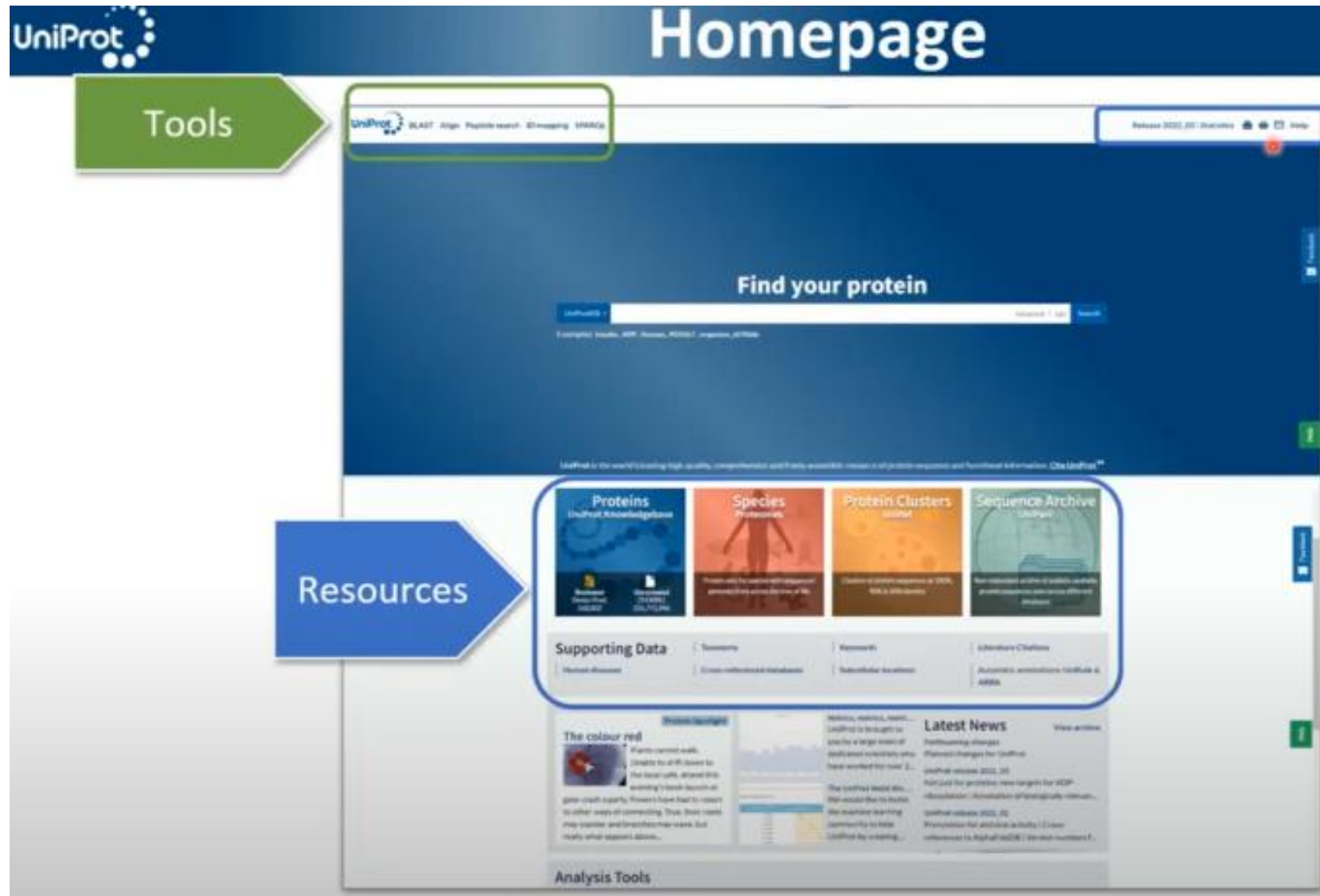


AP1.1 Bases de datos



Universidad
Internacional
de Valencia

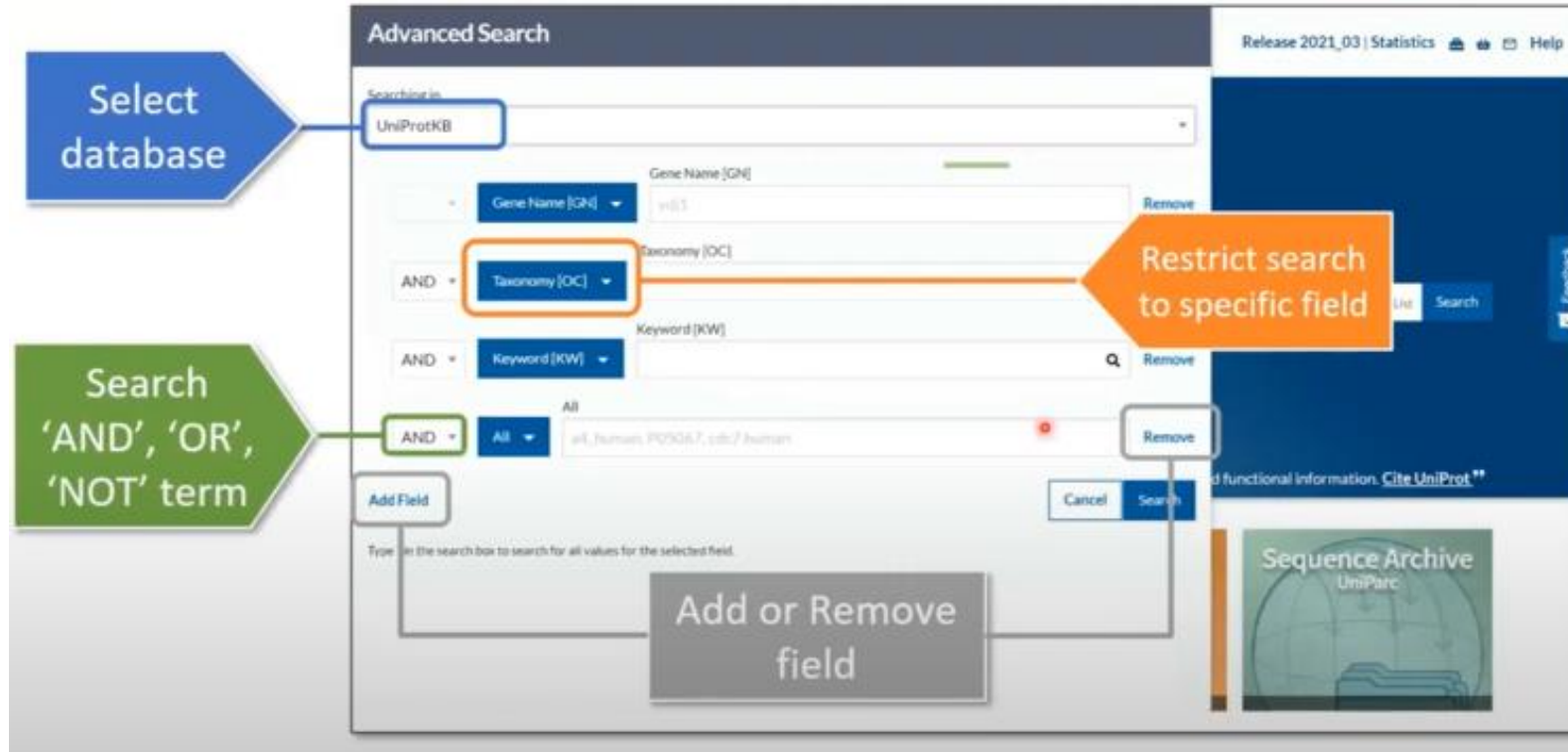
UniProt



UniProt>Búsqueda



UniProt>Búsqueda avanzada



The screenshot displays the UniProt Advanced Search interface. The search is configured with the following criteria:

- Select database:** UniProtKB (indicated by a blue arrow).
- Search 'AND', 'OR', 'NOT' term:** AND (indicated by a green arrow).
- Restrict search to specific field:** Taxonomy [OC] (indicated by an orange arrow).
- Add or Remove field:** A button at the bottom center (indicated by a grey arrow).

The search criteria are as follows:

- Gene Name [GN]: y[0].5
- Taxonomy [OC]: (selected field)
- Keyword [KW]:
- AND: All
- AND: All

The interface includes a search bar, a search button, and a "Sequence Archive UniParc" link. The bottom right corner features a "Sequence Archive UniParc" link.

