

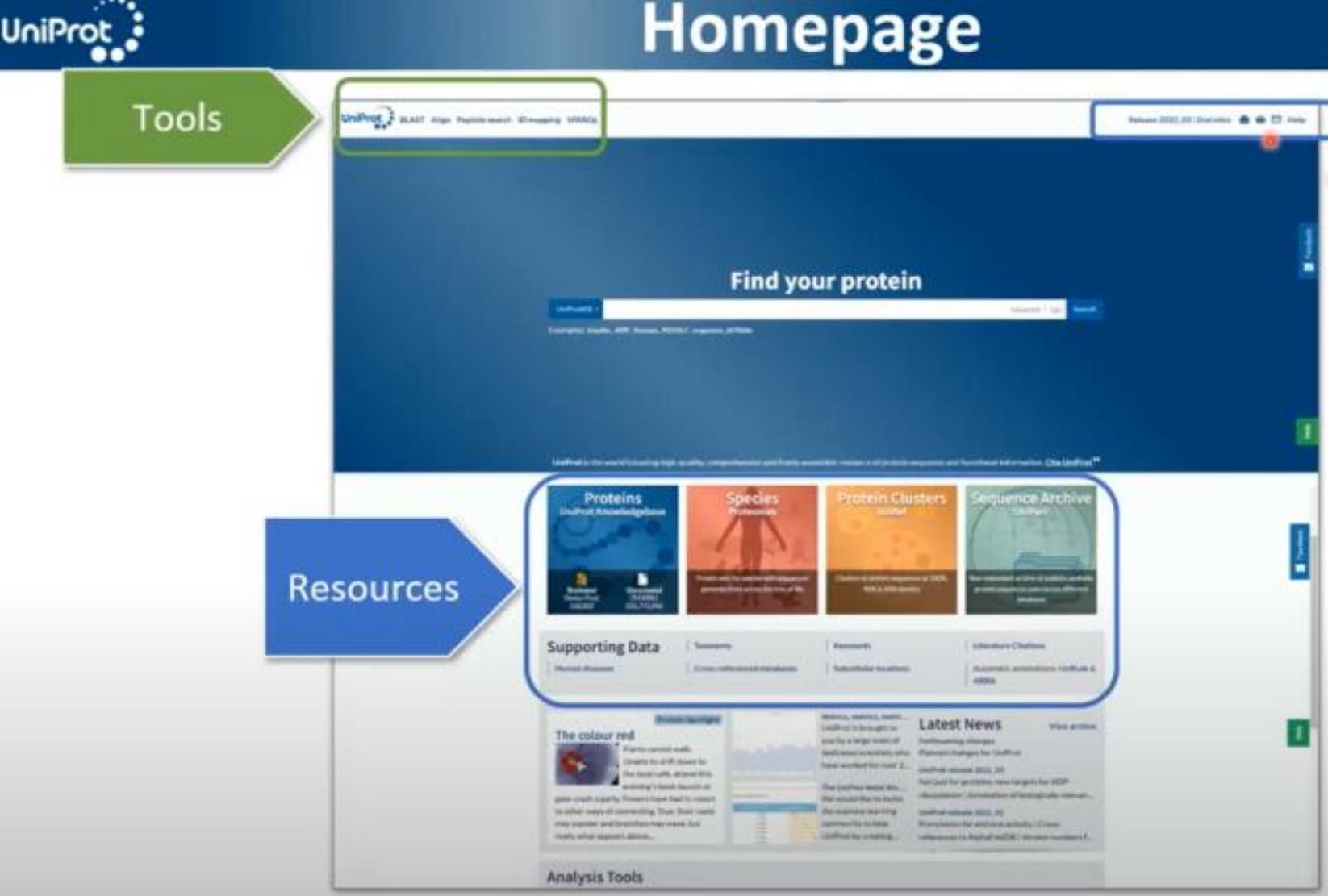
# AP1.1 Bases de datos



viu

**Universidad**  
Internacional  
de Valencia

# UniProt

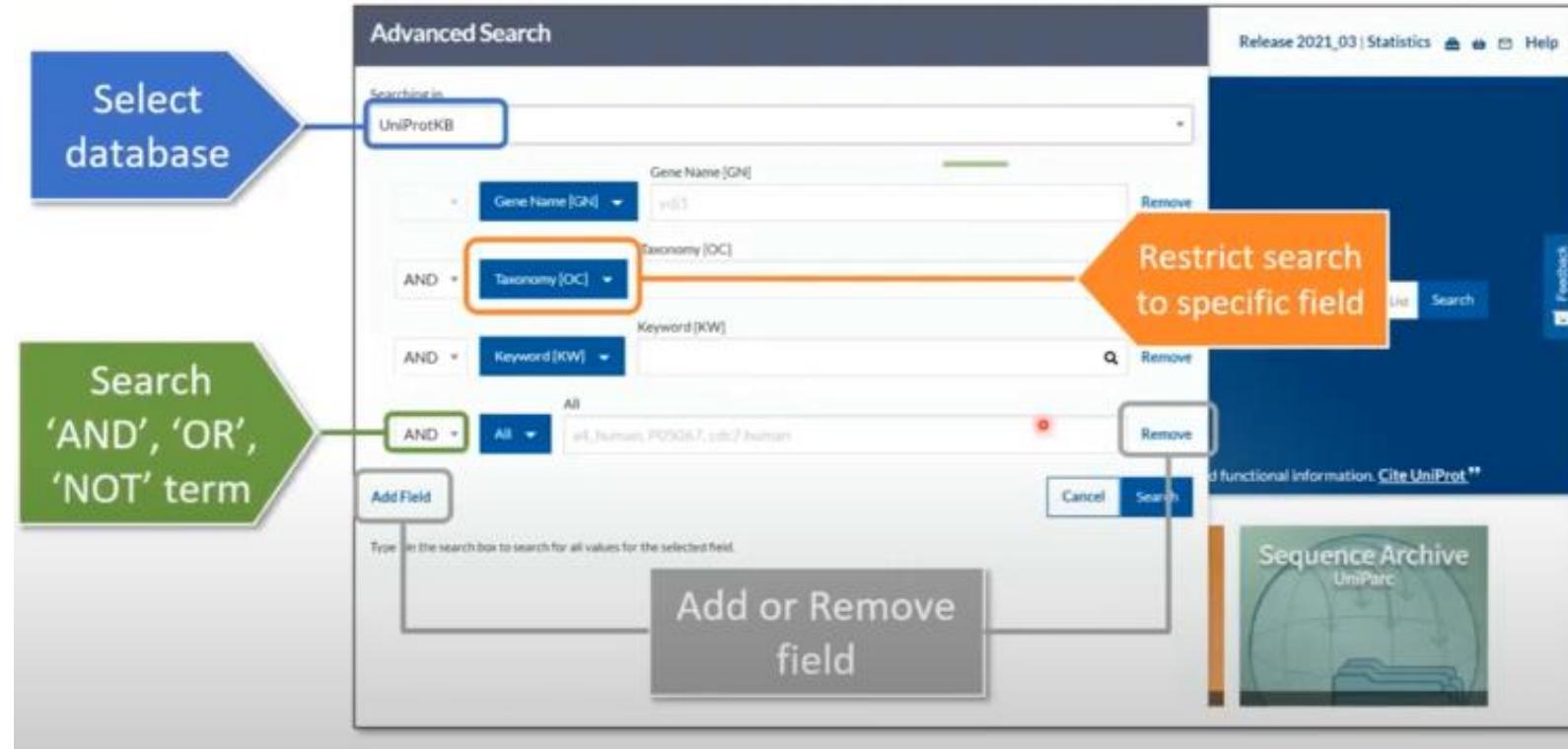


The image shows the UniProt homepage. A green arrow labeled "Tools" points to the top navigation bar, which includes links for BLAST, Align, Peptidomass, IDmapping, and UniRef. A blue arrow labeled "Resources" points to the main content area. The main content area features a search bar with the placeholder "Find your protein". Below the search bar, there is a section titled "UniProt in the world" with a sub-section "UniProt Knowledgebase". This section includes four cards: "Proteins (UniProt Knowledgebase)" (blue background), "Species (Proteomes)" (orange background), "Protein Clusters (SCOPe)" (yellow background), and "Sequence Archive (SRS)" (green background). The "Sequence Archive" card is circled in red. Below this, there are sections for "Supporting Data" and "Latest News".

# UniProt>Búsqueda



# UniProt>Búsqueda avanzada



# 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

| i Your input contains 3 IDs

From database

To database

Restrict by taxonomy

Gene Name

UniProtKB

x

Homo sapiens (Human/Man) [9606]

Human immunodeficiency virus 1 (HIV/AIDS virus) |

Human betapapillomavirus [1188015]

Name your ID Mapping job

# UniProt>Filtrado de búsqueda

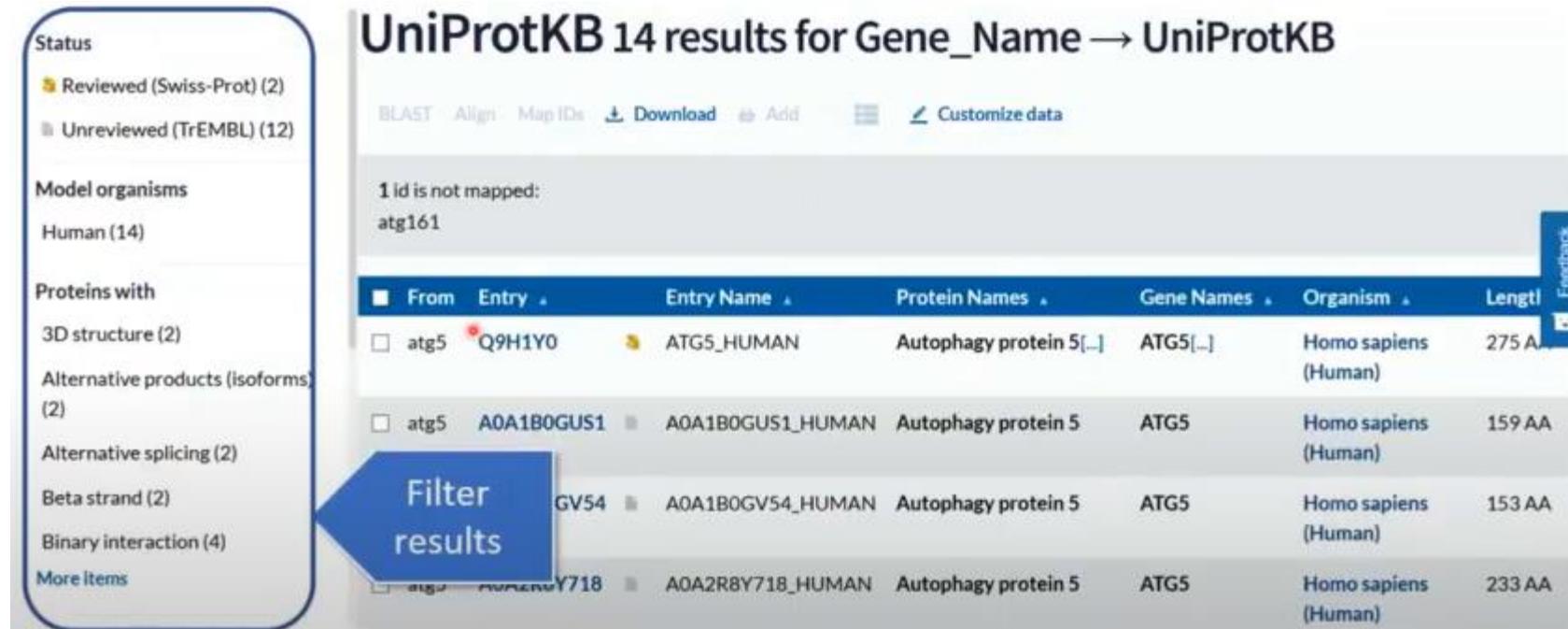
UniProtKB 14 results for Gene\_Name → UniProtKB

