

WEBLEM 4

Introduction to Protein Sequence Database

Introduction:

- **Uniprot:**

The Universal Protein Resource (UniProt) is a comprehensive resource for protein sequence and annotation data. The UniProt databases are the UniProt Knowledgebase (UniProtKB), the UniProt Reference Clusters (UniRef), and the UniProt Archive (UniParc). The UniProt consortium and host institutions EMBL-EBI, SIB and PIR are committed to the long-term preservation of the UniProt databases.

- **UniprotKb:**

The UniProt Knowledgebase (UniProtKB) is the central hub for the collection of functional information on proteins, with accurate, consistent and rich annotation. In addition to capturing the core data mandatory for each UniProtKB entry (mainly, the amino acid sequence, protein name or description, taxonomic data and citation information), as much annotation information as possible is added.

Reviewed(Swiss-Prot)-Manually annotated: Records with information extracted from literature and curator-evaluated computational analysis.

Unreviewed(TeEMBL)-Computationally analyzed: Record that await full manual annotation.

- **Uniref:**

The UniProt Reference Clusters (UniRef) provide clustered sets of sequences from the UniProt Knowledgebase (including isoforms) and selected UniParc records. This hides redundant sequences and obtains complete coverage of the sequence space at three resolution

- **UniParc:**

UniParc is a comprehensive and non-redundant database that contains most of the publicly available protein sequences in the world. Proteins may exist in different sources databases and in multiple copies in the same database. UniParc avoids such redundancy by storing each unique only once and giving it a stable and unique identifier (UPI)

- **Proteomes:**

A proteome is the set of proteins thought to be expressed by an organism. UniProt provides proteomes for species with completely sequenced genomes.

- **PIR:**

The Protein Information Resource (PIR) is an integrated public bioinformatics resource to support genomic, proteomic and systems biology research and scientific studies.

PIR was established in 1984 by the National Biomedical Research Foundation (NBRF) as a resource to assist researchers in the identification and interpretation of protein sequence information. Prior to that, the NBRF compiled the first comprehensive collection of macromolecular sequences in the *Atlas of Protein Sequence and Structure*, published from 1965-1978 under the editorship of Margaret J. Dayhoff. Dr. Dayhoff and her research group pioneered in the development of computer methods for the comparison of protein sequences, for the detection of distantly related sequences and duplications within sequences, and for the inference of evolutionary histories from alignments of protein sequences.

- **PRO:**

PRO provides an ontological representation of protein-related entities by explicitly defining them and showing the relationships between them. Each PRO term represents a distinct class of entities (including specific modified forms, orthologous isoforms, and protein complexes) ranging from the taxon-neutral to the taxon-specific.

- **iPTMnet:**

iPTMnet is a bioinformatics resource for integrated understanding of protein post-translational modification (PTMs) in systems biology context.

It connects multiple disparate bioinformatics tools and systems text mining, data mining, analysis and visualization tools, and databases and ontologies into an integrated cross-cutting research resource to address the knowledge gaps in exploring and discovering PTM networks.

- **iProLINK:**

iProLINK (integrated Protein Literature, Information and knowledge) is a resource with access to text mining tools and annotated corpora developed in house. The collection of data sources can be utilized by computational and biological researches to explore literature information on proteins and their features or properties.

1. **ITextMine:** Integrated text mining tools and relation extraction results from large-scale text processing.
2. **pGenN:** a gene normalization tool tailored for plants.
3. **MiRTex:** a relation extraction tool that identifies miRNA-target relations as well as miRNA-gene and gene-miRNA regulation relations.
4. **EFIP:** A relation extraction tool that identifies information relevant to phosphorylated proteins and phosphorylation-dependent protein-protein interactions.
5. **EmiRIT:** an integrative text mining system collecting miRNA information from the literature.
6. **RLIMS-P:** a generalizable relation extraction system (for developers)
7. **iSimp:** a sentence simplification system (for developers)

WEBLEM 4a

(URL: <https://www.uniprot.org/>)

Aim:

To study 'Rhodopsin' Protein information using UniProt Database.

Introduction:

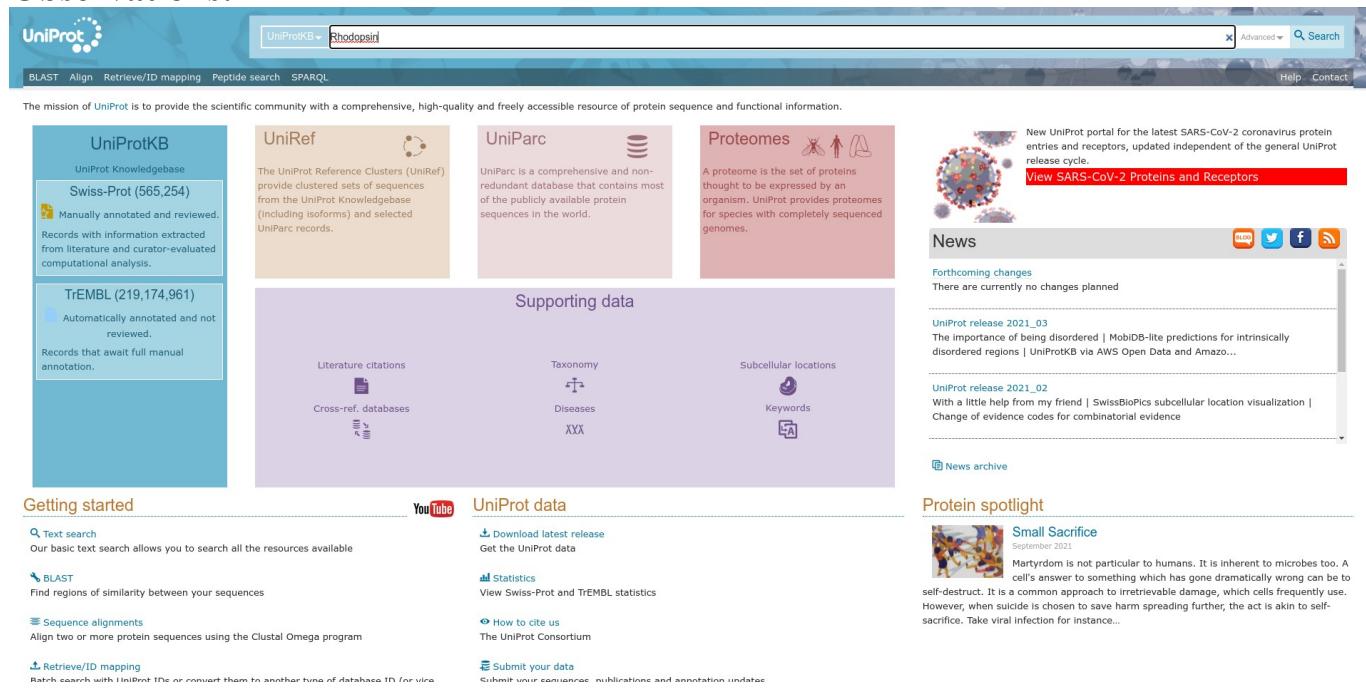
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Rhodopsin is a biological pigment found in the rods of the retina and is a G-protein-coupled receptor (GPCR). It belongs to a group of photoswitchable opsins. Rhodopsin is extremely sensitive to light, and thus enables vision in low-light conditions. When rhodopsin is exposed to light, it immediately photobleaches.

Methodology:

1. Homepage of Uniprot.
2. Enter the UniprotKB and search the query 'Rhodopsin'
3. Interpret the results.

Observations:



The screenshot shows the UniProt homepage with a search bar containing 'Rhodopsin'. The main content area displays various protein databases and supporting data. On the right, there are news items and a protein spotlight. The 'Protein spotlight' section features an image of a virus and the text: 'Small Sacrifice' (September 2021). It discusses the self-destructive behavior of cells.

UniProtKB
UniProt Knowledgebase
Swiss-Prot (565,254)
Manually annotated and reviewed. Records with information extracted from literature and curator-evaluated computational analysis.

UniRef
The UniProt Reference Clusters (UniRef) provide clustered sets of sequences from the UniProt Knowledgebase (including isoforms) and selected UniParc records.

UniParc
UniParc is a comprehensive and non-redundant database that contains most of the publicly available protein sequences in the world.

Proteomes
A proteome is the set of proteins thought to be expressed by an organism. UniProt provides proteomes for species with completely sequenced genomes.

Supporting data

- Literature citations
- Cross-ref. databases
- Taxonomy
- Diseases
- Subcellular locations
- Keywords

News

Forthcoming changes
There are currently no changes planned

UniProt release 2021_03
The importance of being disordered | MobiDB-lite predictions for intrinsically disordered regions | UniProtKB via AWS Open Data and Amazon...

UniProt release 2021_02
With a little help from my friend | SwissBioPics subcellular location visualization | Change of evidence codes for combinatorial evidence

Protein spotlight
Small Sacrifice
September 2021
Martyrdom is not particular to humans. It is inherent to microbes too. A cell's answer to something which has gone dramatically wrong can be to self-destruct. It is a common approach to irretrievable damage, which cells frequently use. However, when suicide is chosen to save harm spreading further, the act is akin to self-sacrifice. Take viral infection for instance...

Fig1. Homepage of Uniprot with query 'Albumin'

UniProtKB 2021_03 results																																																																															
UniProtKB consists of two sections:																																																																															
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Help UniProtKB help video Other tutorials and videos Downloads																																																																															
Filter by BLAST Align Download Add to basket Columns >																																																																															
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Fig2. Hit page of UniprotKB with query 'Rhodopsin'

UniProtKB - P02699 (OPSD_BOVIN)																													
Display Help video BLAST Align Format Add to basket History Add a publication Feedback																													
Protein Rhodopsin Gene RHO Organism Bos taurus (Bovine) Status Reviewed - Annotation score: 5 - Experimental evidence at protein level ¹																													
Function <input checked="" type="checkbox"/> Function <input checked="" type="checkbox"/> Names & Taxonomy <input checked="" type="checkbox"/> Subcellular location <input checked="" type="checkbox"/> Pathology & Biotech <input checked="" type="checkbox"/> PTM / Processing <input checked="" type="checkbox"/> Expression <input checked="" type="checkbox"/> Interaction <input checked="" type="checkbox"/> Structure <input checked="" type="checkbox"/> Family & Domains <input checked="" type="checkbox"/> Sequence <input checked="" type="checkbox"/> Similar proteins <input checked="" type="checkbox"/> Cross-references <input checked="" type="checkbox"/> Entry information <input checked="" type="checkbox"/> Miscellaneous Top																													
Feature table <table border="1"> <thead> <tr> <th>Name</th> <th>Function</th> <th>Position(s)</th> <th>Description</th> <th>Actions</th> <th>Graphical view</th> <th>Length</th> </tr> </thead> <tbody> <tr> <td>Site¹</td> <td>113</td> <td>Plays an important role in the conformation switch to the active conformation</td> <td>3 Publications 1 Publication</td> <td></td> <td></td> <td>1</td> </tr> <tr> <td>Metal binding¹</td> <td>201</td> <td>Zinc</td> <td>Combined sources 2 Publications</td> <td></td> <td></td> <td>1</td> </tr> <tr> <td>Metal binding¹</td> <td>279</td> <td>Zinc</td> <td>Combined sources 2 Publications</td> <td></td> <td></td> <td>1</td> </tr> </tbody> </table> GO - Molecular function¹ <ul style="list-style-type: none"> 11-cis retinal binding Source: UniProtKB arrestin family protein binding Source: CAFA G-protein alpha-subunit binding Source: CAFA G protein-coupled photoreceptor activity Source: UniProtKB guanyl-nucleotide exchange factor activity Source: UniProtKB identical protein binding Source: IntAct opsin binding Source: CAFA zinc ion binding Source: CAFA <p>Complete GO annotation on QuickGO ...</p>		Name	Function	Position(s)	Description	Actions	Graphical view	Length	Site ¹	113	Plays an important role in the conformation switch to the active conformation	3 Publications 1 Publication			1	Metal binding ¹	201	Zinc	Combined sources 2 Publications			1	Metal binding ¹	279	Zinc	Combined sources 2 Publications			1
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Metal binding ¹	279	Zinc	Combined sources 2 Publications			1																							

Fig3. Header page with of result with query 'Rhodopsin'

Display [Help video](#) **Function¹**

Photoreceptor required for image-forming vision at low light intensity. Required for photoreceptor cell viability after birth (By similarity). Light-induced isomerization of 11-cis to all-trans retinal triggers a conformational change that activates signaling via G-proteins (PubMed:10926528, PubMed:12044163, PubMed:11972040, PubMed:16908857, PubMed:16586416, PubMed:17060607, PubMed:17449675, PubMed:18818650, PubMed:21389983, PubMed:22198838, PubMed:23579341, PubMed:25205354, PubMed:27458239). Subsequent receptor phosphorylation mediates displacement of the bound G-protein alpha subunit by the arrestin SAG and terminates signaling (PubMed:1396673, PubMed:15111114).