UniProt>Herramientas


Retrieve/ID mapping

Enter your IDs or [load from a text file](#). Separate IDs by whitespace (space, tab, newline) or commas.

atg5
atg12
atg161

List gene names

Set search parameters

 Your input contains 3 IDs

From database	To database	Restrict by taxonomy
Gene Name ▾	UniProtKB ▾	human ×
		Homo sapiens (Human/Man) [9606]
		Human immunodeficiency virus 1 (HIV/AIDS virus) [10981]
		Human betapapillomavirus [1188015]

Name your ID Mapping job

atg5 +2 Gene_Name → UniProtKB

UniProt>Filtrado de búsqueda

UniProtKB 14 results for Gene_Name → UniProtKB

BLAST Align Map IDs Download Add Customize data

1 id is not mapped:
atg161

From	Entry	Entry Name	Protein Names	Gene Names	Organism	Length
<input type="checkbox"/> atg5	Q9H1Y0	ATG5_HUMAN	Autophagy protein 5[...]	ATG5[...]	Homo sapiens (Human)	275 AA
<input type="checkbox"/> atg5	A0A1B0GUS1	A0A1B0GUS1_HUMAN	Autophagy protein 5	ATG5	Homo sapiens (Human)	159 AA
<input type="checkbox"/> atg5	A0A1B0GV54	A0A1B0GV54_HUMAN	Autophagy protein 5	ATG5	Homo sapiens (Human)	153 AA
<input type="checkbox"/> atg5	A0A2R8Y718	A0A2R8Y718_HUMAN	Autophagy protein 5	ATG5	Homo sapiens (Human)	233 AA

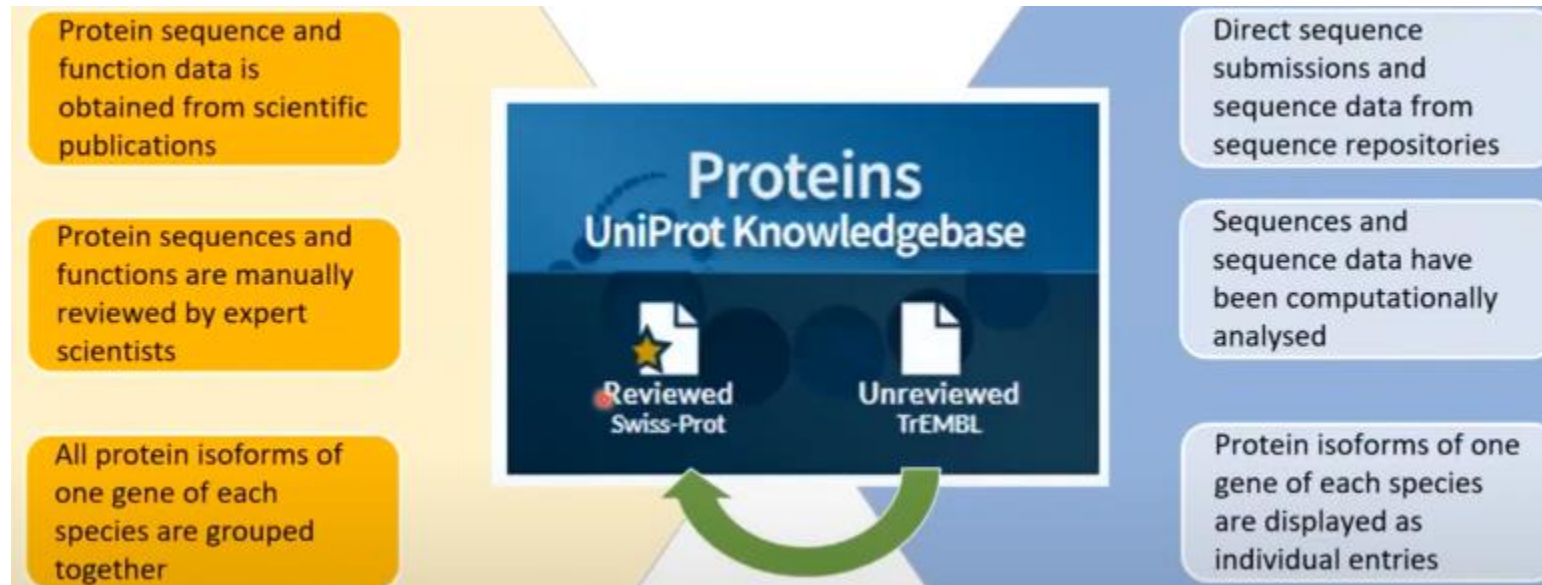
Filter results

Status
Reviewed (Swiss-Prot) (2)
Unreviewed (TrEMBL) (12)

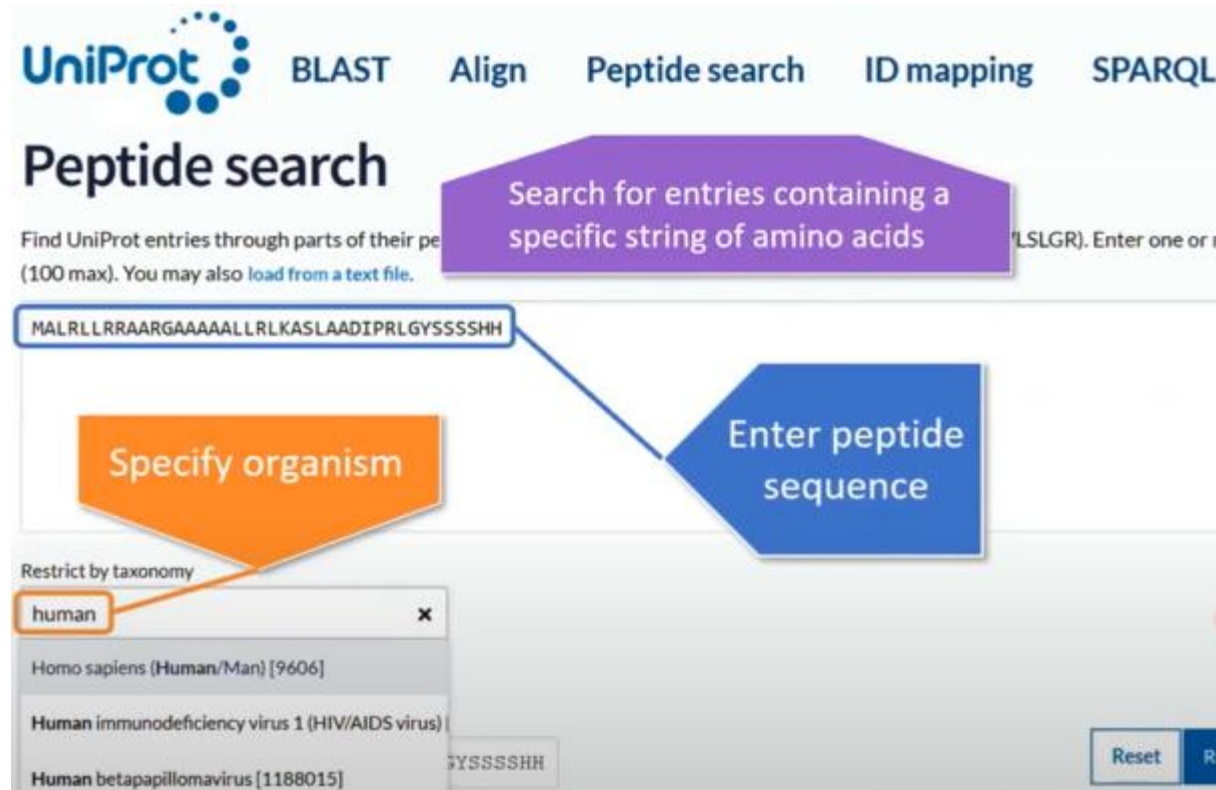
Model organisms
Human (14)

Proteins with
3D structure (2)
Alternative products (isoforms) (2)
Alternative splicing (2)
Beta strand (2)
Binary interaction (4)
More items

UniProt>Revisión de entradas



UniProt>Búsqueda de fragmentos peptídicos



The image shows the UniProt Peptide search interface. At the top, the UniProt logo is followed by navigation links: BLAST, Align, Peptide search, ID mapping, and SPARQL. The main heading is "Peptide search". Below it, a text box explains: "Find UniProt entries through parts of their peptide sequence (100 max). You may also [load from a text file](#)." A purple callout box points to the search input field, stating: "Search for entries containing a specific string of amino acids". The input field contains the peptide sequence "MALRLLRRAARGAAAAALLRLKASLAADIPRLGYSSSSH". A blue callout box points to this field, stating: "Enter peptide sequence". Below the input field, there is a section titled "Restrict by taxonomy" with an orange callout box pointing to it, stating: "Specify organism". The taxonomy dropdown menu is open, showing a list of organisms. The word "human" is highlighted in the list. Other visible entries include "Homo sapiens (Human/Man) [9606]", "Human immunodeficiency virus 1 (HIV/AIDS virus)", and "Human betapapillomavirus [1188015]". A "Reset" button is visible at the bottom right of the form.

