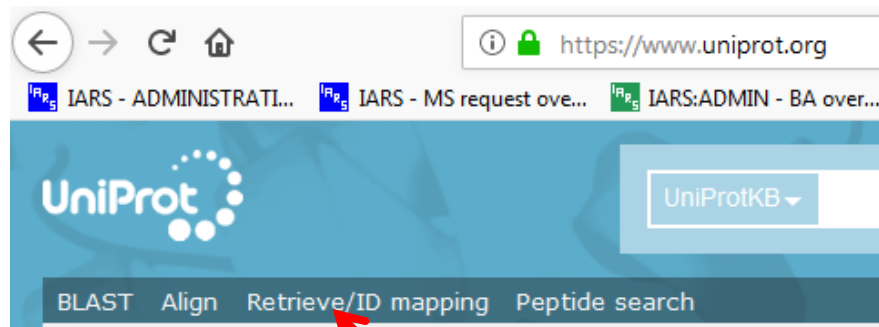


# Kurzanleitung zum Downloaden von Annotationen zu ProteomeDiscoverer Ergebnis-Files von Uniprot

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



The mission of UniProt is to provide the scientific community with a co



Auf "Retrieve/ID mapping" klicken

UniProt

UniProtKB

Advanced Search

BLAST Align Retrieve/ID mapping Peptide search Help Contact

## Retrieve/ID mapping

**How to use Retrieve/ID mapping tool**

Enter or upload a list of identifiers to do one of the following:

- Retrieve the corresponding UniProt entries to download them or work with them on this website.
- Convert identifiers which are of a different type to UniProt identifiers or vice versa and download the identifier lists.

1. Enter identifiers, separated by spaces or new lines, into the form field, for example:  
P31946 P62258  
ALBU\_HUMAN  
EFTU\_ECOLI
2. If you need to convert to another identifier type, select the source and target type from the dropdown menus.
3. Click the Go button.

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

### 1. Provide your identifiers

P31946 P62258

OR upload your own file:  Kostenlos Datei ausgewählt

Run in a new window.

### 2. Select options

From: UniProtKB AC/ID To: UniProtKB

Tools	Core data	Supporting data	Information
<a href="#">BLAST</a> <a href="#">Align</a> <a href="#">Retrieve/ID mapping</a> <a href="#">Peptide search</a>	<a href="#">Protein knowledgebase (UniProtKB)</a> <a href="#">Sequence clusters (UniRef)</a> <a href="#">Sequence archive (UniParc)</a> <a href="#">Proteomes</a>	<a href="#">Literature citations</a> <a href="#">Taxonomy</a> <a href="#">Keywords</a> <a href="#">Subcellular locations</a> <a href="#">Cross-referenced databases</a> <a href="#">Diseases</a>	<a href="#">About UniProt</a> <a href="#">Help</a> <a href="#">FAQ</a> <a href="#">UniProtKB manual</a> <a href="#">Technical corner</a> <a href="#">Expert biocuration</a>

Accession Numbers als Liste oder hintereinander mit Leerzeichen in diese Box kopieren.

## 2. Select options

---

From	To
<input type="text" value="UniProtKB AC/ID"/>	<input type="text" value="UniProtKB"/>
<input type="button" value="Clear"/>	<input type="button" value="Submit"/>

Obige Einstellungen verwenden und "Submit" klicken

Nach einiger Zeit (je nach Zahl der Einträge) geht die Ergebnisliste auf.

UniProtKB results

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2 out of 2 UniProtKB AC/ID identifiers were successfully mapped to 2 UniProtKB IDs in the table below.

Filter by:

Reviewed (2)  
Swiss-Prot

Popular organisms  
Human (2)

View by  
Results table

BLAST Align Download Add to basket Columns

	Your list:...215C2P	Entry	Entry name		Protein names	Gene names	Organism	Length	
<input type="checkbox"/>	P31946	P31946	1433B_HUMAN		14-3-3 protein beta/alpha	YWHAB	Homo sapiens (Human)	246	
<input type="checkbox"/>	P62258	P62258	1433E_HUMAN		14-3-3 protein epsilon	YWHAE	Homo sapiens (Human)	255	

1 to 2 of 2 Show 25

1 to 2 of 2 Show 25

Auf den Button "Columns" klicken

Optionen für zusätzliche Spalten wählen.