By similarity [5 Publications](#) [11 Publications](#)

Sites

Feature key	Position(s)	Description	Actions	Graphical view	Length
Function	113	Plays an important role in the conformation switch to the active conformation	3 Publications	1	1
Names & Taxonomy	201	Zinc Combined sources	2 Publications	1	1
Subcellular location	279	Zinc Combined sources	2 Publications	1	1

GO - Molecular function¹

- 11-cis retinal binding [Source: UniProtKB](#)
- arrestin family protein binding [Source: CAFA](#)
- G-protein alpha-subunit binding [Source: CAFA](#)
- G protein-coupled photoreceptor activity [Source: UniProtKB](#)
- guanyl-nucleotide exchange factor activity [Source: UniProtKB](#)
- identical protein binding [Source: IntAct](#)
- opsin binding [Source: CAFA](#)
- zinc ion binding [Source: CAFA](#)

Complete GO annotation on QuickGO ...

GO - Biological process¹

- absorption of visible light [Source: UniProtKB](#)
- cellular response to light stimulus [Source: GO_Central](#)
- detection of temperature stimulus involved in thermception [Source: Ensembl](#)
- G protein-coupled receptor signaling pathway [Source: GO_Central](#)
- photoreceptor cell maintenance [Source: Ensembl](#)
- phototransduction [Source: GO_Central](#)
- phototransduction, visible light [Source: AgBase](#)
- protein-chromophore linkage [Source: UniProtKB-KW](#)
- protein phosphorylation [Source: Ensembl](#)
- response to light stimulus [Source: CAFA](#)
- retina development in camera-type eye [Source: Ensembl](#)
- rhodopsin mediated signaling pathway [Source: UniProtKB](#)
- thermotaxis [Source: Ensembl](#)
- visual perception [Source: UniProtKB-KW](#)

Complete GO annotation on QuickGO ...

Fig4. Function page of result for query ‘Rhodopsin’

Display [Help video](#) **Structure¹**

Entry

Publications

Feature viewer

Feature table

None

Function Names & Taxonomy Subcellular location Pathology & Biotech PTM / Processing Expression Interaction Structure Family & Domains Sequence Similar proteins Cross-references Entity information Miscellaneous

▲ Top

Structure¹

None

Source Identifier Method Resolution Chain Positions Links

PDB	1BOJ	Model		A	1-348	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1BOK	Model		A	1-348	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1EDS	NMR		A	93-123	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1EDV	NMR		A	172-205	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1EDW	NMR		A	268-293	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1EDX	NMR		A	1-40	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1FRR	X-ray	2.80 Å	A/B	1-348	PDB · RCSB-PDB · PDBJ · PDBsum

Secondary structure

Fig5. Structure of result of query ‘Rhodopsin’

Display [Help video](#) **Sequence¹**

Sequence status¹: Complete.

P02699-1 [UniParc] [FASTA](#) [Add to basket](#)

[Hide](#)

Length: 348
Mass (Da): 39,008
Last modified: July 21, 1986 - v1
Checksum: 33FDA196803E81F3

BLAST [GO](#)

10 20 30 40 50
MNGTEGPNFY VPFNSNKTGVV RSPFEAPOYY LAEPWQFSML AAYMFLLIML
60 70 80 90 100
GFPINFLTLV VTQHMKKLRT PLNYILLNL AVALDFMVFGG FTTTLYTSLH
110 120 130 140 150
GYFVFGPTGC NLEGFFATLG GEIALWLSIV LAIERYVVVC KPMNSNRFGE
160 170 180 190 200
NHAIMGVFTT WVMALACAAP PLVGWRSVTP EGMQCSGID YYTPHEETNN
210 220 230 240 250
ESFVYIMFVV HFIIPILIVF FCYQQLVFTV KEAAQAOQES ATTQKAEKEV
260 270 280 290 300
TRMVIIIMVIA FLICWLPYAS VAFVIFTHQG SDFGPIMFTI PAFFAKTSAV
310 320 330 340
YNPVIYIMMN KOFRNCMVT LCCGKNPLGD DEASTTVSKT ET5QVAPA

Experimental Info

Feature key	Position(s)	Description	Actions	Graphical view	Length
Sequence conflict ¹	281	S → F in AAA30675 (PubMed:2950966). Curated			1

Sequence databases

Select the link	K00506 UniProt K00505 Genomic DNA Translation: AAA30674.1
destinations:	M21606 mRNA Translation: AAA30675.1
<input checked="" type="radio"/> EMBL ¹	
<input type="radio"/> GenBank ¹	
<input type="radio"/> DDBJ ¹	
PIR ¹	A90840, OBO
RefSeq ¹	NP_001014890.1, NM_001014890.2

Genome annotation databases

Ensembl ¹	ENSBTAT00000001730; ENSBTAP00000001730; ENSBTAG000000001310
GeneID ¹	509333

Fig6. Sequences of result for query ‘Rhodopsin’

Display [Help video](#) **Names & Taxonomy¹**

Entry

Publications

Feature viewer

Feature table

None

Function

Names & Taxonomy

Subcellular location

Pathology & Biotech

PTM / Processing

Expression

Interaction

Structure

Family & Domains

Sequence

Similar proteins

Cross-references

Entry information

Miscellaneous

[Top](#)

Protein names¹: Recommended name: Rhodopsin

Gene names¹: Name: RHO

Organism¹: Bos taurus (Bovine)

Taxonomic identifier¹: 9913 [NCBI]

Taxonomic lineage¹: Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Mammalia > Eutheria > Laurasiatheria > Artiodactyla > Ruminantia > Pecora > Bovidae > Bovinae > Bos [2](#)

Proteomes¹: UP000009136 Component¹: Chromosome 2

Organism-specific databases

VGNC¹: VGNC:33942, RHO

Subcellular location¹

UniProt annotation GO - Cellular component

Other locations

- Membrane [1](#) [6 Publications](#) ; Multi-pass membrane protein [1](#) [19 Publications](#)
- photoreceptor outer segment [1](#) [4 Publications](#)

Note: Synthesized in the inner segment (IS) of rod photoreceptor cells before vectorial transport to disk membranes in the rod outer segment (OS) photosensory cilia. [By similarity](#)

Fig7. Names and taxonomy of result for query ‘Rhodopsin’

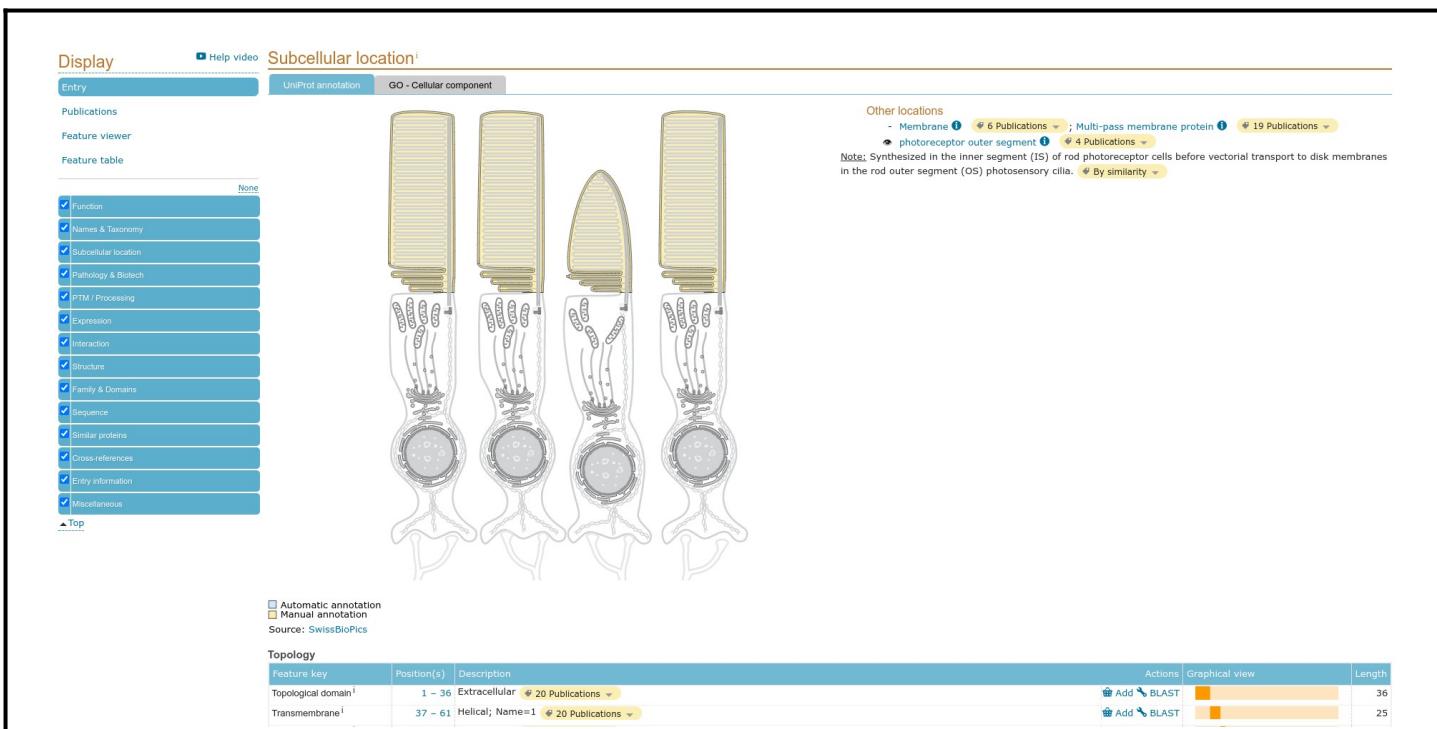


Fig8. Subcellular location of result for query 'Rhodopsin'

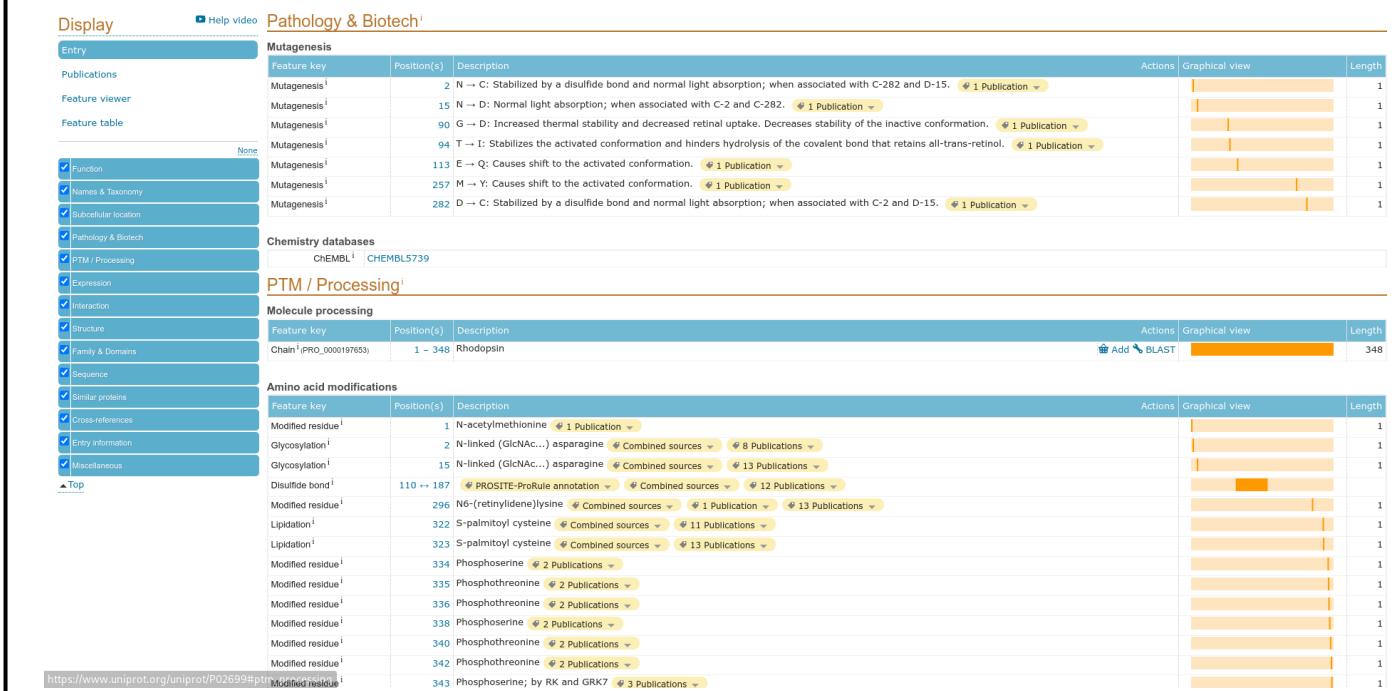


Fig9. Pathology and Biotech of result for query 'Albumin'

Display [Help video](#) **PTM / Processingⁱ**

Molecule processing

Feature key	Position(s)	Description	Actions	Graphical view	Length
Chain ⁱ [PRO_0000197653]	1 – 348	Rhodopsin	Add BLAST		348

Feature table

Amino acid modifications

Feature key	Position(s)	Description	Actions	Graphical view	Length
Function		Modified residue ⁱ	1 N-acetylmethionine		1
Names & Taxonomy		Glycosylation ⁱ	2 N-linked (GlcNAc...) asparagine		1
Subcellular location		Glycosylation ⁱ	15 N-linked (GlcNAc...) asparagine		1
Pathology & Biotech		Disulfide bond ⁱ	110 ↔ 187 N6-(retinylidene)lysine		1
IPTM / Processing		Lipidation ⁱ	296 S-palmitoyl cysteine		1
Expression		Lipidation ⁱ	322 S-palmitoyl cysteine		1
Interaction		Modified residue ⁱ	323 S-palmitoyl cysteine		1
Structure		Modified residue ⁱ	334 Phosphoserine		1
Family & Domains		Modified residue ⁱ	335 Phosphothreonine		1
Sequence		Modified residue ⁱ	336 Phosphothreonine		1
Similar proteins		Modified residue ⁱ	338 Phosphoserine		1
Cross-references		Modified residue ⁱ	340 Phosphothreonine		1
Entity information		Modified residue ⁱ	342 Phosphothreonine		1
Miscellaneous		Modified residue ⁱ	343 Phosphoserine; by Rk and GRK7		1

Post-translational modificationⁱ

Phosphorylated on some or all of the serine and threonine residues present in the C-terminal region.