UniProt BLAST Align Peptide search ID mapping SPARQL

Peptide search

Find UniProt entries through parts of their peptide sequence (100 max). You may also [load from a text file](#).

Search for entries containing a specific string of amino acids

Enter peptide sequence

Specify organism

Restrict by taxonomy

human


Homo sapiens (Human/Man) [9606]

Human immunodeficiency virus 1 (HIV/AIDS virus)

Human betapapillomavirus [1188015]

Reset

UniProt>Información de una entrada



O15111 · IKKA_HUMAN

Inhibitor of nuclear factor kappa-B kinase subunit alpha · *Homo sapiens* (Human) · EC number: 2.7.11.10 · Gene: CHUK (IKKA, TCF16) · 745 amino acids · Evidence at protein level · (5/5)

Entry Feature viewer Publications External links History

BLAST Align Download Add Community curation (1)

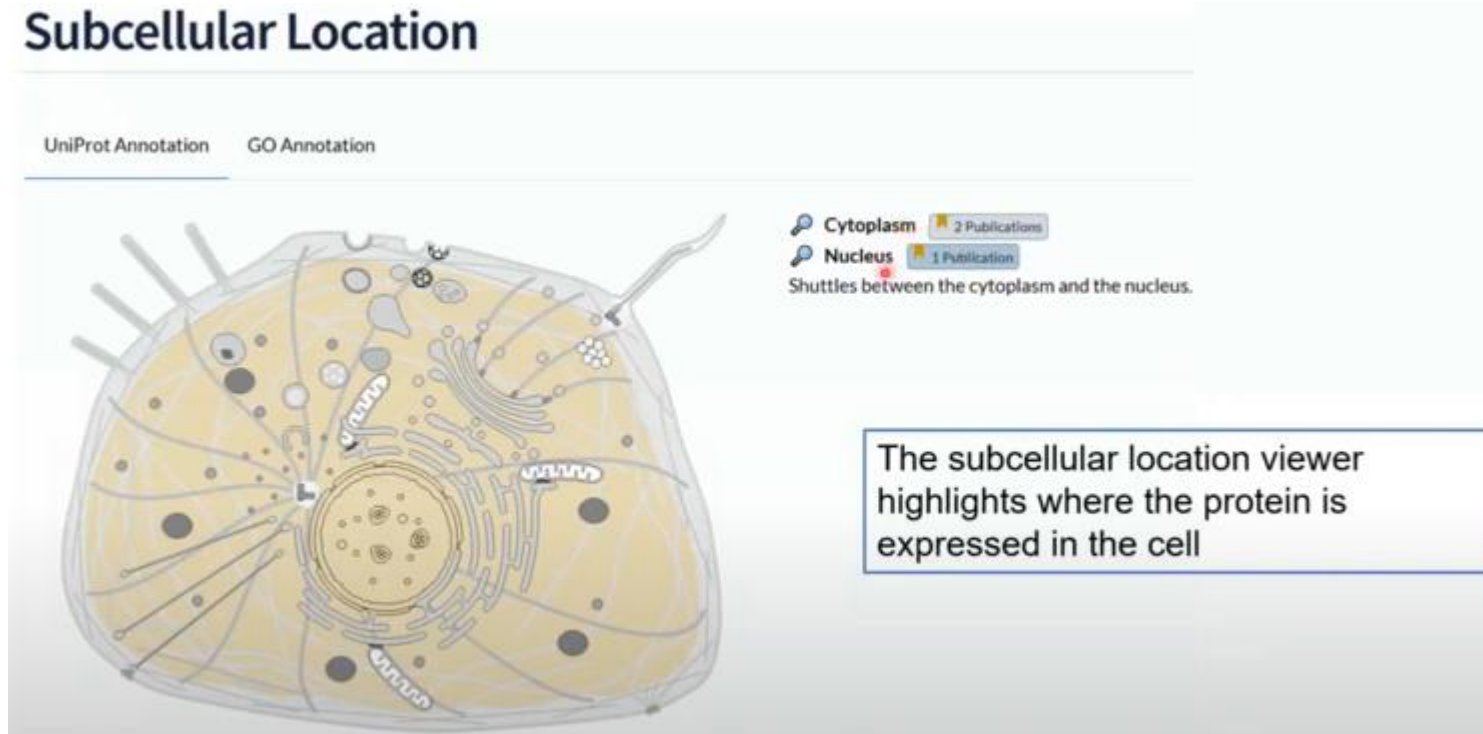
Function

Serine kinase that plays an essential role in the NF-kappa-B signaling pathway which is activated by multiple stimuli such as inflammatory cytokines, bacterial or viral products, DNA damages or other cellular stresses (PubMed:9244310, PubMed:9252186, PubMed:9346484, PubMed:18626576).

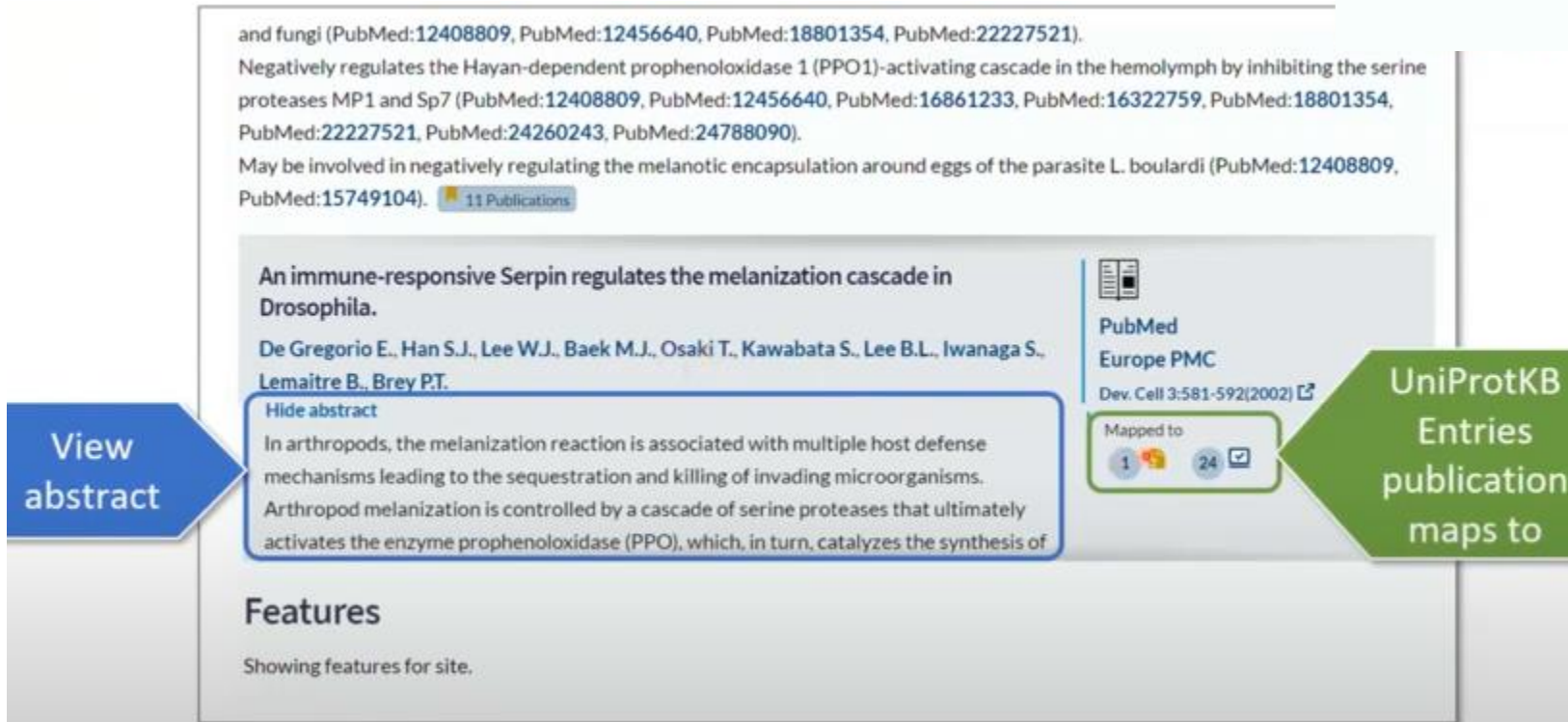
Acts as part of the canonical IKK complex in the conventional pathway of NF-kappa-B activation and phosphorylates inhibitors of NF-kappa-B on serine residues (PubMed:9244310, PubMed:9252186, PubMed:9346484, PubMed:18626576).