BLAST Align Map IDs Download Add Customize data

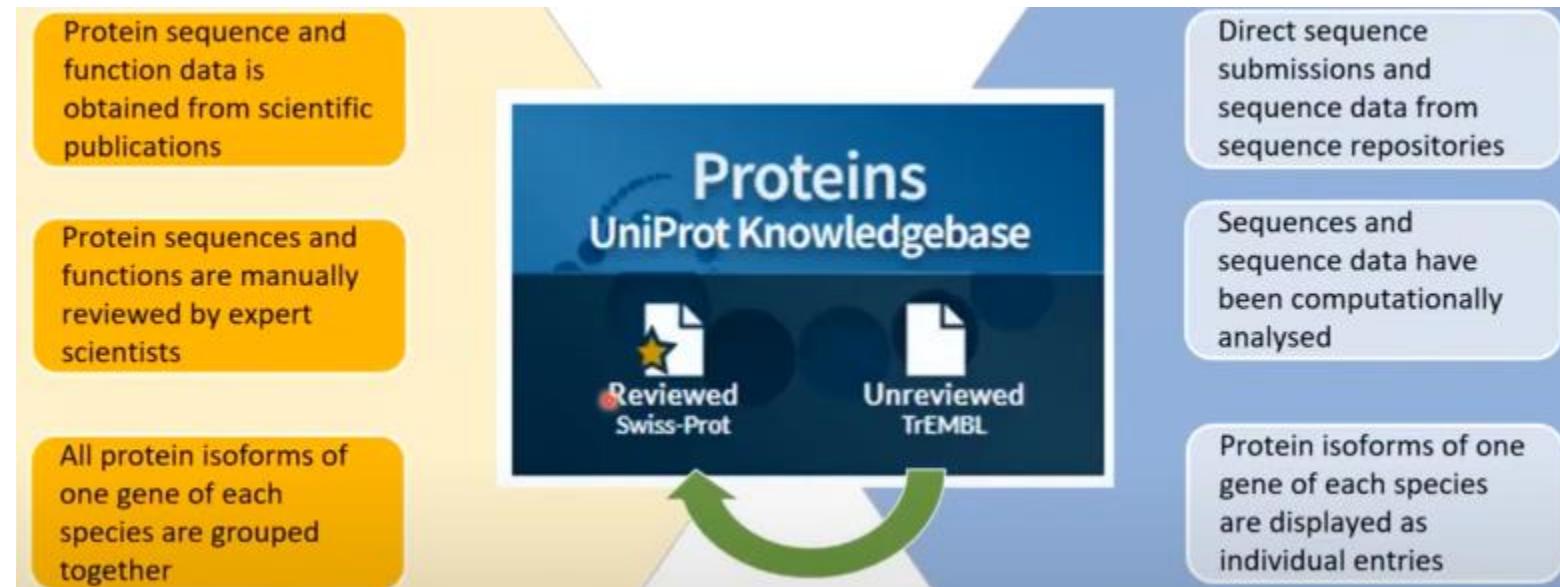
1 id is not mapped:  
atg161

| From | Entry      | Entry Name       | Protein Names            | Gene Names | Organism             | Length |
|------|------------|------------------|--------------------------|------------|----------------------|--------|
| atg5 | Q9H1Y0     | ATG5_HUMAN       | Autophagy protein 5[...] | ATG5[...]  | Homo sapiens (Human) | 275 AA |
| atg5 | A0A1B0GUS1 | A0A1B0GUS1_HUMAN | Autophagy protein 5      | ATG5       | Homo sapiens (Human) | 159 AA |
| GV54 | A0A1B0GV54 | A0A1B0GV54_HUMAN | Autophagy protein 5      | ATG5       | Homo sapiens (Human) | 153 AA |
| Y718 | A0A2R8Y718 | A0A2R8Y718_HUMAN | Autophagy protein 5      | ATG5       | Homo sapiens (Human) | 233 AA |

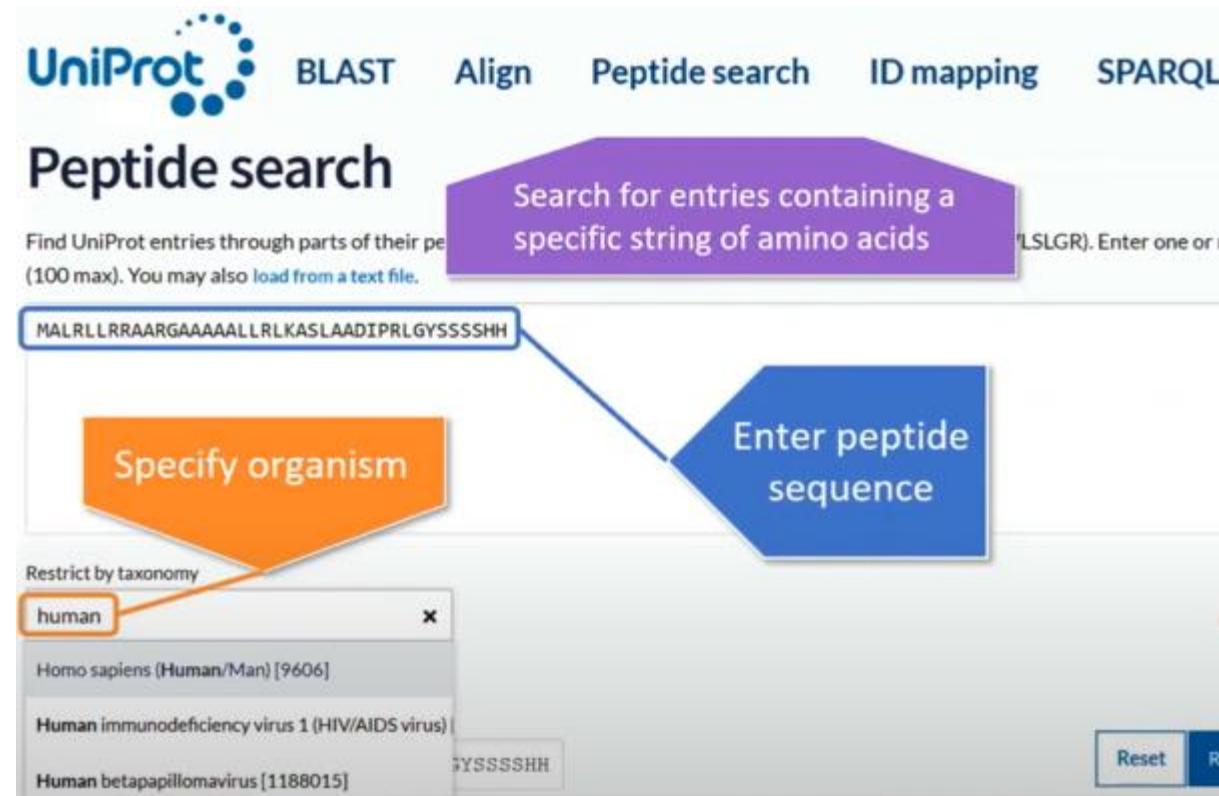
Filter results



# UniProt>Revisión de entradas



# UniProt>Búsqueda de fragmentos peptídicos



The screenshot shows the UniProt Peptide search interface. At the top, there are links for BLAST, Align, Peptide search, ID mapping, and SPARQL. The main title is "Peptide search" with the sub-instruction: "Find UniProt entries through parts of their peptide sequences (100 max). You may also load from a text file." A purple callout box highlights the search input field: "Search for entries containing a specific string of amino acids". Below the input field is the peptide sequence: "MALRLLRRAARGAAAAALLRLKASLAADIPRLGYSSSSHH". To the left of the sequence is an orange callout box labeled "Specify organism" with a sub-instruction: "Restrict by taxonomy". A dropdown menu is open, showing "human" selected. Other options include "Homo sapiens (Human/Man) [9606]", "Human immunodeficiency virus 1 (HIV/AIDS virus)", and "Human betapapillomavirus [1188015]". To the right of the sequence is a blue callout box labeled "Enter peptide sequence". At the bottom right are "Reset" and "Run" buttons.