Contains one covalently linked retinal chromophore. Upon light absorption, the covalently bound 11-cis-retinal is converted to all-trans-retinal. After hydrolysis of the Schiff base and release of the covalently bound all-trans-retinal, active rhodopsin is regenerated by binding of a fresh molecule of 11-cis-retinal.

Keywords - PTMⁱ

Acetylation, Disulfide bond, Glycoprotein, Lipoprotein, Palmitate, Phosphoprotein

Proteomic databases

PaxDbⁱ P02699

PTM databases

GlyConnectⁱ 523, 4 N-Linked glycans
IPTMntⁱ P02699
SwissPalmⁱ P02699

Fig10. PTM/Processing of result for query ‘Rhodopsin’

Display [Help video](#) **Expressionⁱ**

Tissue specificity

Expressed in rod-shaped photoreceptor cells in the retina that mediate vision in dim light (at protein level).

Gene expression databases

Bgeeⁱ ENSBTAG000000001310, Expressed in retina and 18 other tissues

Interactionⁱ

Subunit structureⁱ

Homodimer (PubMed:23303210, PubMed:18563085). May form a complex composed of RHO, GRK1 and RCVN in a Ca²⁺-dependent manner; RCVN prevents the interaction between GRK1 and RHO (PubMed:17020884).
Interacts with GRK1 (By similarity).
Interacts (phosphorylated form) with SAG (PubMed:26200343, PubMed:15111114, PubMed:15351781, PubMed:23579341, PubMed:25205354).
Interacts with GNAT1 (PubMed:23303210, PubMed:28655769, PubMed:18818650, PubMed:21389983, PubMed:23579341, PubMed:26526852).
Interacts with GNAT3 (PubMed:22198830, PubMed:27450239). SAG and G-proteins compete for a common binding site (By similarity).
Interacts with PRCD; the interaction promotes PRCD stability (PubMed:27509380).

Binary interactionsⁱ

Subcellular location

Reset filters

P02699 has binary interactions with 3 proteins

OPSD_BOVIN
ARRS1_BOVIN
GNAT1_BOVIN

OPSD_BOVIN
ARRS1_BOVIN
GNAT1_BOVIN

Hide details

P02699

With	#Exp.	IntAct
GNAT1 [P04695]	3	EBI-8592832, EBI-7052221
itself	6	EBI-8592832, EBI-8592832
SAG - isoform A [P08168-1]	23	EBI-8592832, EBI-15575296

GO - Molecular functionⁱ

Fig11. Expression / Interaction for result of query ‘Rhodopsin’

```
>sp|P02699|OPSD_BOVIN Rhodopsin OS=Bos taurus OX=9913 GN=RHO PE=1 SV=1
MNGTEGPNFYVPFSNKTGVVRSPFEAPQYYLAEPWQFSMLAAYMFLIMLGFPINFLTLY
VTVQHKKLRTPLNYILLNLAVADLFMVFGGFTTLYTSLHGYFVFGPTGCNLEGFFATLG
GEIALWSLVVLAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIP
EGMQCSCGIDYYTPHEETNNESFVIYMFVVFHFIPLIVIFFCYGQLVFTVKEAAAQQQES
ATTQKAKEVTRMVIIMVIAFLICWLKYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAV
YNPVIYIMMNKQFRNCMVTLCCGKNPLGDDEASTTVSKTETSQVAPA
```

Fig12. Fasta Canonical for result for query ‘Rhodopsin’

Conclusions:

Uniprot is a biological database for protein and it has all information regarding the protein sequences, protein structures and UniProt can use as a cross references.

Results:

UniProt is a freely accessible database of protein sequence and functional information, many entries being from genome sequence projects. It contains a larga amount of information about the biological function of proteins derived from the research literatures.

References:

1. <https://www.uniprot.org/>
2. <https://www.uniprot.org/uniprot/?query=Rhodopsin&sort=score>
3. <https://www.uniprot.org/uniprot/P02699#function>
4. https://www.uniprot.org/uniprot/P02699#names_and_taxonomy
5. https://www.uniprot.org/uniprot/P02699#subcellular_location
6. https://www.uniprot.org/uniprot/P02699#pathology_and_biotech
7. https://www.uniprot.org/uniprot/P02699#ptm_processing
8. <https://www.uniprot.org/uniprot/P02699#expression>
9. <https://www.uniprot.org/uniprot/P02699#structure>
10. <https://www.uniprot.org/uniprot/P02699#sequences>
11. <https://www.uniprot.org/uniprot/P02699.fasta>

WEBLEM 4b

(URL: <https://www.uniprot.org/>)

Aim:

To study 'Rhodopsin' Protein information using SwissProt Database: Reviewed and Manually annotated Database.

Introduction:

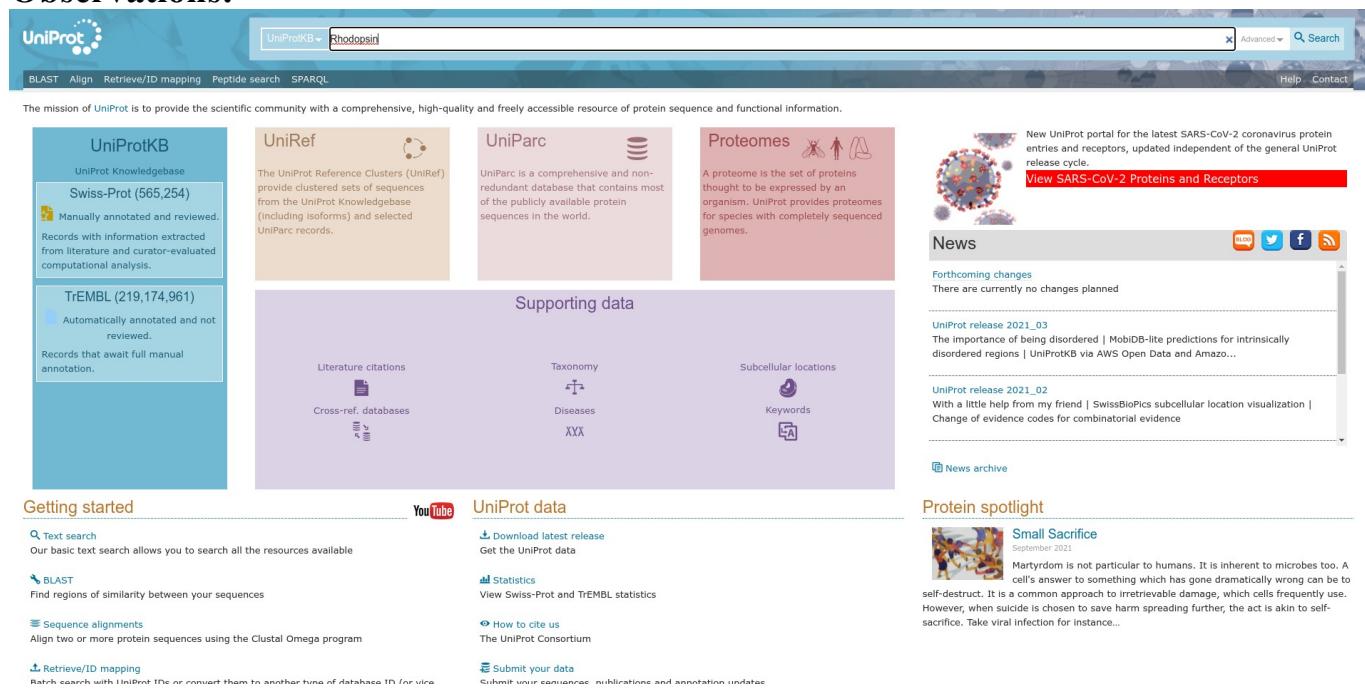
SWISS-PROT is a curated protein sequence database which strives to provide a high level of annotation (such as the description of the function of a protein, its domains structure, post-translational modifications, variants, etc.), a minimal level of redundancy and high level of integration with other databases.

Rhodopsin is a biological pigment found in the rods of the retina and is a G-protein-coupled receptor (GPCR). It belongs to a group of photoswitchable opsins. Rhodopsin is extremely sensitive to light, and thus enables vision in low-light conditions. When rhodopsin is exposed to light, it immediately photobleaches.

Methodology:

- Homepage of Uniprot.
- Enter the UniprotKB and search the query 'Rhodopsin'
- Interpret the results.

Observations:



The screenshot shows the Uniprot homepage with a search query of 'Rhodopsin' entered in the search bar. The page features a navigation bar with links for UniProtKB, UniRef, UniParc, Proteomes, News, and Protein spotlight. Below the navigation is a search bar with dropdowns for UniProtKB, UniRef, UniParc, Proteomes, News, and Protein spotlight. The main content area includes sections for UniProtKB (Swiss-Prot: 565,254, TrEMBL: 219,174,961), UniRef, UniParc, Proteomes, Supporting data (Literature citations, Cross-ref. databases, Taxonomy, Diseases, Subcellular locations, Keywords), News (Forthcoming changes, UniProt release 2021_03, UniProt release 2021_02), and Protein spotlight (Small Sacrifice, Martyrdom is not particular to humans). The footer contains links for Text search, BLAST, Sequence alignments, Retrieve/ID mapping, UniProt data (Download latest release, Statistics, How to cite us, Submit your data), and a link to the News archive.