These modifications allow polyubiquitination of the inhibitors and subsequent degradation by the proteasome (PubMed:9244310,

UniProt>Información de una entrada



UniProt>Citas bibliográficas relacionadas con el contenido





and fungi (PubMed:12408809, PubMed:12456640, PubMed:18801354, PubMed:22227521).
Negatively regulates the Hsyan-dependent prophenoloxidase 1 (PPO1)-activating cascade in the hemolymph by inhibiting the serine proteases MP1 and Sp7 (PubMed:12408809, PubMed:12456640, PubMed:16861233, PubMed:16322759, PubMed:18801354, PubMed:22227521, PubMed:24260243, PubMed:24788090).
May be involved in negatively regulating the melanotic encapsulation around eggs of the parasite *L. boulardi* (PubMed:12408809, PubMed:15749104). 11 Publications

An immune-responsive Serpin regulates the melanization cascade in *Drosophila*.
De Gregorio E., Han S.J., Lee W.J., Baek M.J., Osaki T., Kawabata S., Lee B.L., Iwanaga S., Lemaitre B., Brey P.T.
[Hide abstract](#)
In arthropods, the melanization reaction is associated with multiple host defense mechanisms leading to the sequestration and killing of invading microorganisms. Arthropod melanization is controlled by a cascade of serine proteases that ultimately activates the enzyme prophenoloxidase (PPO), which, in turn, catalyzes the synthesis of

Features
Showing features for site.

PubMed
Europe PMC
Dev. Cell 3:581-592(2002) [↗](#)

Mapped to
1  24 

View abstract

UniProtKB Entries publication maps to

UniProt>Referencias a bases de datos externas

Protein-protein interaction databases

BioGRID | [107569](#) [↗](#) 159 interactors

CORUM | [O15111](#) [↗](#)

ComplexPortal | [CPX-3269](#) [↗](#) IkappaB kinase complex

DIP | [DIP-27526N](#) [↗](#)

ELM | [O15111](#) [↗](#)

 **IntAct** | [O15111](#) [↗](#) 73 interactors

MINT | [O15111](#) [↗](#)

STRING | [9606.ENSP00000359424](#) [↗](#)

Chemistry

BindingDB | [O15111](#) [↗](#)

180 Cross-references to specific external databases that provide additional specialist data

UniProt>Secuencias

Sequence

Tools
Download
Add
Highlight
Copy FASTA

Length 1273
Mass (Da) 141,178

Last updated 2020-04-22 v1
Checksum B17BE6D9F1C4EA34

10	20	30	40	50	60	70	80	90	100	110	120
MFVFLVLLPL	VSSQCVNLTT	RTQLPPAYTN	SFTRGVVYPD	KVFRSSVLHS	TQDLFLPFFS	NVTWFHAIHV	SGTNGTKRFD	NPVLPFNDGV	VFASTKSNI	IRGWIFGTTL	DSKTQSLIIV
130	140	150	160	170	180	190	200	210	220	230	240
NNATNVVIVK	CEQFCNDPF	LGYYVHKNNK	SWMESEFRVY	SSANNCTFEY	VSQPFMDLE	GKQGNFKNLR	EFVFNIDGY	FKIYSKHTPI	NLVRDLPQGF	SALEPLVDLP	IGINITRFQT
250	260	270	280	290	300	310	320	330	340	350	360
LLALHRSYLT	PGDSSSGWTA	GAAAYVGYL	QPRTFLLKYN	ENGTITDAVD	CALDPLSETK	CTLKSFTVEK	GIYQTSNFRV	QPTESIVRFP	NITNLCPFGE	VFNATRFASV	YAWNKRKISN
370	380	390	400	410	420	430	440	450	460	470	480
CVADYSVLIN	SASFSTFKCY	GVSPTKLNDL	CFTNWYADSF	VIRGDEVROI	APGQTGKIAD	YNYKLDDFT	GCVIAWNSNN	LDSKVGGNYN	YLYRLFRKSN	LKPFERDIST	EIQAGSTPC
490	500	510	520	530	540	550	560	570	580	590	600
NGVEGFNCYF	PLQSYGFQPT	NGVGYPYRV	VVLSFELLHA	PATVCGPKKS	TNLVKNKCVN	FNFNGLTGTG	VLTESNKKFL	PFQQFGRDIA	DTTDAVRDPQ	TLEILDITPC	SFGGVSVITP
610	620	630	640	650	660	670	680	690	700	710	720
GTNTSNQVAV	LYQDVNCTEV	PVAIHADQLT	PTWRVYSTGS	NVFQTRAGCL	IGAEHMNNSY	ECDIPIGAGI	CASYQTQINS	PRRARSVASQ	SIIAYTMSLG	AENSVAYSNN	SIAIPTNFTI

UniProt>Caracterización



UniProt>BLAST

BLAST to find similar proteins

P0DTC2 · SPIKE_SARS2
Spike glycoprotein · Severe acute respiratory syndrome coronavirus 2 (2019-nCoV) (SARS-CoV-2) · Gene: 5 - 12731

Entry Feature viewer Publications External links History

BLAST [Align](#) [Download](#) [Add](#) [Community curation \(4\)](#) [Add a publication](#) [Entry feedback](#)

Function

Filters

BLAST results 250 results

Overview Taxonomy Hit Distribution Text Output Input Parameters API Request

[BLAST](#) [Align](#) [Download](#) [Add](#) [Resubmit](#)

Accession	Gene	Protein	Organism	Score	Identity
<input type="checkbox"/> O60260	PRKN	E3 ubiquitin-pro...	Homo sapiens	110%	100%
<input type="checkbox"/> H2QU08	PRKN	E3 ubiquitin-pro...	Pan troglodytes	111.4%	100%
<input type="checkbox"/> A0A2I2YTU5	PRKN	E3 ubiquitin-pro...	Gorilla gorilla go...	101.1%	100%
<input type="checkbox"/> A0A2K6P0M3	PRKN	E3 ubiquitin-pro...	Rhinopithecus ro...	117.4%	100%
<input type="checkbox"/> A0A2K6K8A3	PRKN	E3 ubiquitin-pro...	Rhinopithecus bl...	117.2%	100%
<input type="checkbox"/> A0A096MX93	PRKN	E3 ubiquitin-pro...	Papio anubis	117.6%	100%
<input type="checkbox"/> B8YGJ6	PARK2	E3 ubiquitin-pro...	Macaca fascicula...	117.6%	100%
<input type="checkbox"/> A0A2K5HK82		E3 ubiquitin-pro...	Colobus angolen...		
<input type="checkbox"/> A0A2K6B5N6	PRKN	E3 ubiquitin-pro...	Macaca nemestr...		
<input type="checkbox"/> F6U1L3	PRKN	E3 ubiquitin-pro...	Macaca mulatta		
<input type="checkbox"/> A0A7N9CTJ5	Parkin RBR E3 ub...	Macaca fascicula...			
<input type="checkbox"/> A0A2K5M0T8	PRKN	E3 ubiquitin-pro...	Cercopithecus atys		
<input type="checkbox"/> A0A2K5E771	PRKN	E3 ubiquitin-pro...	Aotus nancymae		

Shows how similar your search query is to individual BLAST hits in the results table

UniProt>BLAST

P0DTC2 · SPIKE_SARS2
Spike glycoprotein · Severe acute respiratory syndrome coronavirus 2 (2019-nCoV) (SARS-CoV-2) · Gene: 5 - 12731

Entry Feature viewer Publications External links History

BLAST [Align](#) [Download](#) [Add](#) [Community curation \(4\)](#) [Add a publication](#) [Entry feedback](#)