# 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

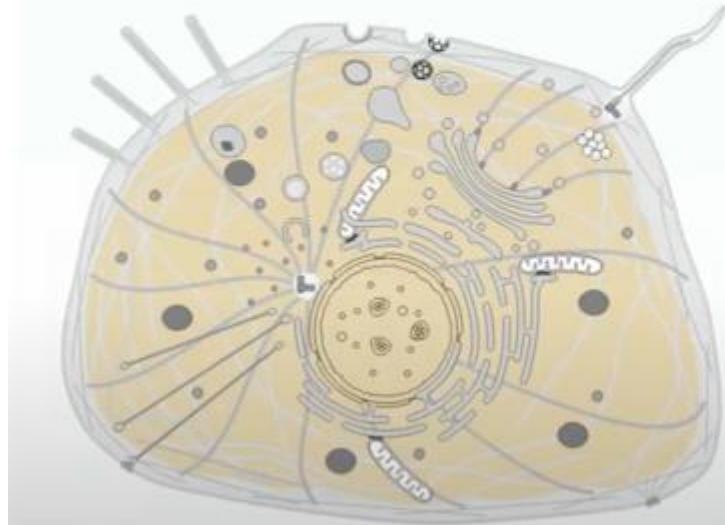
Serine kinase that plays an essential role in the NF-kappa-B signaling pathway which is activated by multiple stimuli such as inflammatory cytokines, bacterial or viral products, DNA damages or other cellular stresses (PubMed:9244310, PubMed:9252186, PubMed:9346484, PubMed:18626576).  
Acts as part of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

Click on any of the quick access tabs to explore specific sections

# UniProt>Información de una entrada

## Subcellular Location

UniProt Annotation   GO Annotation



Cytoplasm

Nucleus

Shuttles between the cytoplasm and the nucleus.

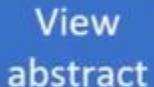
The subcellular location viewer highlights where the protein is expressed in the cell

# UniProt>Citaciones bibliográficas relacionadas con el contenido

and fungi (PubMed:12408809, PubMed:12456640, PubMed:18801354, PubMed:22227521). Negatively regulates the Hayan-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). 

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



 PubMed  
 Europe PMC  
Dev. Cell 3:581-592(2002) ↗  
Mapped to  
1 3 24 ↗



# 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 Last updated 2020-04-22 v1  
Mass(Da) 141,178 Checksum B17BE6D9F1C4EA34

|            |             |             |            |            |            |            |            |            |            |            |            |
|------------|-------------|-------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 10         | 20          | 30          | 40         | 50         | 60         | 70         | 80         | 90         | 100        | 110        | 120        |
| MFVFLVLLPL | VSSQCVNLTT  | RTQLPPIAYTN | SFTRGVYYPD | KVFRSSVLHS | TQDLFLPFFS | NVTWPHAIHV | SGTNGTKRFD | NPVLPFNDGV | YFASTEKSNI | IRGWIFGTTL | DSKTQSLLIV |
| 130        | 140         | 150         | 160        | 170        | 180        | 190        | 200        | 210        | 220        | 230        | 240        |
| NNATNVIK   | CEFAQFCNDPF | LGVYYYHKNNK | SMMESEFRVY | SSANNCTFEY | VSQPFLMDLE | GKQGNFKNLR | EFVFKNIDGY | FKIYSKHTPI | NLVRDLPQGF | SALEPLVDLP | IGINITRFQT |
| 250        | 260         | 270         | 280        | 290        | 300        | 310        | 320        | 330        | 340        | 350        | 360        |
| LLALHRSYLT | PGDSSSGWTA  | GAAYYYYGYL  | QPRTFLLKYN | ENGTITDAVD | CALDPLSETK | CTLKSFTVKE | GIYQTSNFRV | QPTESIVRFP | NITNLCPFGE | VFNATRFASV | YAWNRKRISN |
| 370        | 380         | 390         | 400        | 410        | 420        | 430        | 440        | 450        | 460        | 470        | 480        |
| CVADYSVLYN | SASFSTFKCY  | GVSPTKLNDL  | CFTINVYADF | VIRGDEVRI  | APGQTGKIA  | YNYKLPDDFT | GCVIAWSNSN | LDSKVGNNYN | YLYRLFRKSN | LKPFERDIST | EIYQAGSTPC |
| 490        | 500         | 510         | 520        | 530        | 540        | 550        | 560        | 570        | 580        | 590        | 600        |
| NGVEGFNCYF | PLQSYGFQPT  | NGVGYQPYRV  | VVLSFELLHA | PATVCGPKKS | TNLVVKNCVN | FNFNGLTGTG | VLTESNKKFL | PFQQFGRDIA | DTTDAVRDQ  | TLEILDITPC | SFGGVSVITP |
| 610        | 620         | 630         | 640        | 650        | 660        | 670        | 680        | 690        | 700        | 710        | 720        |
| GTNTSNQAV  | LYQDQNCTEV  | PVAIHADQLT  | PTWRVYSTGS | NVFQTRAGCL | IGAEHMNSY  | ECDIPIGAGI | CASYQTQTN  | PRRARVASQ  | SIIAYTMSLG | AENSVAYSNN | SIAIPTNFTI |

# UniProt>Caracterización



# UniProt>BLAST

**P0DTC2 · SPIKE\_SARS2**

Spike glycoprotein · Severe acute respiratory syndrome coronavirus 2 (2019-nCoV) (SARS-CoV-2) · Gene: S - 1273 ·

