Search, Visualize, Analyze, Download, Learn, About, Documentation, Careers, and COVID-19, along with 'MyPDB' and 'Contact us' buttons. Below this, the main header features the RCSB PDB logo, statistics (218,500 Structures from the PDB and 1,068,577 Computed Structure Models (CSM)), a search bar with a dropdown for '3D Structures', and an 'Include CSM' toggle. A secondary navigation bar includes logos for PDB-101, wwPDB, EMDatabank, NAKB, wwPDB Foundation, and PDB-Dev, along with social media icons. A teal banner promotes 'Access Computed Structure Models (CSMs) of available model organisms' with a 'Learn more' button.

The main content area is divided into three sections:

- Left Sidebar:** A dark blue vertical menu with icons and text for 'Welcome', 'Deposit', 'Search', 'Visualize', 'Analyze', 'Download', and 'Learn'.
- Center Text:**

RCSB Protein Data Bank (RCSB PDB) enables breakthroughs in science and education by providing access and tools for exploration, visualization, and analysis of:

 - Experimentally-determined 3D structures from the **Protein Data Bank (PDB)** archive
 - Computed Structure Models (CSM)** from AlphaFold DB and ModelArchive

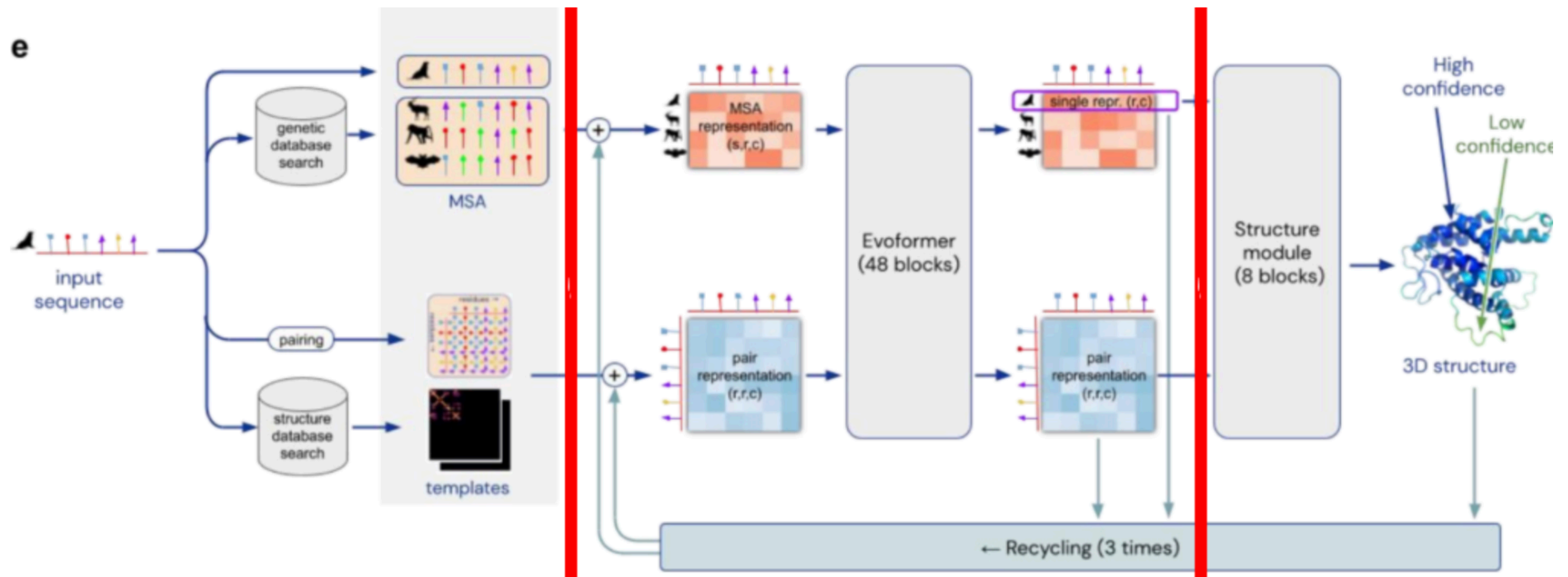
These data can be explored in context of external annotations providing a structural view of biology.
- Right Section:**