Function

BLAST to find similar proteins

Blast parameters
Identity: 40.2 (0 to 100)
Score: 100

Accession	Protein Name	Organism	Score	Identity	Positives	Negatives
A0A2K5HKB2	E3 ubiquitin-pro...	Colobus argole...	41%	100/271	17	104
A0A6J3FUQ0	PRKN	Sapajus apella	41%	100/269	17	100
A0A6J3FTP4	PRKN	Sapajus apella	41%	100/271	17	104
Q5J4W3	prkn	Takifugu rubripes	41%	100/269	17	104
G1MBM1	PRKN	Parkin RBR E3 u...	41%	100/271	17	104
A0A6J3FTN6	PRKN	Sapajus apella	41%	100/271	17	104

Q9WVS6 · E3 ubiquitin-protein ligase parkin · Mus musculus

Highlight properties Select annotation View: Overview Wrapped

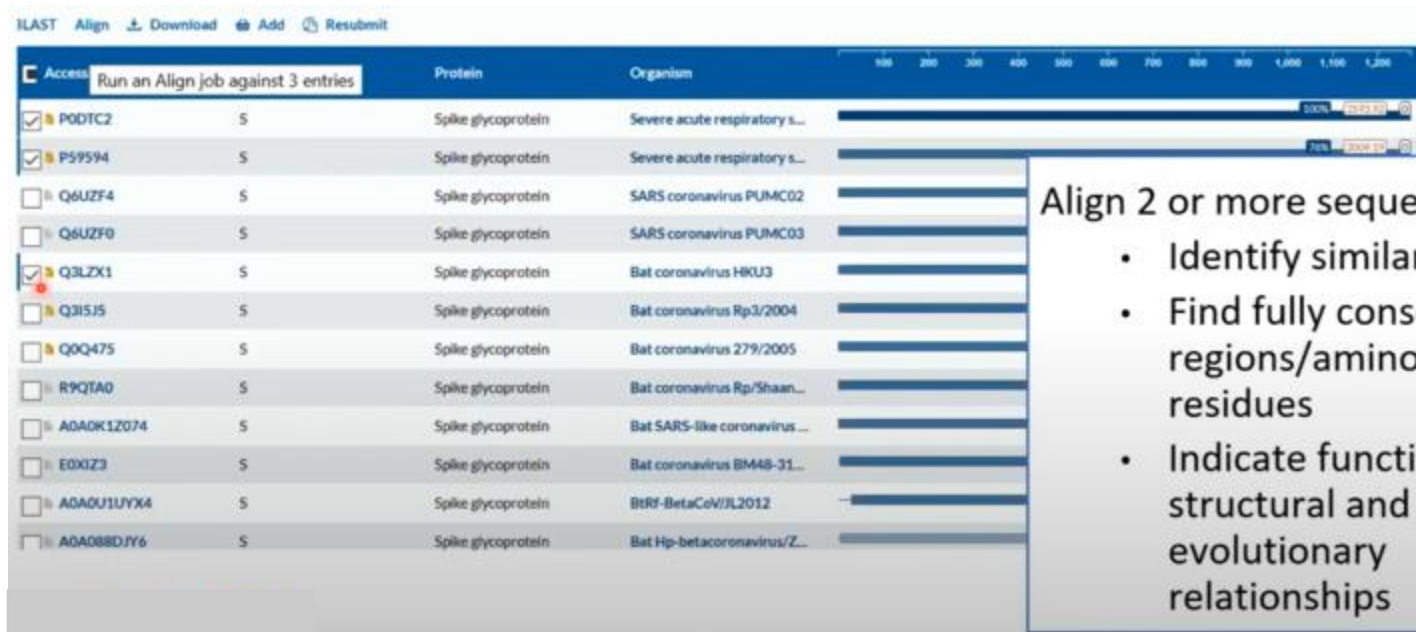
Overview

Q9WVS6.Chain

Query: IYKTNITGKTLTYNLEPOWDIKNVKELVAPQLBLOPDDKIIFAGKELSDATTIEGCDLGQGSVLHAIRLRPPVOROKIOSA81
Match: Q9WVS6 VVIRFNSSYGFPVEVDSDTSLQLKEVAKROGVPAOLRVIFAGKELPNHLIVQNCLEQGSIVHIVQ-RR-RRRSHETN81

Alignment with query sequence loads within the results page window

UniProt>Alineamiento con Clustal



The screenshot shows the UniProt Clustal alignment interface. At the top, there are buttons for 'Align', 'Download', 'Add', and 'Resubmit'. Below these is a table of protein sequences. The table has columns for 'Accession', 'Protein', and 'Organism'. The 'Accession' column contains a list of protein IDs, some of which are checked. The 'Protein' column contains the protein names, and the 'Organism' column contains the organism names. A progress bar at the top right indicates the alignment progress, showing 100% completion for the first two sequences and 75% for the third.

Accession	Protein	Organism
<input checked="" type="checkbox"/> P0DTC2	Spike glycoprotein	Severe acute respiratory s...
<input checked="" type="checkbox"/> P59594	Spike glycoprotein	Severe acute respiratory s...
<input type="checkbox"/> Q6UZF4	Spike glycoprotein	SARS coronavirus PUMC02
<input type="checkbox"/> Q6UZF0	Spike glycoprotein	SARS coronavirus PUMC03
<input checked="" type="checkbox"/> Q3LZX1	Spike glycoprotein	Bat coronavirus HKU3
<input type="checkbox"/> Q315J5	Spike glycoprotein	Bat coronavirus Rp3/2004
<input type="checkbox"/> Q0Q475	Spike glycoprotein	Bat coronavirus 279/2005
<input type="checkbox"/> R9QTA0	Spike glycoprotein	Bat coronavirus Rp/Shaan...
<input type="checkbox"/> A0A0K1Z074	Spike glycoprotein	Bat SARS-like coronavirus ...
<input type="checkbox"/> E0X0Z3	Spike glycoprotein	Bat coronavirus BM48-31...
<input type="checkbox"/> A0A0U1UYX4	Spike glycoprotein	BtRF-BetaCoV/IL2012
<input type="checkbox"/> A0A088DJY6	Spike glycoprotein	Bat Hp-betacoronavirus/Z...

Align 2 or more sequences:

- Identify similar regions
- Find fully conserved regions/amino acid residues
- Indicate functional, structural and evolutionary relationships

UniProt>Alineamiento con Clustal

Align Results

Overview | Phylogenetic Tree | Percent Identity Matrix | Text Output | Input Parameters | API Request

Download | Resubmit

Highlight properties | Select annotation | View: Overview | **Wrapped**

☐ sp|Q7KTX7|PRKN_DROME MSFIFKFIATFVRKMLELLQFGGKTLTHTLSIYVKTNTGKTLTVNL 46

☐ sp|O60260|PRKN_HUMAN MIVFVRFNSSHGFPVEV 17

☐ sp|Q9WVS6|PRKN_MOUSE MIVFVRFNSSYGFPVEV 17

☐ sp|Q9JK66|PRKN_RAT MIVFVRFNSSYGFPVEV 17

sp|Q9JK66-4|PRKN-4_RAT MIVFVRFNSSYGFPVEV 17

Q7KTX7:Chain

☐ sp|Q7KTX7|PRKN_DROME EPOWDIKNVKELVAPQLGLOPDDLKIIFAGKELSDATTI 85

☐ sp|O60260|PRKN_HUMAN DSDTSIFQLKEVVAKRQGV PADQLRVIFAGKELRNDWTV 56

☐ sp|Q9WVS6|PRKN_MOUSE DSDTSIFQLKEVVAKRQGV PADQLRVIFAGKELPNHLTV 56

☐ sp|Q9JK66|PRKN_RAT DSDTSIFQLKEVVAKRQGV PADQLRVIFAGKELQNHLTV 56

sp|Q9JK66-4|PRKN-4_RAT DSDTSIFQLKEVVAKRQGV PADQLRVIFAGKELQNHLTVQHPQDGF 63

Q7KTX7:Chain

Display user-requested protein features tracks

UniProt>Búsqueda de información sobre patologías



The screenshot shows the UniProt homepage. At the top, there are four main sections: **Proteins** (UniProt Knowledgebase), **Species** (Proteomes), **Protein Clusters** (UniRef), and **Sequence Archive** (UniParc). Below these is a 'Supporting Data' section with a grid of links. An orange arrow labeled 'Search specific diseases' points to the 'Diseases' link in this grid. Other links in the grid include Taxonomy, Subcellular locations, UniRule automatic annotation, Keywords, Literature Citations, Cross-referenced databases, and ARBA automatic annotation. Below the 'Supporting Data' section, there are three featured articles: 'On guard' (about space humans), 'AlphaFold structure pred...' (about molecular structural research), and 'Latest News' (about UniProt changes and release 2021_03).