Entry Feature viewer Publications External links History

**BLAST** Align Download Add Community curation (4) Add a publication Entry feedback

**Function**

**BLAST results 250 results**

Overview Taxonomy Hit Distribution Text Output Input Parameters API Request

BLAST Args Download Resubmit

| Accession  | Gene  | Protein                                | Organism                | Identity | Score | E-value  |
|------------|-------|--|-------------------------|----------|-------|----------|
| O60260     | PRKN  | E3 ubiquitin-protein ligase            | Homo sapiens            | 53.6     | 265   | 2.10e-22 |
| H2QJ08     | PRKN  | E3 ubiquitin-protein ligase            | Pan troglodytes         | 53.6     | 2593  |          |
| A0A212YTU5 | PRKN  | E3 ubiquitin-protein ligase            | Gorilla gorilla gorilla | 53.6     |       |          |
| A0A2K6P0M3 | PRKN  | E3 ubiquitin-protein ligase            | Rhinopithecus roxellana | 53.6     |       |          |
| A0A2K6K8A3 | PRKN  | E3 ubiquitin-protein ligase            | Rhinopithecus bieti     | 53.6     |       |          |
| A0A096MX93 | PRKN  | E3 ubiquitin-protein ligase            | Papilio anubis          | 53.6     |       |          |
| B8YGJ6     | PARK2 | E3 ubiquitin-protein ligase            | Macaca fasciata         | 53.6     |       |          |
| A0A2K5HKB2 |       | E3 ubiquitin-protein ligase            | Colobus angolensis      | 53.6     |       |          |
| A0A2K6BSN6 | PRKN  | E3 ubiquitin-protein ligase            | Macaca nemestrina       | 53.6     |       |          |
| F6U1L3     | PRKN  | E3 ubiquitin-protein ligase            | Macaca mulatta          | 53.6     |       |          |
| A0A7N9CTJ5 |       | Parkin RBR E3 ubiquitin-protein ligase | Macaca fasciata         | 53.6     |       |          |
| A0A2K5M0T8 | PRKN  | E3 ubiquitin-protein ligase            | Cercopithecus atys      | 53.6     |       |          |
| A0A2K5E771 | PRKN  | E3 ubiquitin-protein ligase            | Aotus nancymai          | 53.6     |       |          |

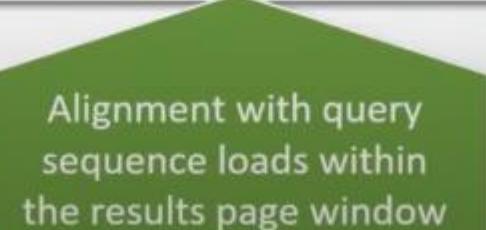
**Shows how similar your search query is to individual BLAST hits in the results table**

**Filters**

BLAST to find similar proteins

# UniProt>BLAST

 BLAST to find similar proteins

 Alignment with query sequence loads within the results page window

**P0DTC2 · SPIKE\_SARS2**  
Spike glycoprotein · Severe acute respiratory syndrome coronavirus 2 (2019-nCoV) (SARS-CoV-2) · Gene: S-1273 ·

Entry Feature viewer Publications External links History

BLAST  Download Add Community curation (4) Add a publication Entry feedback

### Function

Blast parameters

Identity: 40.2 Score: 100

Q9WVS6 · E3 ubiquitin-protein ligase parkin · *Mus musculus*

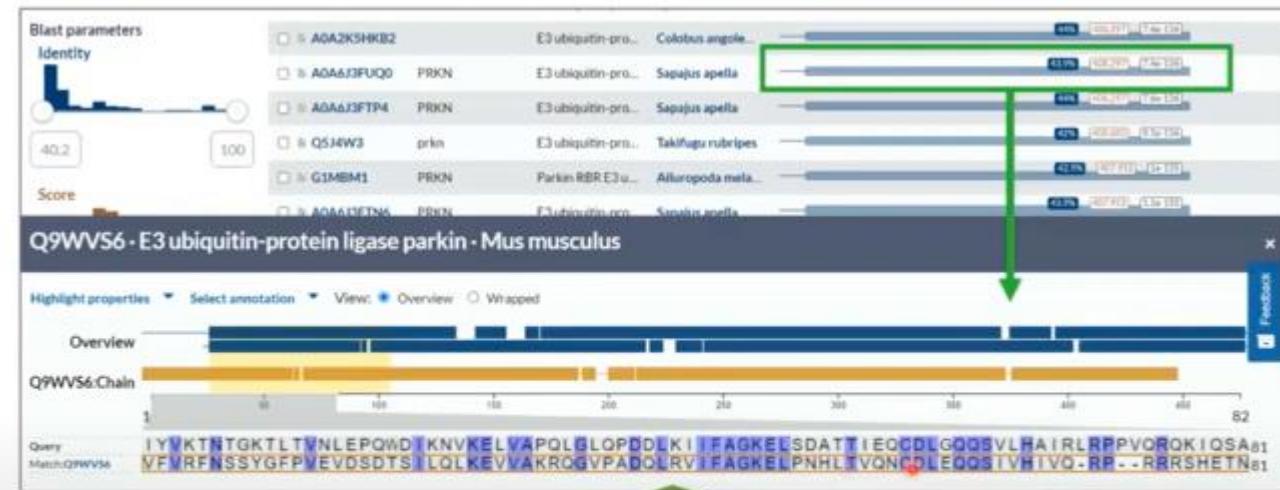
Highlight properties Select annotation View: Overview Wrapped

Overview

Q9WVS6\_Chain

Query Match: Q9WVS6

Sequence alignment showing the alignment of the query sequence (Q9WVS6) with the target sequence (P0DTC2). The alignment highlights conserved regions with blue shading. A green arrow points from the green arrow at the bottom to the alignment window, indicating that the alignment with the query sequence loads directly within the results page window.



# UniProt>Alineamiento con Clustal

ILAST Align ↗ Download Add Resubmit

Access Run an Align job against 3 entries

|                                     | Protein    | Organism           | 100                           | 200   | 300     | 400    | 500      | 600      | 700      | 800          | 900         | 1,000  | 1,100         | 1,200  |
|-------------------------------------|------------|--------------------|-------------------------------|-------|---------|--------|----------|----------|----------|--------------|-------------|--------|---------------|--------|
| <input checked="" type="checkbox"/> | P0DTG2     | Spike glycoprotein | Severe acute respiratory s... | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |
| <input checked="" type="checkbox"/> | P59594     | Spike glycoprotein | Severe acute respiratory s... | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |
| <input type="checkbox"/>            | Q6UZF4     | Spike glycoprotein | SARS coronavirus PUMC02       | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |
| <input type="checkbox"/>            | Q6UZF0     | Spike glycoprotein | SARS coronavirus PUMC03       | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |
| <input checked="" type="checkbox"/> | Q3LZX1     | Spike glycoprotein | Bat coronavirus HKU3          | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |
| <input type="checkbox"/>            | Q3I5J5     | Spike glycoprotein | Bat coronavirus Rp3/2004      | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |
| <input type="checkbox"/>            | Q0Q475     | Spike glycoprotein | Bat coronavirus 279/2005      | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |
| <input type="checkbox"/>            | R9QTA0     | Spike glycoprotein | Bat coronavirus Rp/Shaan...   | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |
| <input type="checkbox"/>            | AOA0K1Z074 | Spike glycoprotein | Bat SARS-like coronavirus ... | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |
| <input type="checkbox"/>            | E0XIZ3     | Spike glycoprotein | Bat coronavirus BM48-31...    | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |
| <input type="checkbox"/>            | AOA0U1UYX4 | Spike glycoprotein | BtRf-BetaCoV/JL2012           | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |
| <input type="checkbox"/>            | AOA088DJY6 | Spike glycoprotein | Bat Hp-beta-coronavirus/Z...  | [red] | [green] | [blue] | [orange] | [purple] | [yellow] | [light blue] | [dark blue] | [pink] | [light green] | [grey] |