Vorschlag, alle Punkte unter Gene Ontology durch setzen eines Häkchens aktivieren:

▼ Gene Ontology (GO)

- Gene ontology (biological process)
- Gene ontology (cellular component)
- Gene ontology (GO)
- Gene ontology (molecular function)
- Gene ontology IDs

Das sollte dann so aussehen:

### Customize results table

#### Unsaved columns<sup>i</sup>

Click on the + to add to 'Columns to be displayed' and to the 'Miscellaneous' section below for future use.



Your list: M20181112..215C2P

#### Columns to be displayed<sup>i</sup>


Drag and drop to re-order.

Reset to default Save Cancel

Entry	Entry name		Protein names	Gene names	Organism	Length	Gene ontology (biological process)	Gene ontology (cellular component)	Gene ontology (GO)	Gene ontology (molecular function)	Gene ontology IDs
-------	------------	--	---------------	------------	----------	--------	------------------------------------	------------------------------------	--------------------	------------------------------------	-------------------

Auf "Save" klicken

# Um Annotationen erweiterte Tabelle:



UniProtKB -

Advanced

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

## UniProtKB results [Basket](#)

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**Popular organisms**  
Human (2)

**View by**

[Results table](#)

[Taxonomy](#)

[Keywords](#)

[Gene Ontology](#)

[Enzyme class](#)

[Pathway](#)

**UniRef**

Your results in sequence clusters with identity of:  
100%, 90% or 50%

**Demo**

[Help video](#)

BLAST [Align](#) [Download](#) [Add to basket](#) [Columns](#)
1 to 2 of 2 Show 25

	Your list...215C2P	Entry	Entry name	Protein names	Gene names	Organism	Length	Gene ontology (biological process)	Gene ontology (cellular component)	Gene ontology (GO)	Gene ontology
<input type="checkbox"/>	P31946	P31946	1433B_HUMAN	<b>14-3-3 protein beta/alpha</b>	<b>YWHAB</b>	Homo sapiens (Human)	246	cytoplasmic sequestering of protein; hippo signaling; MAPK cascade; membrane organization; negative regulation of G-protein coupled receptor protein signaling pathway; negative regulation of protein dephosphorylation; negative regulation of transcription, DNA-templated; positive regulation of catalytic activity; positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway; protein heterooligomerization; protein targeting; regulation of mRNA stability; viral process	cytoplasm; cytosol; extracellular exosome; focal adhesion; melanosome; membrane; mitochondrion; nucleus; perinuclear region of cytoplasm; transcriptional repressor complex	cytoplasm; cytosol; extracellular exosome; focal adhesion; melanosome; membrane; mitochondrion; nucleus; perinuclear region of cytoplasm; transcriptional repressor complex; cadherin binding; enzyme binding; histone deacetylase binding; identical protein binding; phosphoprotein binding; phosphoserine residue binding; protein C-terminus binding; protein domain specific binding; protein-containing complex binding;	cadherin binding; histone deacetylase binding; identical protein phosphoserine r protein-containing binding; protein binding; protein binding

are here (nucleotides) mapped to 2 amino acids (see in the table below).

The screenshot shows a web interface with a 'Download' dialog box open over a table of search results. The dialog box has the following options:

- Download selected (0)
- Download all (2)
- Format: Excel
- Compressed
- Uncompressed
- Preview first 10 <sup>i</sup>
- Go

The table below has the following columns: 'Gene names', 'Gene names', and 'Organism'. The first row shows '3 protein' and 'alpha' in the first column, 'YWHAB' in the second column, and 'Homo sapiens (Human)' in the third column.

1. Auf "Download" klicken
2. Format wählen (Empfehlung Excel oder FASTA)
3. Entscheiden ob die Files "compressed" oder "uncompressed" heruntergeladen werden sollen → Empfehlung: "uncompressed"
4. Auf "GO" klicken
5. Die Ergebnisse können z.B. mit den Suchergebnislisten in Excel zusammenkopiert werden → ACHTUNG: Durch "missing annotations" kann es gerade bei langen Listen leicht zu Verschiebungen kommen. Das automatische Sortieren über Excel ist wohl nur dem fortgeschrittenen Excel-Anwender möglich