Fig1. Homepage of Uniprot with query 'Albumin'

UniProtKB 2021_03 results																																																																															
UniProtKB consists of two sections:																																																																															
 Reviewed (Swiss-Prot) - Manually annotated	Records with information extracted from literature and curator-evaluated computational analysis.																																																																														
 Unreviewed (TrEMBL) - Computationally analyzed	Records that await full manual annotation.																																																																														
Help UniProtKB help video Other tutorials and videos Downloads																																																																															
Filter by BLAST Align Download Add to basket Columns >																																																																															
<table border="1"> <thead> <tr> <th>Entry</th> <th>Entry name</th> <th>Protein names</th> <th>Gene names</th> <th>Organism</th> <th>Length</th> </tr> </thead> <tbody> <tr> <td><input type="checkbox"/> P02699</td> <td>OPSD_BOVIN</td> <td> Rhodopsin</td> <td>RHO</td> <td>Bos taurus (Bovine)</td> <td>348</td> </tr> <tr> <td><input type="checkbox"/> P08100</td> <td>OPSD_HUMAN</td> <td> Rhodopsin</td> <td>RHO OPN2</td> <td>Homo sapiens (Human)</td> <td>348</td> </tr> <tr> <td><input type="checkbox"/> P28327</td> <td>GRK1_BOVIN</td> <td> Rhodopsin kinase GRK1</td> <td>GRK1 RHOK</td> <td>Bos taurus (Bovine)</td> <td>561</td> </tr> <tr> <td><input type="checkbox"/> Q15835</td> <td>GRK1_HUMAN</td> <td> Rhodopsin kinase GRK1</td> <td>GRK1 RHOK</td> <td>Homo sapiens (Human)</td> <td>563</td> </tr> <tr> <td><input type="checkbox"/> P15409</td> <td>OPSD_MOUSE</td> <td> Rhodopsin</td> <td>Rho</td> <td>Mus musculus (Mouse)</td> <td>348</td> </tr> <tr> <td><input type="checkbox"/> Q63651</td> <td>GRK1_RAT</td> <td> Rhodopsin kinase GRK1</td> <td>Grk1 Rhok</td> <td>Rattus norvegicus (Rat)</td> <td>564</td> </tr> <tr> <td><input type="checkbox"/> Q9WVL4</td> <td>GRK1_MOUSE</td> <td> Rhodopsin kinase GRK1</td> <td>Grk1 Rhok</td> <td>Mus musculus (Mouse)</td> <td>564</td> </tr> <tr> <td><input type="checkbox"/> Q8WTQ7</td> <td>GRK7_HUMAN</td> <td> Rhodopsin kinase GRK7</td> <td>GRK7 GPRK7</td> <td>Homo sapiens (Human)</td> <td>553</td> </tr> <tr> <td><input type="checkbox"/> P31356</td> <td>OPSD_TODPA</td> <td> Rhodopsin</td> <td>RHO</td> <td>Todarodes pacificus (Japanese flying squid) (Ommastrephes pacificus)</td> <td>448</td> </tr> <tr> <td><input type="checkbox"/> P22328</td> <td>OPSD_CHICK</td> <td> Rhodopsin</td> <td>RHO</td> <td>Gallus gallus (Chicken)</td> <td>351</td> </tr> <tr> <td><input type="checkbox"/> P32308</td> <td>OPSD_CANLF</td> <td> Rhodopsin</td> <td>RHO</td> <td>Canis lupus familiaris (Dog) (Canis familiaris)</td> <td>348</td> </tr> <tr> <td><input type="checkbox"/> Q49HM9</td> <td>GRK7A_DANRE</td> <td> Rhodopsin kinase grk7a</td> <td>grk7a grk7-1, dkeyp-13a.1</td> <td>Danio rerio (Zebrafish) (Brachydanio rerio)</td> <td>549</td> </tr> </tbody> </table>		Entry	Entry name	Protein names	Gene names	Organism	Length	<input type="checkbox"/> P02699	OPSD_BOVIN	 Rhodopsin	RHO	Bos taurus (Bovine)	348	<input type="checkbox"/> P08100	OPSD_HUMAN	 Rhodopsin	RHO OPN2	Homo sapiens (Human)	348	<input type="checkbox"/> P28327	GRK1_BOVIN	 Rhodopsin kinase GRK1	GRK1 RHOK	Bos taurus (Bovine)	561	<input type="checkbox"/> Q15835	GRK1_HUMAN	 Rhodopsin kinase GRK1	GRK1 RHOK	Homo sapiens (Human)	563	<input type="checkbox"/> P15409	OPSD_MOUSE	 Rhodopsin	Rho	Mus musculus (Mouse)	348	<input type="checkbox"/> Q63651	GRK1_RAT	 Rhodopsin kinase GRK1	Grk1 Rhok	Rattus norvegicus (Rat)	564	<input type="checkbox"/> Q9WVL4	GRK1_MOUSE	 Rhodopsin kinase GRK1	Grk1 Rhok	Mus musculus (Mouse)	564	<input type="checkbox"/> Q8WTQ7	GRK7_HUMAN	 Rhodopsin kinase GRK7	GRK7 GPRK7	Homo sapiens (Human)	553	<input type="checkbox"/> P31356	OPSD_TODPA	 Rhodopsin	RHO	Todarodes pacificus (Japanese flying squid) (Ommastrephes pacificus)	448	<input type="checkbox"/> P22328	OPSD_CHICK	 Rhodopsin	RHO	Gallus gallus (Chicken)	351	<input type="checkbox"/> P32308	OPSD_CANLF	 Rhodopsin	RHO	Canis lupus familiaris (Dog) (Canis familiaris)	348	<input type="checkbox"/> Q49HM9	GRK7A_DANRE	 Rhodopsin kinase grk7a	grk7a grk7-1, dkeyp-13a.1	Danio rerio (Zebrafish) (Brachydanio rerio)	549
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Fig2. Hit page of UniprotKB with query 'Rhodopsin'

UniProtKB - P02699 (OPSD_BOVIN)																							
Display	Help video BLAST Align Format Add to basket History																						
Entry	Add a publication Feedback																						
Publications																							
Feature viewer																							
Feature table																							
Protein Rhodopsin Gene RHO Organism Bos taurus (Bovine) Status  Reviewed - Annotation score:  - Experimental evidence at protein level ¹																							
Function <input checked="" type="checkbox"/> Function <input checked="" type="checkbox"/> Names & Taxonomy <input checked="" type="checkbox"/> Subcellular location <input checked="" type="checkbox"/> Pathology & Biotech <input checked="" type="checkbox"/> PTM / Processing <input checked="" type="checkbox"/> Expression <input checked="" type="checkbox"/> Interaction <input checked="" type="checkbox"/> Structure <input checked="" type="checkbox"/> Family & Domains <input checked="" type="checkbox"/> Sequence <input checked="" type="checkbox"/> Similar proteins <input checked="" type="checkbox"/> Cross-references <input checked="" type="checkbox"/> Entry information <input checked="" type="checkbox"/> Miscellaneous Top																							
Sites <table border="1"> <thead> <tr> <th>Feature key</th> <th>Position(s)</th> <th>Description</th> <th>Actions</th> <th>Graphical view</th> <th>Length</th> </tr> </thead> <tbody> <tr> <td>Site¹</td> <td>113</td> <td>Plays an important role in the conformation switch to the active conformation</td> <td> 3 Publications  1 Publication</td> <td></td> <td>1</td> </tr> <tr> <td>Metal binding¹</td> <td>201</td> <td>Zinc  Combined sources  2 Publications</td> <td></td> <td>1</td> </tr> <tr> <td>Metal binding¹</td> <td>279</td> <td>Zinc  Combined sources  2 Publications</td> <td></td> <td>1</td> </tr> </tbody> </table>		Feature key	Position(s)	Description	Actions	Graphical view	Length	Site ¹	113	Plays an important role in the conformation switch to the active conformation	 3 Publications  1 Publication		1	Metal binding ¹	201	Zinc  Combined sources  2 Publications		1	Metal binding ¹	279	Zinc  Combined sources  2 Publications		1
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Metal binding ¹	279	Zinc  Combined sources  2 Publications		1																			
GO - Molecular function¹  11-cis retinal binding   arrestin family protein binding   G-protein alpha-subunit binding   G protein-coupled photoreceptor activity   guanyl-nucleotide exchange factor activity   identical protein binding   opsin binding   zinc ion binding 																							
Complete GO annotation on QuickGO ...																							

Fig3. Header page with of result with query 'Rhodopsin'

Display [Help video](#) **Function¹**

Entry

Publications

Feature viewer

Feature table

Sites

Feature key	Position(s)	Description	Actions	Graphical view	Length
Site ¹	113	Plays an important role in the conformation switch to the active conformation	3 Publications	1 Publication	1
Metal binding ¹	201 Zinc	Combined sources	2 Publications	1	
Metal binding ¹	279 Zinc	Combined sources	2 Publications	1	

GO - Molecular function¹

- 11-cis retinal binding [Source: UniProtKB](#)
- arrestin family protein binding [Source: CAFA](#)
- G-protein alpha-subunit binding [Source: CAFA](#)
- G protein-coupled photoreceptor activity [Source: UniProtKB](#)
- guanyl-nucleotide exchange factor activity [Source: UniProtKB](#)
- identical protein binding [Source: IntAct](#)
- opsin binding [Source: CAFA](#)
- zinc ion binding [Source: CAFA](#)

Complete GO annotation on QuickGO ...

GO - Biological process¹

- absorption of visible light [Source: UniProtKB](#)
- cellular response to light stimulus [Source: GO_Central](#)
- detection of temperature stimulus involved in thermception [Source: Ensembl](#)
- G protein-coupled receptor signaling pathway [Source: GO_Central](#)
- photoreceptor cell maintenance [Source: Ensembl](#)
- phototransduction [Source: GO_Central](#)
- phototransduction, visible light [Source: AgBase](#)
- protein-chromophore linkage [Source: UniProtKB-KW](#)
- protein phosphorylation [Source: Ensembl](#)
- response to light stimulus [Source: CAFA](#)
- retina development in camera-type eye [Source: Ensembl](#)
- rhodopsin mediated signaling pathway [Source: UniProtKB](#)
- thermotaxis [Source: Ensembl](#)
- visual perception [Source: UniProtKB-KW](#)

Complete GO annotation on QuickGO ...

Fig4. Function page of result for query ‘Rhodopsin’

Display [Help video](#) **Structure¹**

Entry

Publications

Feature viewer

Feature table

Sites

Source	Identifier	Method	Resolution	Chain	Positions	Links
PDB	1BOJ	Model		A	1-348	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1BOK	Model		A	1-348	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1EDS	NMR		A	93-123	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1EDV	NMR		A	172-205	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1EDW	NMR		A	268-293	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1EDX	NMR		A	1-40	PDB · RCSB-PDB · PDBJ · PDBsum
PDB	1FRR	X-ray	2.80 Å	A/B	1-348	PDB · RCSB-PDB · PDBJ · PDBsum

Secondary structure

Fig5. Structure of result of query ‘Rhodopsin’

Display [Help video](#) **Sequence¹**

Sequence status¹: Complete.

P02699-1 [UniParc] [FASTA](#) [Add to basket](#)

[Hide](#)

Length: 348
Mass (Da): 39,008
Last modified: July 21, 1986 - v1
Checksum: 33FDA196803E81F3

BLAST [GO](#)

10 20 30 40 50
MNGTEGPNFY VPFNSNKTGVV RSPFEAPOYY LAEPWQFSML AAYMFLLIML
60 70 80 90 100
GFPINFLTLV VTQHMKKLRT PLNYILLNL AVALDFMVFGG FTTTLYTSLH
110 120 130 140 150
GYFVFGPTGC NLEGFFATLG GEIALWLSIV LAIERYVVVC KPMNSNRFGE
160 170 180 190 200
NHAIMGVFTT WVMALACAAP PLVGWRSRIP EGMOCSGCGID YYTPHEETNN
210 220 230 240 250
ESFVYIMFVV HFIIPILIVF FCYQQLVFTV KEAAQAOQES ATTQKAEKEV
260 270 280 290 300
TRMVIIIMVIA FLICWLPYAS VAFVIFTHQG SDFGPIMFTI PAFFAKTSAV
310 320 330 340
YNPVIYIMMN KOFRNCMVT LCCGKNPLGD DEASTTVSKT ET5QVAPA

Experimental Info

Feature key	Position(s)	Description	Actions	Graphical view	Length
Sequence conflict ¹	281	S → F in AAA30675 (PubMed:2950966). Curated			1

Sequence databases

Select the link	K00506 UniProt K00505 Genomic DNA Translation: AAA30674.1
destinations:	M21606 mRNA Translation: AAA30675.1
<input checked="" type="radio"/> EMBL ¹	
<input type="radio"/> GenBank ¹	
<input type="radio"/> DDBJ ¹	
PIR ¹	A90840, OBO
RefSeq ¹	NP_001014890.1, NM_001014890.2

Genome annotation databases

Ensembl ¹	ENSBTAT00000001730; ENSBTAP00000001730; ENSBTAG000000001310
GeneID ¹	509333

Fig6. Sequences of result for query ‘Rhodopsin’

Display [Help video](#) **Names & Taxonomy¹**

Entry

Publications

Feature viewer

Feature table

None

Function

Names & Taxonomy

Subcellular location

Pathology & Biotech

PTM / Processing

Expression

Interaction

Structure

Family & Domains

Sequence

Similar proteins

Cross-references

Entry information

Miscellaneous

[Top](#)

Protein names¹: Recommended name: Rhodopsin

Gene names¹: Name: RHO

Organism¹: Bos taurus (Bovine)

Taxonomic identifier¹: 9913 [NCBI]

Taxonomic lineage¹: Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Mammalia > Eutheria > Laurasiatheria > Artiodactyla > Ruminantia > Pecora > Bovidae > Bovinae > Bos [2](#)

Proteomes¹: UP00000136 Component¹: Chromosome 2

Organism-specific databases

VGNC¹: VGNC:33942, RHO

Subcellular location¹

UniProt annotation GO - Cellular component

Other locations

- Membrane [1](#) [6 Publications](#) ; Multi-pass membrane protein [1](#) [19 Publications](#)
- photoreceptor outer segment [1](#) [4 Publications](#)

Note: Synthesized in the inner segment (IS) of rod photoreceptor cells before vectorial transport to disk membranes in the rod outer segment (OS) photosensory cilia. [By similarity](#)

Fig7. Names and taxonomy of result for query ‘Rhodopsin’