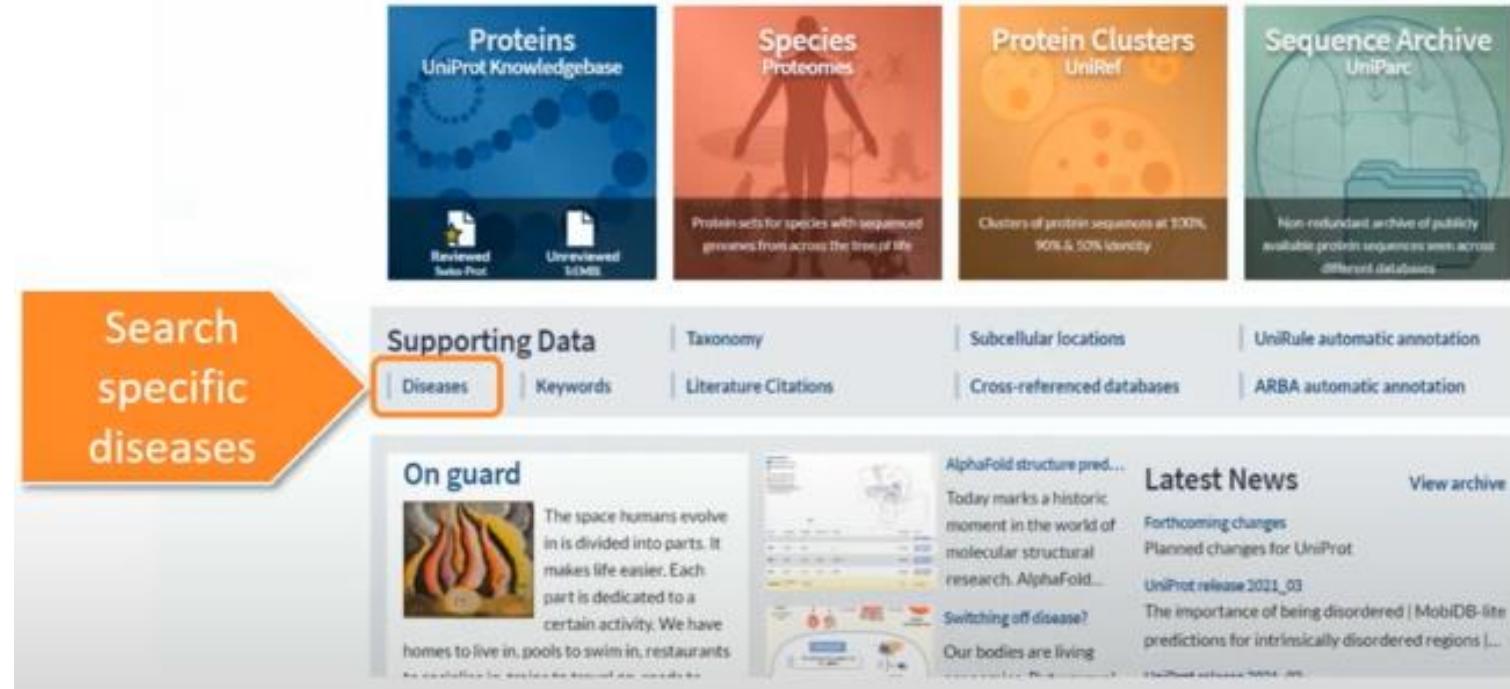
Align 2 or more sequences:

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

# UniProt>Alineamiento con Clustal

The screenshot shows a protein sequence alignment interface. At the top, there are tabs for Overview, Phylogenetic Tree, Percent Identity Matrix, Text Output, Input Parameters, and API Request. Below these are buttons for Download and Resubmit. A blue arrow on the left points to the 'Highlight properties' dropdown menu, which is open to 'Select annotation'. The main area displays two sequence blocks. The first block is labeled 'Q7KTX7:Chain' and contains sequences for various species. The second block is also labeled 'Q7KTX7:Chain' and shows a longer sequence. Both blocks have highlighted regions in blue, indicating specific annotations or features.

# UniProt>Búsqueda de información sobre patologías



The screenshot shows the UniProt homepage with a search result for "Search specific diseases". The results include:

- Proteins**: UniProt Knowledgebase. Includes "Reviewed Swiss-Prot" and "Unreviewed TrEMBL" sections.
- Species Proteomes**: Protein sets for species with sequenced genomes from across the tree of life.
- Protein Clusters**: UniRef. Clusters of protein sequences at 100%, 90% & 50% identity.
- Sequence Archive**: UniParc. Non-redundant archive of publicly available protein sequences from across different databases.

Below these are sections for **Supporting Data** (with **Diseases** highlighted), **Taxonomy**, **Subcellular locations**, **UniRule automatic annotation**, **Keywords**, **Literature Citations**, **Cross-referenced databases**, **ARBA automatic annotation**, and news items like "On guard" and "Latest News".

# UniProt>Búsqueda de información sobre patologías



**Access disease data**

**Disease & Variants**

**Involvement in disease**

**Parkinson disease (PARK)**

**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 cholinerexia, dystonic cramps, and dementia. The pathology of Parkinson disease involves the loss of dopaminergic neurons in the substantia nigra and the accumulations of aggregated protein, 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:166600 [F]

**Natural variants in PARK**

| VARIANT ID | POSITION(S) | CHANGE | DESCRIPTION  |
|------------|-------------|--------|--|
| VAR_019736 | 42          | R>P    | In PARK2 and PARK6 induces a conformational change in the PSMD4-binding site of Ubl resulting in impaired proteasomal binding; decreases increased aggregation; impairs the ability to ubiquitinate and degrade SYT11; dbSNPrs368134308 [2 Publications] |
| VAR_019749 | 253         | C>Y    | In PARK6 late onset; dbSNPrs747427602 [2 Publications]   |
| VAR_019750 | 258         | R>C    | In PARK2 and PARK6 at heterozygosity it is associated with late onset Parkinson disease; impairs the ability to ubiquitinate SNCAIP and ZNF promoter; abolishes TPS3 transcriptional repression; dbSNPrs150562946 [2 Publications]                       |
| VAR_019752 | 275         | R>W    | In PARK2 and PARK6 at heterozygosity it is associated with late onset Parkinson disease; impairs the ability to ubiquitinate SNCAIP; abolishes the ability to ubiquitinate and degrade SYT11; dbSNPrs34424956 [2 Publications]                           |
| VAR_019753 | 200         | D>N    | In PARK6 does not affect PINK-1 dependent localization to depolarized mitochondria; dbSNPrs72480422 [2 Publications]   |