Proteins
UniProt Knowledgebase

Species
Proteomes

Protein Clusters
UniRef

Sequence Archive
UniParc

Reviewed Swiss-Prot | Unreviewed TrEMBL

Protein sets for species with sequenced genomes from across the tree of life

Clusters of protein sequences at 100%, 90% & 50% identity

Non-redundant archive of publicly available protein sequences from across different databases

Search specific diseases

Supporting Data

- Diseases
- Taxonomy
- Subcellular locations
- UniRule automatic annotation
- Keywords
- Literature Citations
- Cross-referenced databases
- ARBA automatic annotation

On guard

The space humans evolve in is divided into parts. It makes life easier. Each part is dedicated to a certain activity. We have homes to live in, pools to swim in, restaurants

AlphaFold structure pred...

Today marks a historic moment in the world of molecular structural research. AlphaFold...

Latest News

View archive

Forthcoming changes
Planned changes for UniProt
UniProt release 2021_03
The importance of being disordered | MobiDB-lite predictions for intrinsically disordered regions |...

UniProt>Búsqueda de información sobre patologías



- Function
- Names & Taxonomy
- Subcellular Location
- Disease & Variants**
- PTM/Processing
- Expression
- Interaction
- Structure
- Family & Domains
- Sequence & Isoforms
- Similar Proteins

Disease & Variants¹

Involvement in disease¹

Parkinson disease (PARK)

[4 Publications](#)

Note Disease susceptibility may be associated with variants affecting the gene represented in this entry. Heterozygous mutations act as susceptibility alleles for (PubMed:12730996 and PubMed:12629236)

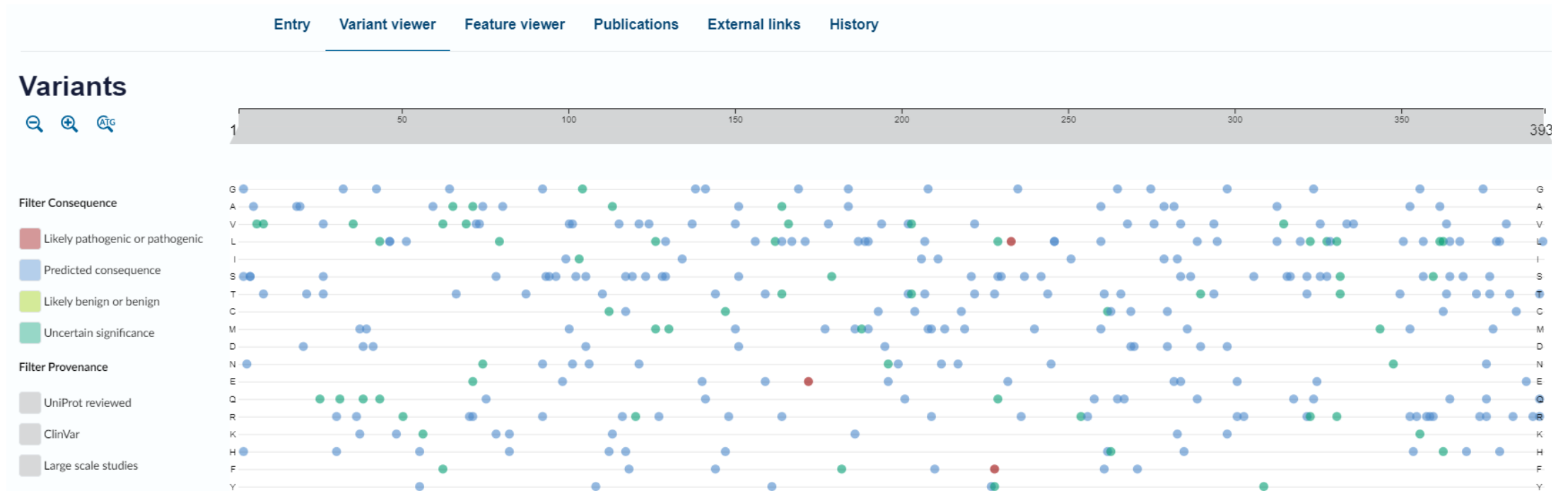
Description A complex neurodegenerative disorder characterized by bradykinesia, resting tremor, muscular rigidity and postural instability. Additional features are chorea, dysautonomia, dystonic cramps, and dementia. The pathology of Parkinson disease involves the loss of dopaminergic neurons in the substantia nigra and the accumulations of aggregated proteins in surviving neurons in various areas of the brain. The disease is progressive and usually manifests after the age of 50 (before 50 years) are known. The majority of the cases are sporadic suggesting a multifactorial etiology based on environmental and genetic factors. However, family history for the disease. Familial forms of the disease usually begin at earlier ages and are associated with atypical clinical features.

See also [MIM:168600](#) [2]