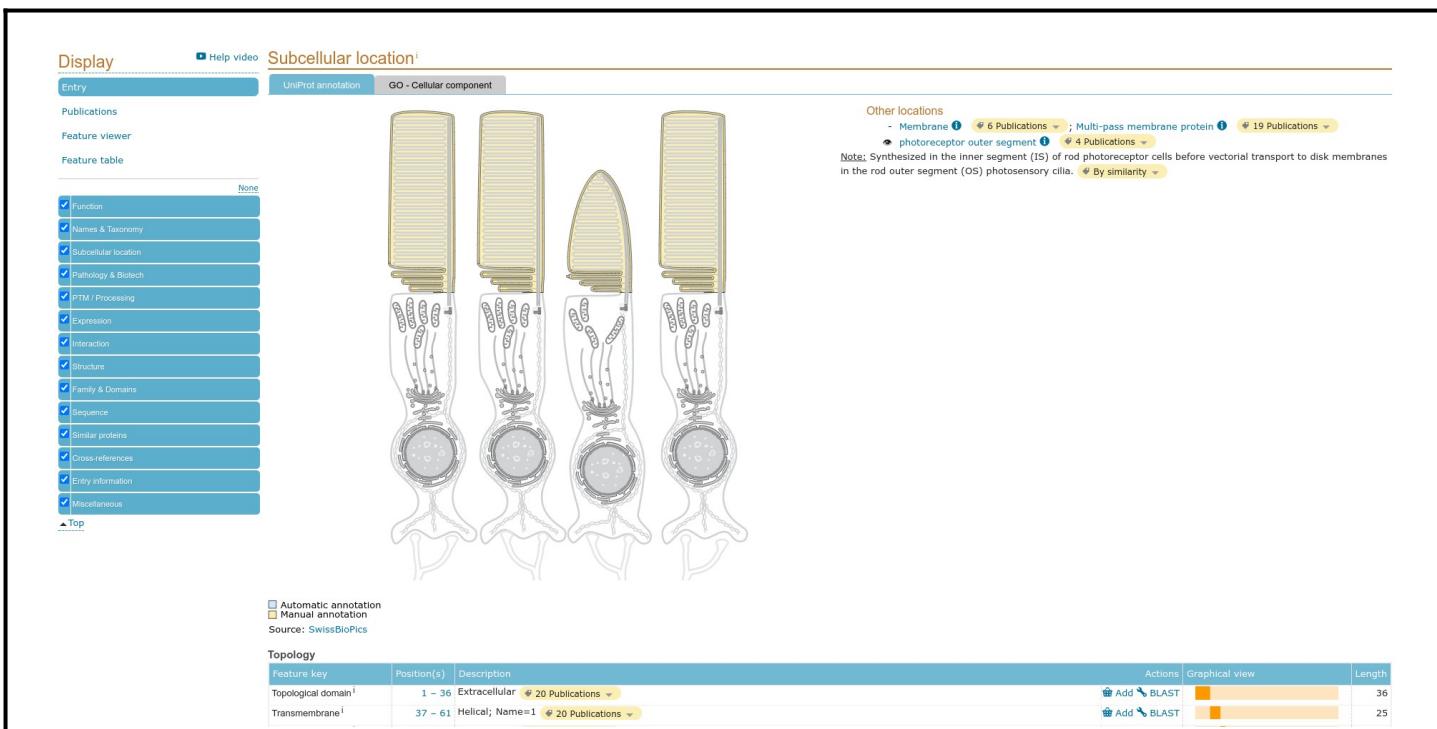


Fig8. Subcellular location of result for query 'Rhodopsin'

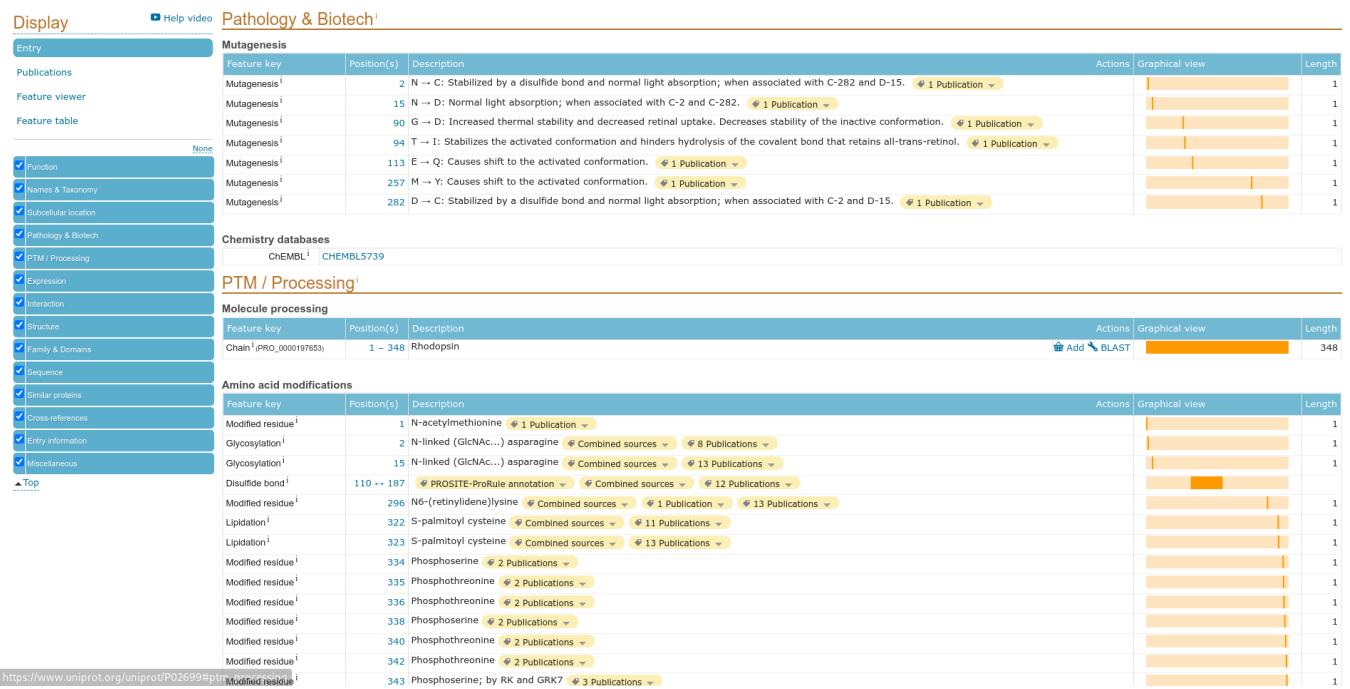


Fig9. Pathology and Biotech of result for query 'Albumin'

Display Help video **PTM / Processingⁱ**

Molecule processing

Feature key	Position(s)	Description	Actions	Graphical view	Length
Chain ⁱ [PRO_0000197653]	1 – 348	Rhodopsin	 		348

Feature table

Amino acid modifications

Feature key	Position(s)	Description	Actions	Graphical view	Length
Function		Modified residue ⁱ	1 N-acetylmethionine  1 Publication		1
Names & Taxonomy		Glycosylation ⁱ	2 N-linked (GlcNAc...) asparagine  Combined sources  8 Publications		1
Subcellular location		Glycosylation ⁱ	15 N-linked (GlcNAc...) asparagine  Combined sources  13 Publications		1
Pathology & Biotech		Disulfide bond ⁱ	110 ↔ 187  PROSITE-ProRule annotation  Combined sources  12 Publications		1
IPTM / Processing		Modified residue ⁱ	296 N6-(retinylidene)lysine  Combined sources  1 Publication  13 Publications		1
Expression		Lipidation ⁱ	322 S-palmitoyl cysteine  Combined sources  11 Publications		1
Interaction		Lipidation ⁱ	323 S-palmitoyl cysteine  Combined sources  13 Publications		1
Structure		Modified residue ⁱ	334 Phosphoserine  2 Publications		1
Family & Domains		Modified residue ⁱ	335 Phosphothreonine  2 Publications		1
Sequence		Modified residue ⁱ	340 Phosphothreonine  2 Publications		1
Similar proteins		Modified residue ⁱ	342 Phosphothreonine  2 Publications		1
Cross-references		Modified residue ⁱ	343 Phosphoserine; by RK and GRK7  3 Publications		1
Entity information					
Miscellaneous					



Post-translational modificationⁱ

Phosphorylated on some or all of the serine and threonine residues present in the C-terminal region.  3 Publications

Contains one covalently linked retinal chromophore. Upon light absorption, the covalently bound 11-cis-retinal is converted to all-trans-retinal. After hydrolysis of the Schiff base and release of the covalently bound all-trans-retinal, active rhodopsin is regenerated by binding of a fresh molecule of 11-cis-retinal.  1 Publication  14 Publications

Keywords - PTMⁱ

Acetylation, Disulfide bond, Glycoprotein, Lipoprotein, Palmitate, Phosphoprotein

Proteomic databases

PaxDbⁱ P02699

PTM databases

GlyConnectⁱ 523, 4 N-Linked glycans
IPTMntⁱ P02699
SwissPalmⁱ P02699

Fig10. PTM/Processing of result for query ‘Rhodopsin’

Display Help video **Expressionⁱ**

Tissue specificityⁱ

Expressed in rod-shaped photoreceptor cells in the retina that mediate vision in dim light (at protein level).  4 Publications

Gene expression databases

Bgeeⁱ ENSBTAG000000001310, Expressed in retina and 18 other tissues

Interactionⁱ

Subunit structureⁱ

Homodimer (PubMed:23303210, PubMed:18563085). May form a complex composed of RHO, GRK1 and RCVN in a Ca²⁺-dependent manner; RCVN prevents the interaction between GRK1 and RHO (PubMed:17020884).
Interacts with GRK1 (By similarity).
Interacts (phosphorylated form) with SAG (PubMed:26200343, PubMed:15111114, PubMed:15351781, PubMed:23579341, PubMed:25205354).
Interacts with GNAT1 (PubMed:23303210, PubMed:28655769, PubMed:18818650, PubMed:21389983, PubMed:23579341, PubMed:26526852).
Interacts with GNAT3 (PubMed:22198830, PubMed:27450239). SAG and G-proteins compete for a common binding site (By similarity).
Interacts with PRCD; the interaction promotes PRCD stability (PubMed:27509380).
 18 Publications

Binary interactionsⁱ

Subcellular location 

OPSD_BOVIN has binary interactions with 3 proteins













Hide details

P02699

With	#Exp.	IntAct
GNAT1 [P04695]	3	EBI-8592832, EBI-7052221
itself	6	EBI-8592832, EBI-8592832
SAG - isoform A [P08168-1]	23	EBI-8592832, EBI-15575296

GO - Molecular functionⁱ

Fig11. Expression / Interaction for result of query ‘Rhodopsin’

```
>sp|P02699|OPSD_BOVIN Rhodopsin OS=Bos taurus OX=9913 GN=RHO PE=1 SV=1
MNGTEGPNFYVPFSNKTGVVRSPFEAPQYYLAEPWQFSMLAAYMFLIMLGFPINFLTLY
VTVQHKKLRTPLNYILLNLAVADLFMVFGGFTTLYTSLHGYFVFGPTGCNLEGFFATLG
GEIALWSLVVLAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIP
EGMQCSCGIDYYTPHEETNNESFVIYMFVVFHIPLIVIFFCYGQLVFTVKEAAAQQQES
ATTQKAEKEVTRMVIIMVIAFLICWLKYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAV
YNPVIYIMMNKQFRNCMVTLCCGKNPLGDDEASTVSKTETSQVAPA
```

Fig12. Fasta Canonical for result for query ‘Rhodopsin’

Conclusions:

Uniprot is a biological database for protein and it has all information regarding the protein sequences, protein structures and UniProt can use as a cross references.

Results:

In UniprotKB it consist SwissProt that is Reviewed paper and for the query ‘Albumin’ is contain 511 papers .

References:

1. <https://www.uniprot.org/>
2. <https://www.uniprot.org/uniprot/?query=Rhodopsin&sort=score>
3. <https://www.uniprot.org/uniprot/P02699#function>
4. https://www.uniprot.org/uniprot/P02699#names_and_taxonomy
5. https://www.uniprot.org/uniprot/P02699#subcellular_location
6. https://uniprot.org/uniprot/P02699#pathology_and_biotech
7. https://www.uniprot.org/uniprot/P02699#ptm_processing
8. <https://www.uniprot.org/uniprot/P02699#expression>
9. <https://www.uniprot.org/uniprot/P02699#structure>
10. <https://www.uniprot.org/uniprot/P02699#sequences>
11. <https://www.uniprot.org/uniprot/P02699.fasta>

WEBLEM 4c (URL: <https://www.uniprot.org/>)

Aim:

To study ‘Rhodopsin’ Protein information using TrEMBL Database: Unreviewed and manually annotated Database.