# UniProt>Búsqueda de información sobre patologías



# Protein Data Bank

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

 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 www.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 property (length, size, resolution, ...)
- Chemical property (name, weight, ...)
- Sequence identity search (mmseqs2)
- Amino acid regular expression (pattern, e.g. /MM\*G/)
- Structure similarity search (in-house algorithm)
- Structural pattern search (local geometric pattern)
- Chemical structure search (smiles / 2D graph molecule)

### Structure Attributes

### Chemical Attributes

### Sequence Similarity

### Sequence Motif

### Structure Similarity

### Structure Motif

### Chemical Similarity

Return Structures  grouped by  

Include Computed Structure Models (CSM)  Count Clear 

# Protein Data Bank>Resultados de búsqueda

Refinements 

Structure Determination Methodology

experimental (2)  
 computational (1)

CSM Source Database

AlphaFoldDB (1)

pLDDT Global Quality Score

50.0 - 75.0 (1)

Scientific Name of Source Organism

Homo sapiens (3)

Taxonomy

Eukaryota (3)

Experimental Method

X-RAY DIFFRACTION (2)

Polymer Entity Type

Protein (3)  
 RNA (1)

Refinement Resolution (Å)

2.0 - 2.5 (2)

Release Date

2000 - 2004 (2)  
 2005 - 2014 (1)

Symmetry Type

Asymmetric (3)

SCOP Classification

Alpha and beta proteins (α+β) (2)  
 Artifacts (1)

1 to 2 of 3 Structures

Page 1 of 1 | 25 | Sort by: ↓ Score

  
1DTJ CRYSTAL STRUCTURE OF NOVA-2 KH3 K-HOMOLOGY RNA-BINDING DOMAIN  
Lewis, H.A., Chen, H., Edo, C., Buckanovich, R.J., Yang, Y.Y., Matsuura, K., Zhong, R., Damert, 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)  
[Download File](#) [View File](#)

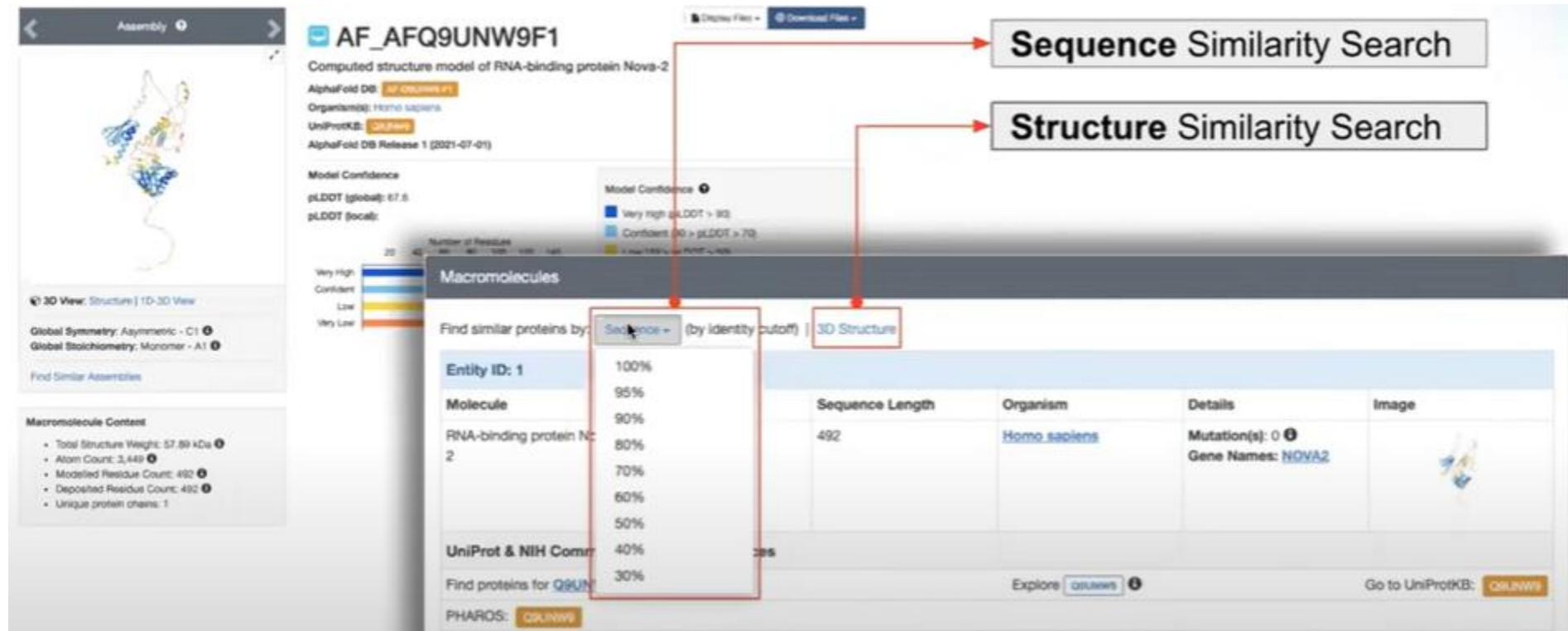
  
1EC6 CRYSTAL STRUCTURE OF NOVA-2 KH3 K-HOMOLOGY RNA-BINDING DOMAIN BOUND TO 20-MER RNA HAIRPIN  
Lewis, H.A., Matsuura, K., Jensen, K.E., Edo, C., Chen, H.  
(2000) Cell 100: 323-332  
Released 2000-02-21  
Method X-RAY DIFFRACTION 2.4 Å  
Organisms Homo sapiens  
Macromolecule RNA-BINDING PROTEIN NOVA-2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

  
AF\_AFQ9UNW9F1 Computed structure model of RNA-binding protein Nova-2  
AlphaFold DB   
pLDDT (global) 67.6  
Organisms Homo sapiens  
Macromolecule RNA-binding protein Nova-2 (protein)  
[Download File](#)

1 to 2 of 3 Structures

Page 1 of 1 | 25 | Sort by: ↓ Score

# Protein Data Bank>Enlaces a búsqueda dentro de resultados



The screenshot shows the PDB entry for AF\_AFQ9UNW9F1, which is a Computed structure model of RNA-binding protein Nova-2. The interface includes a 3D structure viewer, assembly information, and a 'Macromolecules' search panel.