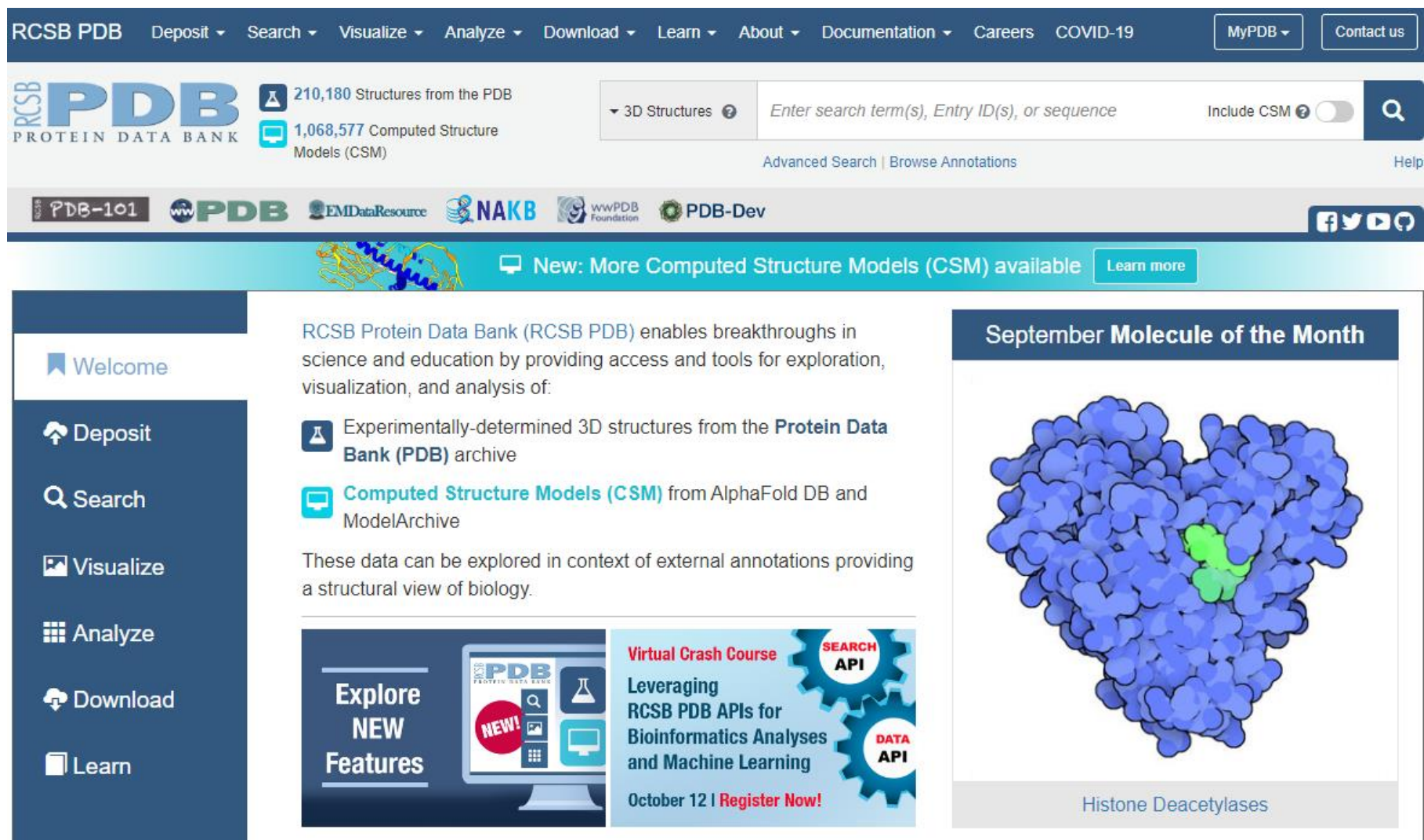
Natural variants in PARK

VARIANT ID	POSITION(S)	CHANGE	DESCRIPTION
VAR_019736	42	R>P	In PARK2 and PARK; induces a conformational change in the PSMD4-binding site of Ubl resulting in impaired proteasomal binding; decrease increased aggregation; impairs the ability to ubiquitinate and degrade SYT11; dbSNP:rs308134306 7 Publications
VAR_019749	253	C>Y	In PARK; late onset; dbSNP:rs747427602 1 Publication
VAR_019750	256	R>C	In PARK2 and PARK; at heterozygosity it is associated with late onset Parkinson disease; impairs the ability to ubiquitinate SNCAIP and ZNF promoter; abolishes TP53 transcriptional repression; dbSNP:rs150562946 7 Publications
VAR_019752	275	R>W	In PARK2 and PARK; at heterozygosity it is associated with late onset Parkinson disease; impairs the ability to ubiquitinate SNCAIP; abolish impairs the ability to ubiquitinate and degrade SYT11; dbSNP:rs34424956 12 Publications
VAR_019753	300	D>N	In PARK; does not affect PINK-1 dependent localization to depolarized mitochondria; dbSNP:rs72480422 3 Publications

UniProt>Búsqueda de información sobre patologías



Protein Data Bank



The screenshot shows the RCSB PDB website homepage. The top navigation bar includes links for Deposit, Search, Visualize, Analyze, Download, Learn, About, Documentation, Careers, and COVID-19, along with MyPDB and Contact us buttons. The main header displays the RCSB PDB logo and statistics: 210,180 Structures from the PDB and 1,068,577 Computed Structure Models (CSM). A search bar is present with a dropdown for '3D Structures' and a search button. Below the header, there are logos for PDB-101, PDB, EMDDataResource, NAKB, wwPDB Foundation, and PDB-Dev, along with social media icons. A banner for 'New: More Computed Structure Models (CSM) available' is visible. The main content area features a 'Welcome' message, a list of services (Deposit, Search, Visualize, Analyze, Download, Learn), and a description of the PDB's mission. It also highlights 'Experimentally-determined 3D structures from the Protein Data Bank (PDB) archive' and 'Computed Structure Models (CSM) from AlphaFold DB and ModelArchive'. A section for 'September Molecule of the Month' features a 3D model of Histone Deacetylases. At the bottom, there is a 'Virtual Crash Course' announcement for leveraging RCSB PDB APIs for bioinformatics analyses and machine learning, scheduled for October 12.

RCSB PDB Deposit Search Visualize Analyze Download Learn About Documentation Careers COVID-19 MyPDB Contact us

RCSB PDB PROTEIN DATA BANK

210,180 Structures from the PDB

1,068,577 Computed Structure Models (CSM)

3D Structures ? Enter search term(s), Entry ID(s), or sequence Include CSM ?

Advanced Search | Browse Annotations Help

PDB-101 PDB EMDDataResource NAKB wwPDB Foundation PDB-Dev

New: More Computed Structure Models (CSM) available Learn more

Welcome

Deposit Search Visualize Analyze Download Learn

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.

Explore NEW Features

Virtual Crash Course
Leveraging RCSB PDB APIs for Bioinformatics Analyses and Machine Learning
October 12 | Register Now!

SEARCH API
DATA API

September Molecule of the Month

Histone Deacetylases

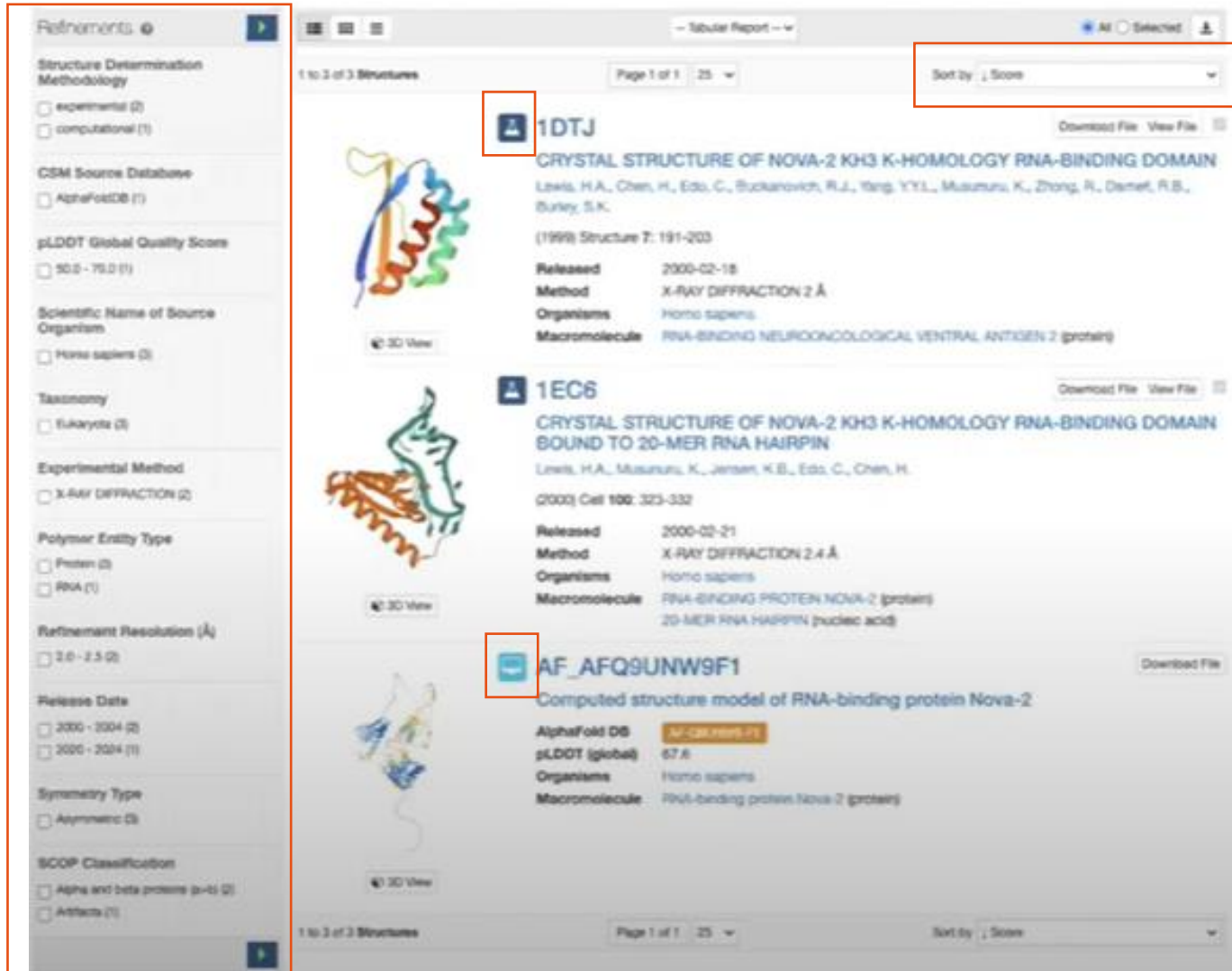
Protein Data Bank>Búsqueda avanzada

Advanced Search Query Builder

Full Text	Free text search (google-like)
Structure Attributes	Structure property (length, size, resolution, ...)
Chemical Attributes	Chemical property (name, weight, ...)
Sequence Similarity	Sequence identity search (mmseqs2)
Sequence Motif	Amino acid regular expression (pattern, e.g. /MM*G/)
Structure Similarity	Structure similarity search (in-house algorithm)
Structure Motif	Structural pattern search (local geometric pattern)
Chemical Similarity	Chemical structure search (smiles / 2D graph molecule)

Return Structures grouped by No Grouping Include Computed Structure Models (CSM) ☒ Count Clear Search