Introduction:

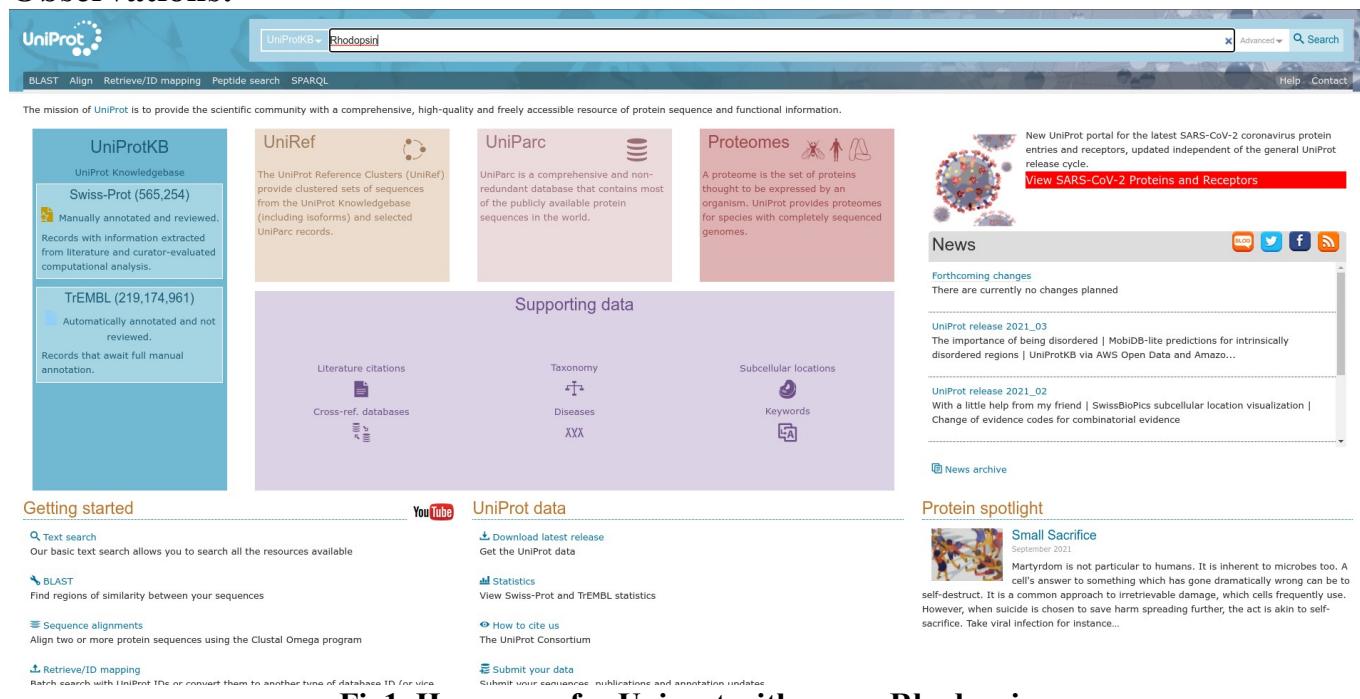
UniProtKB/TrEMBL is a computer-annotated protein sequence database complementing . UniProtKB/TrEMBL contains the translations of all coding sequences (CDS) present in the EMBL/GenBank/DDBJ Nucleotide Sequence Databases and also protein sequences extracted. The database is enriched with automated classification and annotation.

Rhodopsin is a biological pigment found in the rods of the retina and is a G-protein-coupled receptor (GPCR). It belongs to a group of photoswitchable opsins. Rhodopsin is extremely sensitive to light, and thus enables vision in low-light conditions. When rhodopsin is exposed to light, it immediately photobleaches.

Methodology:

- Homepage of Uniprot.
- Enter the UniprotKB and search the query ‘Rhodopsin’
- Open Unreviewed paper.
- Interpret the results.

Observations:



The screenshot shows the UniProt homepage with the search term 'Rhodopsin' entered in the search bar. The results page displays various protein databases and supporting data. Key sections include:

- UniProtKB**: UniProt Knowledgebase (Swiss-Prot: 565,254, TrEMBL: 219,174,961).
- UniRef**: The UniProt Reference Clusters (UniRef) provide clustered sets of sequences from the UniProt Knowledgebase (including isoforms) and selected UniParc records.
- UniParc**: UniParc is a comprehensive and non-redundant database that contains most of the publicly available protein sequences in the world.
- Proteomes**: A proteome is the set of proteins thought to be expressed by an organism. UniProt provides proteomes for species with completely sequenced genomes.
- Supporting data**: Includes Literature citations, Cross-ref. databases, Taxonomy, Diseases, Subcellular locations, and Keywords.
- News**: Forthcoming changes (no changes planned), UniProt release 2021_03 (importance of being disordered, MobiDB-lite predictions), UniProt release 2021_02 (with a little help from my friend, SwissBioPics subcellular location visualization), and a news archive.
- Protein spotlight**: Small Sacrifice (September 2021) discusses martyrdom in cells.

Fig1. Homepage for Uniprot with query Rhodopsin

UniProtKB - rhodopsin AND reviewed:no

Advanced Search

BLAST Align Retrieve/ID mapping Peptide search SPARQL Help Contact Basket

UniProtKB 2021_03 results

UniProtKB consists of two sections:

Reviewed (Swiss-Prot) - Manually annotated
Records with information extracted from literature and curator-evaluated computational analysis.

Unreviewed (TrEMBL) - Computationally analyzed
Records that await full manual annotation.

The UniProt Knowledgebase (UniProtKB) is the central hub for the collection of functional information on proteins, with accurate, consistent and rich annotation. In addition to capturing the core data mandatory for each UniProtKB entry (mainly, the amino acid sequence, protein name or description, taxonomic data and citation information), as much annotation information as possible is added.

Help UniProtKB help video Other tutorials and videos Downloads

Filter by:

Popular organisms:
Zebrafish (53)
Fruit fly (48)
Human (27)
Rat (22)
Bovine (20)
Other organisms Go

Search terms:
Filter "rhodopsin" as:
gene name (47)
gene ontology (1,134)
protein name (26,101)
strain (1)
taxonomy (1)

Table: 1 to 25 of 54,696 Show 25

Entry	Entry name	Protein names	Gene names	Organism	Length
<input type="checkbox"/> F1P3Y2	F1P3Y2_CHICK	Rhodopsin	RHO	Gallus gallus (Chicken)	351
<input type="checkbox"/> Q9VTU7	Q9VTU7_DROME	Rhodopsin	Rh7	Rh7 anon-WO0170980.34, anon-WO0170980.35, Dmel\CG5638, DMELRH7, Rh	483
<input type="checkbox"/> U3KGW6	U3KGW6_FICAL	Rhodopsin	RHO	Ficedula albicollis (Collared flycatcher) (Muscicapa albicollis)	351
<input type="checkbox"/> Q9IA36	Q9IA36_TAEGU	Rhodopsin	RHO	Taeniopygia guttata (Zebra finch) (Poephila guttata)	351
<input type="checkbox"/> G1ND14	G1ND14_MELGA	Rhodopsin	RHO	Meleagris gallopavo (Wild turkey)	351
<input type="checkbox"/> U3IBZ9	U3IBZ9_ANAPP	Rhodopsin	RHO	Anas platyrhynchos platyrhynchos (Northern mallard)	351
<input type="checkbox"/> A0A093Q1T7	A0A093Q1T7_9PASS	Rhodopsin	N305_14752	Manacus vitellinus (golden-collared manakin)	351
<input type="checkbox"/> Q9VDS3	Q9VDS3_DROME	Exit protein of rhodopsin and TRP A	Xport-A	Drosophila melanogaster (Fruit fly)	116
<input type="checkbox"/> A4ZIS8	A4ZIS8_ORNAN	Rhodopsin	RHO	Ornithorhynchus anatinus (Duckbill platypus)	353
<input type="checkbox"/> Q9PTX9	Q9PTX9_DANRE	Rhodopsin	exorh exo-rod	Danio rerio (Zebrafish) (Brachydanio rerio)	354
<input type="checkbox"/> H2QNC5	H2QNC5_PANTR	Rhodopsin	RHO	Pan troglodytes (Chimpanzee)	348
<input type="checkbox"/> G3R589	G3R589_GORGO	Rhodopsin	RHO	Gorilla gorilla gorilla (Western lowland gorilla)	348

Fig2. Hit page for Unreviewed for query Rhodopsin

UniProtKB - F1P3Y2 (F1P3Y2_CHICK)

Advanced Search Help video Add to basket History Add a publication Feedback

Display:

Entry: Rhodopsin, RHO, Gallus gallus (Chicken)

Status: Unreviewed - Annotation score: - Protein inferred from homology

Function:

GO - Molecular function:

- G-protein alpha-subunit binding Source: AgBase
- G protein-coupled photoreceptor activity Source: GO_Central
- protein homodimerization activity Source: AgBase

Complete GO annotation on QuickGO ...

GO - Biological process:

- cellular response to light stimulus Source: GO_Central
- detection of temperature stimulus involved in thermoreception Source: Ensembl
- G protein-coupled receptor signaling pathway Source: GO_Central
- light absorption Source: AgBase
- photoreceptor cell maintenance Source: Ensembl
- phototransduction Source: GO_Central
- protein-chromophore linkage Source: AgBase
- protein phosphorylation Source: Ensembl
- retina development in camera-type eye Source: Ensembl
- thermotaxis Source: Ensembl
- visual perception Source: UniProtKB-KW

Complete GO annotation on QuickGO ...

Keywords:

- Molecular function: G-protein coupled receptor UniRule annotation ARBA annotation Photoreceptor protein, Receptor, Retinal protein UniRule annotation ARBA annotation Transducer
- Biological process: Sensory transduction, Vision ARBA annotation

Fig3. Header page for query Rhodopsin

Display Help video Function¹

Entry

Publications

Feature viewer

Feature table

None

Function¹

- G-protein alpha-subunit binding Source: AgBase
- G protein-coupled photoreceptor activity Source: GO_Central
- protein homodimerization activity Source: AgBase

Complete GO annotation on QuickGO ...

GO - Molecular function¹

- cellular response to light stimulus Source: GO_Central
- detection of temperature stimulus involved in thermoreception Source: Ensembl
- G protein-coupled receptor signaling pathway Source: GO_Central
- light absorption Source: AgBase
- photoreceptor cell maintenance Source: Ensembl
- phototransduction Source: GO_Central
- protein-chromophore linkage Source: AgBase
- protein phosphorylation Source: Ensembl
- retina development in camera-type eye Source: Ensembl
- thermotaxis Source: Ensembl
- visual perception Source: UniProtKB-KW

Complete GO annotation on QuickGO ...

Biological process¹

Keywords¹

Molecular function	G-protein coupled receptor UniRule annotation ARBA annotation , Photoreceptor protein, Receptor, Retinal protein UniRule annotation ARBA annotation , Transducer
Biological process	Sensory transduction, Vision ARBA annotation
Ligand	Chromophore

Enzyme and pathway databases

Reactome¹

- R-GGA-2453902, The canonical retinoid cycle in rods (twilight vision)
- R-GGA-2485179, Activation of the phototransduction cascade
- R-GGA-2514859, Inactivation, recovery and regulation of the phototransduction cascade
- R-GGA-418594, G alpha (i) signalling events
- R-GGA-419771, Opsins
- R-GGA-5620916, VxPx cargo-targeting to cilium

Names & Taxonomy¹

Protein names ¹	Recommended name: Rhodopsin UniRule annotation
Gene names ¹	Name: RHO Imported
Organism ¹	Galus gallus [Chicken] Imported
Taxonomic identifier	9031 [NCBI]

<https://www.ebi.ac.uk/QuickGO/annotations?geneProduct=RHO>

Fig4. Function page for query Rhodopsin

```
>tr|F1P3Y2|F1P3Y2_CHICK Rhodopsin OS=Gallus gallus OX=9031 GN=RHO PE=3 SV=2
MNGTEGQDFYVPMNSNKTGVVRSPFEYPQYYLAEPWKFSALAAYMFMLILLGFPVNFLTLY
VTIQHKKLRTPLNYILLNLAVADLFMVFGGFTTMYTSMNGYFVFGVTGCYIEGFFATLG
GEIALWSLVLVLAVERYVVVCKPMNSNFRFGENHAIMGVAFSWIMAMACAAPPLFGWSRYIP
EGMQCSCGIDYYTLKPEINNESFVIYMFVVHFMIPLAVIDFCYGNLVCTVKEAAAQQQES
ATTQKAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTNQGSDFGPIFMTIPAFFAKSSAI
YNPVIYIVMNKQFRNCMITTLCGKNPLGDEDTSAGKTETSSVSVSPA
```