**Search Options:**

- Display File: [Display File](#) | [Download File](#)
- Sequence Similarity Search
- Structure Similarity Search

**Macromolecules Panel:**

- Model Confidence: pLDDOT (global): 67.6
- Number of Residues: 492
- Find similar proteins by: Sequence (selected) | 3D Structure
- Entity ID: 1
- Molecule: RNA-binding protein N<sub>2</sub>
- UniProt & NIH Comm: Find proteins for Q8UNW
- PHAROS: [Q8UNW](#)

**Similarity Results:**

| Identity (%) | Sequence Length | Organism     | Details                            | Image   |
|--------------|-----------------|--------------|------------------------------------|---|
| 100%         | 492             | Homo sapiens | Mutation(s): 0   Gene Names: NOVA2 |  |
| 95%          |                 |              |                                    |   |
| 90%          |                 |              |                                    |   |
| 80%          |                 |              |                                    |   |
| 70%          |                 |              |                                    |   |
| 60%          |                 |              |                                    |   |
| 50%          |                 |              |                                    |   |
| 40%          |                 |              |                                    |   |
| 30%          |                 |              |                                    |   |

Explore: [Q8UNW](#) | Go to UniProtKB: [Q8UNW](#)

# Protein Data Bank>Búsqueda avanzada

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|                                     |                            |              |   |    |    |              |   |       |       |       |                 |
|-------------------------------------|----------------------------|--------------|---|----|----|--------------|---|-------|-------|-------|-----------------|
| Structure Determination Methodology | X                          | ▼            | ▼ | is | ▼  | experimental | ▼ | + NOT | Count | x     |                 |
| AND                                 | Data Collection Resolution | X            | ▼ | ▼  | <= | ▼            | 4 | A     | + NOT | Count | x               |
| AND / OR                            | Add Attribute              | Add Subquery |   |    |    |              |   |       |       |       | Remove Subquery |
| Add Subquery                        |                            |              |   |    |    |              |   |       |       |       |                 |

Chemical Attributes [?](#)

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

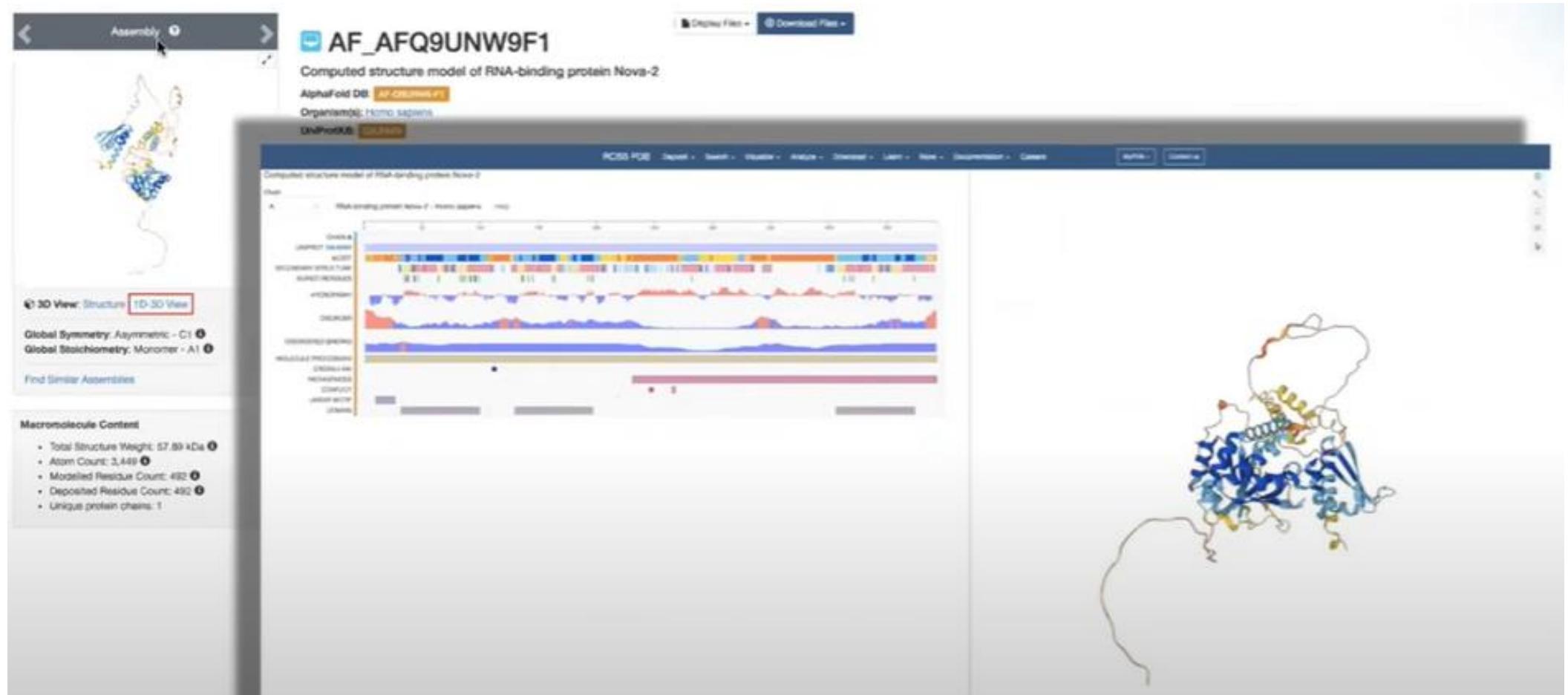
AND MTTAPQEPPARPLQAGSGAGPAPGRAMRSTTLALLALVLLYLVSGALVFALEQPHEQQAQRELGEVREKFLRAHPCVSDQELGLIKEVADALGGGADPETQSTSQSSHSAWDLGSAFFSGTIITIGYGN  
VALRTDAGRLFCIFYALVGIPLFAGILLAGVGDRGLGSSLRHGIGHIEAIFLKWHVPPELVRVLSAMLFLIGCLLFVLTPTFVFCYMEDWSKLEAIYFVIVTLLTVGFGLDYVAGADPRQDSPAYQPLVWFWILLGLAYFA

Entry ID  Sequence Type  E-Value Cutoff  Identity Cutoff  % (Integer only)

Sequence Motif [?](#)

Structure Similarity [?](#)

# Protein Data Bank>Visor 1D-3D





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