Protein Data Bank>Resultados de búsqueda



Refinements

Structure Determination Methodology

- ☐ experimental (2)
- ☐ computational (1)

CSM Source Database

- ☐ AlphaFoldDB (1)

pLDDT Global Quality Score

- ☐ 90.0 - 95.0 (1)

Scientific Name of Source Organism

- ☐ Homo sapiens (2)

Taxonomy

- ☐ Eukaryote (2)

Experimental Method

- ☐ X-RAY DIFFRACTION (2)

Polymer Entity Type

- ☐ Protein (2)
- ☐ RNA (1)

Refinement Resolution (Å)

- ☐ 2.0 - 2.5 (2)

Release Date

- ☐ 2000 - 2004 (2)
- ☐ 2000 - 2004 (1)

Symmetry Type

- ☐ Asymmetric (2)

SCOP Classification


- ☐ Alpha and beta proteins (a-b) (2)
- ☐ Antifolds (1)

1DTJ
CRYSTAL STRUCTURE OF NOVA-2 KH3 K-HOMOLOGY RNA-BINDING DOMAIN
Lewis, H.A., Chen, H., Edo, C., Buckanovich, R.J., Teng, Y.Y.L., Musumeci, K., Zhong, R., Darnell, R.B., Burley, S.K.
(1999) Structure 7: 191-203
Released: 2000-02-18
Method: X-RAY DIFFRACTION 2 Å
Organisms: Homo sapiens
Macromolecule: RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2 (protein)

1EC6
CRYSTAL STRUCTURE OF NOVA-2 KH3 K-HOMOLOGY RNA-BINDING DOMAIN BOUND TO 20-MER RNA HAIRPIN
Lewis, H.A., Musumeci, K., Jensen, K.B., Edo, C., Chen, H.
(2000) Cell 100: 323-332
Released: 2000-02-21
Method: X-RAY DIFFRACTION 2.4 Å
Organisms: Homo sapiens
Macromolecule: RNA-BINDING PROTEIN NOVA-2 (protein); 20-MER RNA HAIRPIN (nucleic acid)


AF_AFQ9UNW9F1
Computed structure model of RNA-binding protein Nova-2
AlphaFold DB: AF-Q8U9UNW9F1
pLDDT (global): 67 Å
Organisms: Homo sapiens
Macromolecule: RNA-binding protein Nova-2 (protein)

Protein Data Bank>Enlaces a búsqueda dentro de resultados



The screenshot displays the PDB entry page for AF_AFQ9UNW9F1, a computed structure model of RNA-binding protein Nova-2. The page includes a 3D structure viewer, a table of similar proteins, and a dropdown menu for finding similar proteins by sequence or structure.

Entity ID: 1

Entity ID: 1	Sequence Length	Organism	Details	Image
Molecule				
RNA-binding protein Nova-2	492	Homo sapiens	Mutation(s): 0 Gene Names: NOVA2	

Find similar proteins by: **Sequence** (by identity cutoff) | **3D Structure**

Sequence Similarity Search

Structure Similarity Search

Macromolecules

Model Confidence

pLDDT (global): 87.5
pLDDT (local):

Macromolecule Content

- Total Structure Weight: 57.89 kDa
- Atom Count: 3,449
- Modelled Residue Count: 492
- Deposited Residue Count: 492
- Unique protein chains: 1

UniProt & NIH Commons

Find proteins for [Q9UNW9](#)

PHAROS: [Q9UNW9](#)

Explore [Q9UNW9](#)

Go to UniProtKB: [Q9UNW9](#)

Protein Data Bank>Búsqueda avanzada

Advanced Search Query Builder [Help](#)

Full Text [?](#)

Structure Attributes [?](#) [Help](#)

	Structure Determination Methodology	x	is	experimental		+ NOT	Count	x
AND	Data Collection Resolution	x	<=	4	Å	+ NOT	Count	x

AND / OR Add Attribute Add Subquery Remove Subquery

Add Subquery

Chemical Attributes [?](#)

Sequence Similarity [?](#) [Help](#)

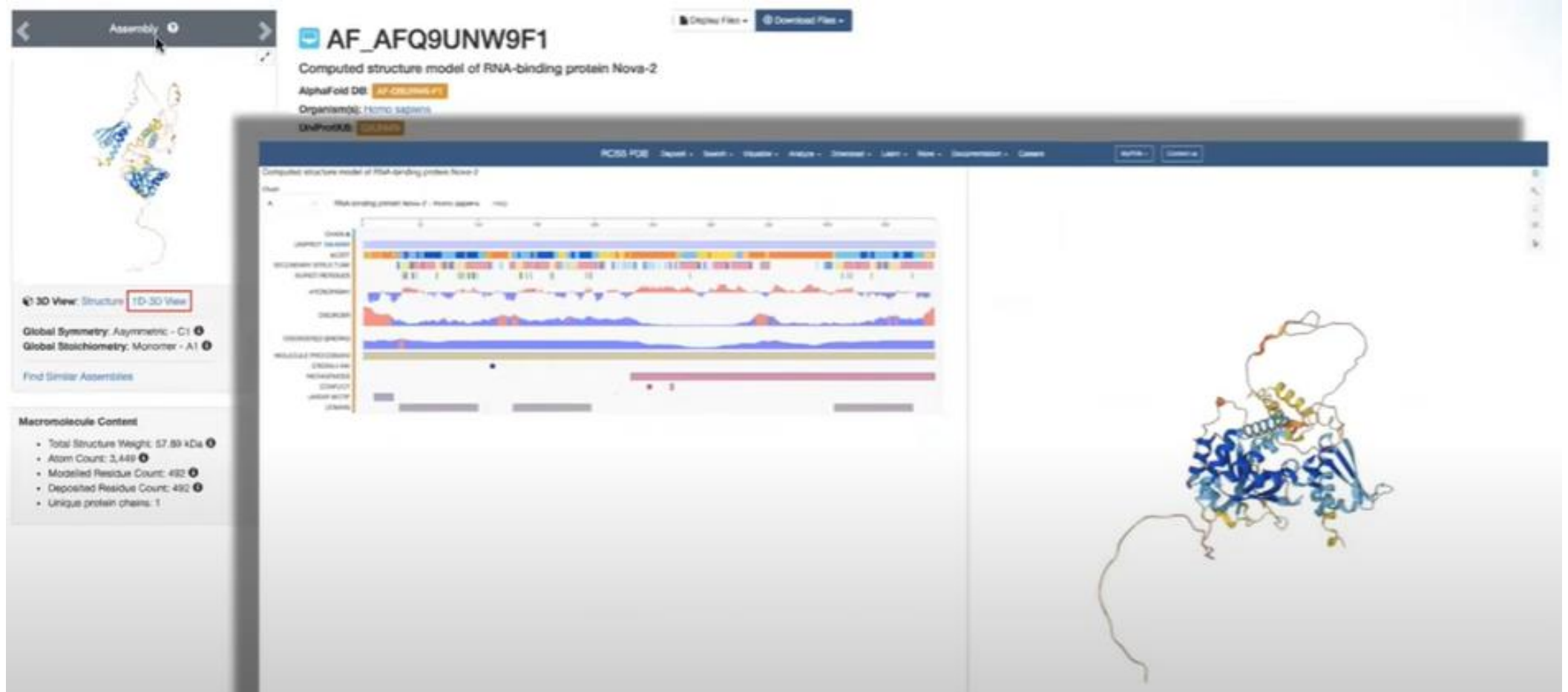
AND MTTAPQEPPARPLQAGSGAGPAPGRAMRSTLLALLALVLLYLVSGALVFRALEQPHEQQAQRELGEVREKFLRAHPCVSDQELGLLIKEVADALGGGADPETQSTSQSSHSAWDLGSAFFFSGTIITIGYGN
VALRTDAGRLFCIFYALVGIFLFGILLAGVGDRLGSSLRHGIGHIEAIFLKWHPPELVRVLSAMFLLLIGCLLFVLTPTFVFCYMEDWSKLEAIYFVIVTLTTVGFGDYVAGADPRQDSPAYQPLVWFWILLGLAYFA

Entry ID Sequence Type [?](#) E-Value Cutoff [?](#) Identity Cutoff % (Integer only) [?](#) Count Clear

Sequence Motif [?](#)

Structure Similarity [?](#)

Protein Data Bank>Visor 1D-3D





viu

Universidad
Internacional
de Valencia

universidadviu.com

De:
 Planeta Formación y Universidades