April Molecule of the Month

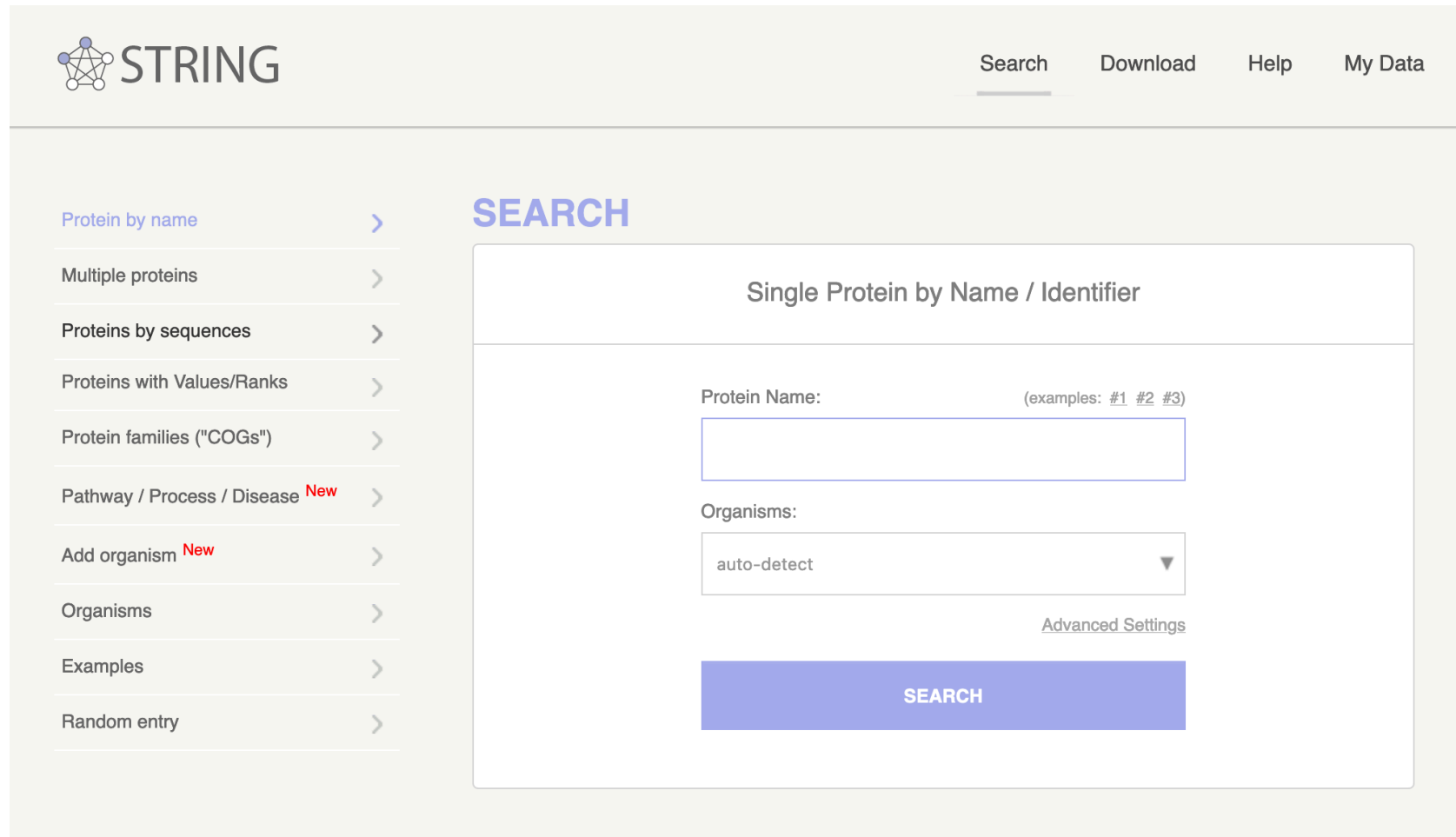
PhiX174 YES Complex

At the bottom of the main content area, there are three promotional banners: 'Explore NEW Features' with a computer monitor icon, 'PDB-101 Training Resources' with a lightbulb icon, and a central graphic with a magnifying glass over a PDB-101 label.

AlphaFold: Protein Structure Prediction



String: Protein Interactions Prediction



The screenshot shows the STRING database search interface. At the top left is the STRING logo. To the right are navigation links: Search, Download, Help, and My Data. On the left side, there is a vertical menu with the following options: Protein by name, Multiple proteins, Proteins by sequences, Proteins with Values/Ranks, Protein families ("COGs"), Pathway / Process / Disease (marked as New), Add organism (marked as New), Organisms, Examples, and Random entry. The main content area is titled "SEARCH" and contains a sub-section "Single Protein by Name / Identifier". This section includes a "Protein Name:" label with a text input field and a note "(examples: #1 #2 #3)". Below it is an "Organisms:" label with a dropdown menu currently set to "auto-detect". A link for "Advanced Settings" is located below the dropdown. At the bottom of the search area is a large blue "SEARCH" button.