Fig5. FASTA Canonical for result page of query Rhodopsin

Display Help video Names & Taxonomy¹

Entry

Publications

Feature viewer

Feature table

None

Function

Names & Taxonomy

Subcellular location¹

Pathology & Biotech

PTM / Processing

Expression

Interaction

Structure

Family & Domains

Sequence

Similar proteins

Cross-references

Entry information

Miscellaneous

Top

Protein names¹ Recommended name: **Rhodopsin** UniRule annotation

Gene names¹ Name: **RHO** Imported

Organism¹ **Galus gallus (Chicken)** Imported

Taxonomic identifier¹ 9031 [NCBI]

Taxonomic lineage¹ Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Archelosuria > Archosaura > Dinosauria > Saurischia > Theropoda > Coelurosauria > Aves > Neognathae > Galloanserae > Galliformes > Phasianidae > Phasianinae > Galus

Proteomes¹ UP000000539 Component¹: Chromosome 12

Subcellular location¹

UniProt annotation GO - Cellular component

Other locations

- Membrane UniRule annotation ARBA annotation; Multi-pass membrane protein
- UniRule annotation ARBA annotation

https://www.uniprot.org/uniprot/F1P3Y2#names_and_taxonomy Automatic annotation

Fig6. Names and Taxonomy of result page for query Rhodopsin

Display Help video Subcellular location¹

Entry

Publications

Feature viewer

Feature table

None

Function

Names & Taxonomy

Subcellular location¹

Pathology & Biotech

PTM / Processing

Expression

Interaction

Structure

Family & Domains

Sequence

Similar proteins

Cross-references

Entry information

Miscellaneous

Top

Automatic annotation

Manual annotation

Source: SwissBioPics

Topology

Feature key	Position(s)	Description	Actions	Graphical view	Length
Transmembrane ¹	40 – 63	Helical UniRule annotation	Add BLAST		24
Transmembrane ¹	75 – 9	Helical UniRule annotation	Add BLAST		22
Transmembrane ¹	102 – 133	Helical UniRule annotation	Add BLAST		32
Transmembrane ¹	153 – 173	Helical UniRule annotation	Add BLAST		21
Transmembrane ¹	203 – 223	Helical UniRule annotation	Add BLAST		21
Transmembrane ¹	254 – 277	Helical UniRule annotation	Add BLAST		24

https://www.uniprot.org/uniprot/F1P3Y2#names_and_taxonomy

Fig7. Subcellular location of result page for query Rhodopsin

Display [Help video](#)

PTM / Processing

Keywords - PTM¹
Disulfide bond ARBA annotation Glycoprotein ARBA annotation Phosphoprotein ARBA annotation

Expression

Gene expression databases
Bgee¹ ENSGALG00000020745, Expressed in cerebellum and 1 other tissue

Interaction

GO - Molecular function¹
▪ G-protein alpha-subunit binding Source: AgBase
▪ protein homodimerization activity Source: AgBase
Complete GO annotation on QuickGO ...

Structure

No structure information available for F1P3Y2

Family & Domains

Domains and Repeats

Feature key	Position(s)	Description	Actions	Graphical view	Length
Domain ¹	54 – 306	G_PROTEIN_RECEP_F1_2 <input checked="" type="checkbox"/> InterPro annotation <input type="checkbox"/>	Add BLAST		253

Region

Feature key	Position(s)	Description	Actions	Graphical view	Length
Region ¹	331 – 351	Disordered <input checked="" type="checkbox"/> Sequence analysis <input type="checkbox"/>	Add BLAST		21

Compositional bias

Feature key	Position(s)	Description	Actions	Graphical view	Length
Compositional bias ¹	333 – 351	Polar residues <input checked="" type="checkbox"/> Sequence analysis <input type="checkbox"/>	Add BLAST		19

Sequence similarities¹
Belongs to the G-protein coupled receptor 1 family, Opsin subfamily. UniRule annotation

Keywords - Domain¹
Transmembrane, Transmembrane helix UniRule annotation ARBA annotation

<https://www.uniprot.org/uniprot/F1P3Y2#ptm>

Phylogenomic databases

Fig8. PTM processing for result of query Rhodopsin

Display [Help video](#)

Expression

Gene expression databases
Bgee¹ ENSGALG00000020745, Expressed in cerebellum and 1 other tissue

Interaction

GO - Molecular function¹
▪ G-protein alpha-subunit binding Source: AgBase
▪ protein homodimerization activity Source: AgBase
Complete GO annotation on QuickGO ...

Structure

No structure information available for F1P3Y2

Family & Domains

Domains and Repeats

Feature key	Position(s)	Description	Actions	Graphical view	Length
Domain ¹	54 – 306	G_PROTEIN_RECEP_F1_2 <input checked="" type="checkbox"/> InterPro annotation <input type="checkbox"/>	Add BLAST		253

Region

Feature key	Position(s)	Description	Actions	Graphical view	Length
Region ¹	331 – 351	Disordered <input checked="" type="checkbox"/> Sequence analysis <input type="checkbox"/>	Add BLAST		21

Compositional bias

Feature key	Position(s)	Description	Actions	Graphical view	Length
Compositional bias ¹	333 – 351	Polar residues <input checked="" type="checkbox"/> Sequence analysis <input type="checkbox"/>	Add BLAST		19

Sequence similarities¹
Belongs to the G-protein coupled receptor 1 family, Opsin subfamily. UniRule annotation

Keywords - Domain¹
Transmembrane, Transmembrane helix UniRule annotation ARBA annotation

Phylogenomic databases

GeneTree ¹	ENSGT01030000234549
HOGENOM ¹	CLU_009579_3_0_1
InParanoid ¹	F1P3Y2
OMA ¹	Rhodopsin

Fig9. Expression for result of query Rhodopsin

Display Help video Interaction¹

Entry Publications Feature viewer Feature table

None

Function Names & Taxonomy Subcellular location Pathology & Biotech PTM / Processing Expression Interaction Structure Family & Domains Sequence Similar proteins Cross-references Entry information Miscellaneous

► Top

Interaction¹

GO - Molecular function¹

- G-protein alpha-subunit binding Source: AgBase
- protein homodimerization activity Source: AgBase

Complete GO annotation on QuickGO ...

Structure¹

No structure information available for F1P3Y2

Family & Domains¹

Domains and Repeats

Feature key	Position(s)	Description	Actions	Graphical view	Length
Domain ¹	54 – 306	G_PROTEIN_RECEP_F1_2 InterPro annotation	Add BLAST		253

Region

Feature key	Position(s)	Description	Actions	Graphical view	Length
Region ¹	331 – 351	Disordered Sequence analysis	Add BLAST		21

Compositional bias

Feature key	Position(s)	Description	Actions	Graphical view	Length
Compositional bias ¹	333 – 351	Polar residues Sequence analysis	Add BLAST		19

Sequence similarities¹

Belongs to the G-protein coupled receptor 1 family. Opsin subfamily. UniRule annotation

Keywords - Domain¹

Transmembrane, Transmembrane helix UniRule annotation ARBA annotation

Phylogenomic databases

GeneTree ¹	ENSGT01030000234549
HOGENOM ¹	CLU_009579_3_0_1
InParanoid ¹	F1P3Y2
OMA ¹	EQPQYLYL
TreeFam ¹	TF324998

Family and domain databases

► Top View protein in InterPro

Fig10. Interaction for result of query Rhodopsin

Display Help video Similar proteins¹

Entry Publications Feature viewer Feature table

None

Function Names & Taxonomy Subcellular location Pathology & Biotech PTM / Processing Expression Interaction Structure Family & Domains Sequence Similar proteins Cross-references Entry information Miscellaneous

► Top

Similar proteins¹

Protein	Similar proteins	Species	Score	Length	Source
F1P3Y2	Rhodopsin	BAMTH	●●●○	351	UniRef100_F1P3Y2

Full view

Cross-references¹

Sequence databases

Select the link [AADN05000356](#) Genomic DNA No translation available.

destination: EMBL¹ GenBank¹ DDBJ¹

3D structure databases

ModBase¹ [Search...](#) SWISS-MODEL-Workspace¹ [Submit a new modelling project...](#)

Protein family/group databases

GPCRD¹ [Search...](#)

Genome annotation databases

Ensembl¹ [ENSGALT00000033236; ENSGALP00000032596; ENSGALG00000020745](#)

Phylogenomic databases

GeneTree ¹	ENSGT01030000234549
HOGENOM ¹	CLU_009579_3_0_1
InParanoid ¹	F1P3Y2
OMA ¹	EQPQYLYL
TreeFam ¹	TF324998

Enzyme and pathway databases

Reactome¹

- R-GGA-2453902, The canonical retinoid cycle in rods (twilight vision)
- R-GGA-2485179, Activation of the phototransduction cascade
- R-GGA-2514859, Inactivation, recovery and regulation of the phototransduction cascade
- R-GGA-418594, G alpha (I) signalling events
- R-GGA-419771, Opsins
- R-GGA-5620916, VxPx cargo-targeting to cilium

Fig11. Similar proteins for result of query Rhodopsin

Conclusions:

A computer annotated supplement to Swiss-Prot .Contains all the translations of EMBL nucleotide sequences entries not yet integrated in Swiss-Prot and cross-referenced to many other databases.

Results:

In UniprotKB it consist TrEMBL that is Unreviewed paper and for the query 'Rhodopsin' is contain 54,696 papers

References:

1. <https://www.uniprot.org/>
2. <https://www.uniprot.org/uniprot/?query=rhodopsin&fil=reviewed%3A0&sort=score>
3. <https://www.uniprot.org/uniprot/F1P3Y2>
4. <https://www.uniprot.org/uniprot/F1P3Y2#function>
5. https://www.uniprot.org/uniprot/F1P3Y2#names_and_taxonomy
6. https://uniprot.org/uniprot/F1P3Y2#subcellular_location
7. https://www.uniprot.org/uniprot/F1P3Y2#ptm_processing
8. <https://www.uniprot.org/uniprot/F1P3Y2#expression>
9. <https://www.uniprot.org/uniprot/F1P3Y2#interaction>
10. https://www.uniprot.org/uniprot/F1P3Y2#similar_proteins
11. <https://www.uniprot.org/uniprot/F1P3Y2.fasta>

WEBLEM 4d

(URL: <https://www.uniprot.org/>)

Aim:

To study 'Rhodopsin' Protein information using PIR Database: An Integrated Protein Informatics Database.

Introduction:

The Protein Information Resource (PIR) is an integrated public bioinformatics resource to support genomic, proteomic and systems biology research and scientific studies (Wu et al., 2003). PIR was established in 1984 by the National Biomedical Research Foundation (NBRF) as a resource to assist researchers in the identification and interpretation of protein sequence information.

Rhodopsin is a biological pigment found in the rods of the retina and is a G-protein-coupled receptor (GPCR). It belongs to a group of photoswitchable opsins. Rhodopsin is extremely sensitive to light, and thus enables vision in low-light conditions. When rhodopsin is exposed to light, it immediately photobleaches.

Methodology:

- Homepage of Uniprot.
- Enter the UniprotKB and search the query 'Rhodopsin'
- Interpret the results.

Observations:

Fig1. Homepage of PIR

About PIR		Resources		Search/Analysis		Download		Support		Protein Search	
<input type="checkbox"/> (search) <input type="text" value="rhodopsin"/> <input type="button" value="GO"/>		<input type="button" value="All Fields"/> <input type="button" value="AND"/> <input type="button" value="All Fields"/> <input type="button" value="AND"/> <input type="button" value="All Fields"/>		<input type="button" value="+ add input box"/> <input type="button" value="del input box"/>						<input type="checkbox"/> Text Search Result	
Display Options	<input type="checkbox"/> Help ?	42785 proteins 856 pages 50 / page <input type="button" value="<<"/> <input type="button" value="1"/> <input type="button" value="2"/> <input type="button" value="3"/> <input type="button" value="4"/> <input type="button" value="5"/> <input type="button" value=">>"/>								Save Result As: <input type="checkbox"/> TABLE <input type="checkbox"/> FASTA	
<input type="checkbox"/> check & analyze		<input type="checkbox"/> GO Slim / Pathway...								<input type="checkbox"/> Pairwise Alignment <input type="checkbox"/> Multiple Alignment <input type="checkbox"/> Domain Display	
<input type="checkbox"/> Protein AC/ID	Protein Name			Length	Organism Name	PRO ID	PIRSF ID			UniRef50	
<input type="checkbox"/> A3KFT3/0R2M5_HUMAN	Olfactory receptor 2M5			312	Homo sapiens (Human)	PR:000011781; PR:A3KFT3	PIRSF003152; PIRSF00006	UniRef50_Q8NH8C			
<input type="checkbox"/> A4D2G3/0A2A5_HUMAN	Olfactory receptor 2A5			310	Homo sapiens (Human)	PR:000011746; PR:A4D2G3	PIRSF003152; PIRSF00006	UniRef50_A4D2G3			
<input type="checkbox"/> A6NCV1/00C74_HUMAN	Olfactory receptor 6C74			312	Homo sapiens (Human)	PR:000011968; PR:A6NCV1	PIRSF003152; PIRSF00006	UniRef50_A6NCV1			
<input type="checkbox"/> A6ND48/0I411_HUMAN	Olfactory receptor 1411			311	Homo sapiens (Human)	PR:000011712; PR:A6ND48	PIRSF003152; PIRSF00006	UniRef50_A6ND48			
<input type="checkbox"/> A6NDH6/0SH15_HUMAN	Olfactory receptor 5H15			313	Homo sapiens (Human)	PR:000011931; PR:A6NDH6	PIRSF003152; PIRSF00006	UniRef50_A6NNKO			
<input type="checkbox"/> A6NDL8/0GC68_HUMAN	Olfactory receptor 6C68			312	Homo sapiens (Human)	PR:000011966; PR:A6NDL8	PIRSF003152; PIRSF00006	UniRef50_A6NDL8			
<input type="checkbox"/> A6NET4/0RK53_HUMAN	Olfactory receptor 5K3			321	Homo sapiens (Human)	PR:000011928; PR:A6NET4	PIRSF003152; PIRSF00006	UniRef50_Q8VGQZ			
<input type="checkbox"/> A6GNF89/0RC66_HUMAN	Olfactory receptor 6C6			314	Homo sapiens (Human)	PR:000011964; PR:A6GNF89	PIRSF003152; PIRSF00006	UniRef50_A6GNF89			
<input type="checkbox"/> A6NGY5/0S1F1_HUMAN	Olfactory receptor 5F1			319	Homo sapiens (Human)	PR:000011867; PR:A6NGY5	PIRSF003651; PIRSF00006	UniRef50_A6NGY5			
<input type="checkbox"/> A6NH00/0R278_HUMAN	Olfactory receptor 2T8			312	Homo sapiens (Human)	PR:000011798; PR:A6NH00	PIRSF003152; PIRSF00006	UniRef50_A6NH00			
<input type="checkbox"/> A6NH9A/0Q4C6_HUMAN	Olfactory receptor 4C6			309	Homo sapiens (Human)	PR:000011820; PR:A6NH9A	PIRSF003152; PIRSF00006	UniRef50_Q6NGL6			
<input type="checkbox"/> A6NH9G/0SH14_HUMAN	Olfactory receptor 5H14			310	Homo sapiens (Human)	PR:000011930; PR:A6NH9G	PIRSF003152; PIRSF00006	UniRef50_A6NH9G			
<input type="checkbox"/> A6N1J9/0C670_HUMAN	Olfactory receptor 5C70			312	Homo sapiens (Human)	PR:000011967; PR:A6N1J9	PIRSF003152; PIRSF00006	UniRef50_Q6R6D1			
<input type="checkbox"/> A6NZ3/0GC65_HUMAN	Olfactory receptor 6C65			312	Homo sapiens (Human)	PR:000011965; PR:A6NZ3	PIRSF003152; PIRSF00006	UniRef50_Q6R6D1			
<input type="checkbox"/> A6NKK0/0R5H1_HUMAN	Olfactory receptor 5H1			313	Homo sapiens (Human)	PR:000011929; PR:A6NKK0	PIRSF003152; PIRSF00006	UniRef50_A6NNKO			
<input type="checkbox"/> A6NL08/0QC75_HUMAN	Olfactory receptor 6C75			312	Homo sapiens (Human)	PR:000011969; PR:A6NL08	PIRSF003152; PIRSF00006	UniRef50_A6NL08			
<input type="checkbox"/> A6NI26/0RS51_HUMAN	Olfactory receptor 5R31			309	Homo sapiens (Human)	PR:000011931; PR:A6NI26	PIRSF003152; PIRSF00006	UniRef50_A6NI26			

Fig2. Hit page for PIR for query Rhodopsin

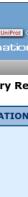
 PIR A  CONSORTIUM MEMBER Protein Information Resource	<p>TL ALPN-----KEVAVABULLB LIGGLNNSAVTIAAKQULAE VTOF8RN-----AKTTAQWKE Protein Search  </p>						
/ProClass Summary Report for UniProtKB Entry: A3KFT3							
ID Mapping							
GENERAL INFORMATION							
Protein Name and ID	<table border="1"> <tr> <td>UniProtKB ID</td><td>UniProtKB Accession</td><td>Protein Name</td></tr> <tr> <td>OR2M5_HUMAN</td><td>A3KFT3</td><td>Olfactory receptor 2M5</td></tr> </table> <p>RefSeq: NP_001004690.1 GenBank: LAU977216.1 CCDS: CCDS31105.1</p>	UniProtKB ID	UniProtKB Accession	Protein Name	OR2M5_HUMAN	A3KFT3	Olfactory receptor 2M5
UniProtKB ID	UniProtKB Accession	Protein Name					
OR2M5_HUMAN	A3KFT3	Olfactory receptor 2M5					
Taxonomy	<p>Source Organism: Homo sapiens (Human) Taxon Group: Euk/mammal NCBI Taxon: 9606 Lineage: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.</p>						
Gene Name	OR2M5; OR2M5P						
Keywords	cell membrane; disulfide bond; g-protein coupled receptor; glycoprotein; membrane; olfaction; receptor; reference proteome; sensory transduction; transducer; transmembrane; transmembrane helix						
Function	Odorant receptor.						
CROSS-REFERENCES							
Bibliography	<p>► View Bibliography Information Annotated references: PMID: 16710414; 21248752 [UniProt] Other references: 14983052; 21873635</p>						
DNA Sequence	<p>EMBL: AL592313 DDBJ: AL592313 GenBank: AL592313</p>						
Genome/Gene	<p>Gene Name: OR2M5; olfactory receptor family 2 subfamily M member 5 Synonyms: OR2M5P; Map Location: 1q44 Enzrez Gene: 127058 UniGene: 16s.553580 RefSeq: NM_001004690.1 NP_001004690.1 [Map Viewer] Entrez: ENSG00000166476; ENSP00000355432; ENSG00000162727 UCSC: OR2M5.2 human KEGG: hsa127059</p>						
Gene Expression	<p>CleanEx SOURCE Bgee: ENSG00000162727</p>						
Genetic Variation/Disease	<p>HapMap: OR2M5</p>						
Protein Ontology:							

Fig3. Result page for query Rhodopsin

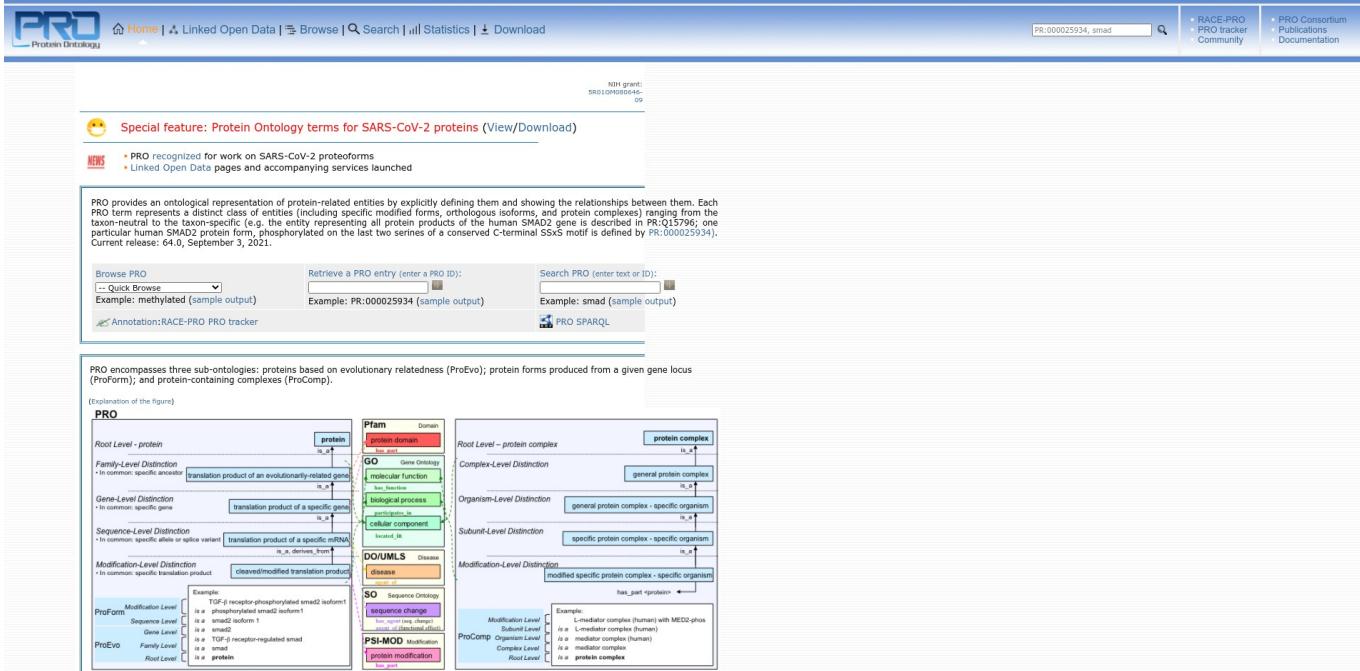


Fig4. Home page of PRO with PR ID

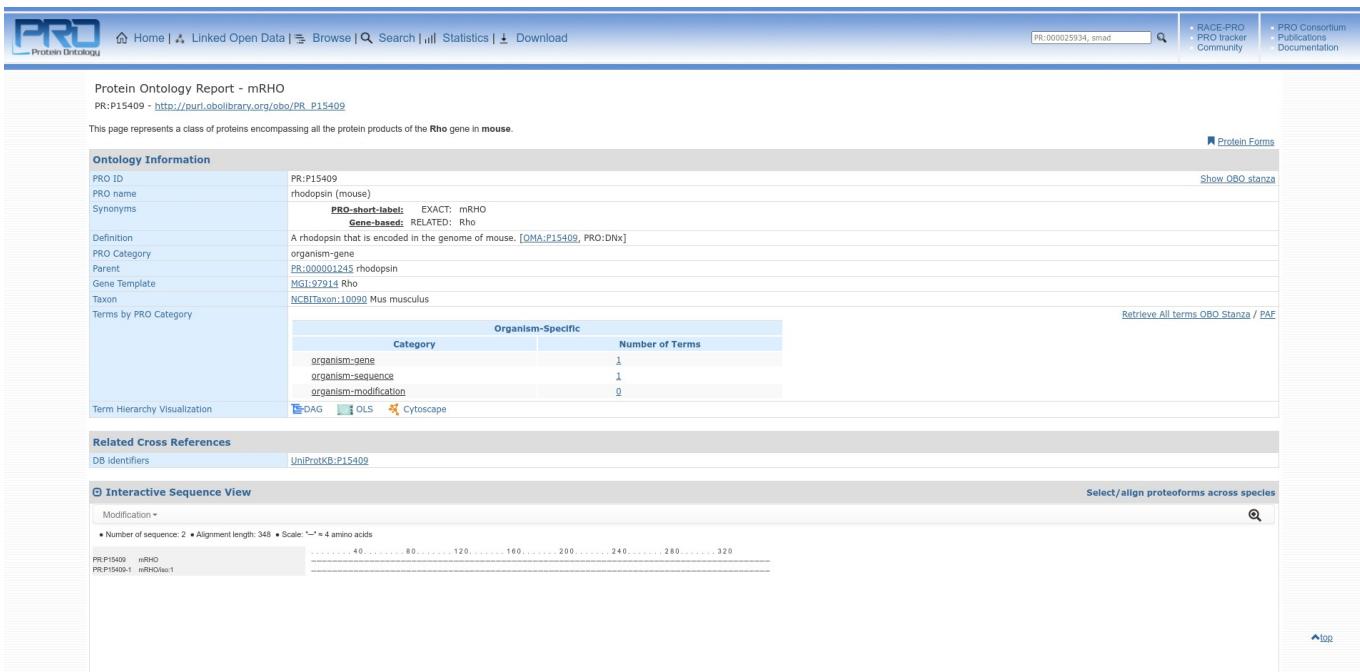


Fig5. Result page of PRO for query rhodopsin

PIR A UniProt CONSORTIUM MEMBER
Protein Information Resource

About PIR Resources Search/Analysis Download Support

(NSF grants ABI-1062320)
NIH/NIGMS grants U01GM120953

iPTMnet

iPTMnet is a bioinformatics resource for integrated understanding of protein post-translational modifications (PTMs) in systems biology context.

It connects multiple disparate bioinformatics tools and systems text mining, data mining, analysis and visualization tools, and databases and ontologies into an integrated cross-cutting research resource to address the knowledge gaps in exploring and discovering PTM networks.

- Browse
- Statistics
- Project Info
- API
- Help
- License
- Citation



Search for proteins in iPTMnet database

All

PTM type Has Role Restrict by Organism Sample Report Batch Retrieval (New!)

Search phosphorylation information in the literature

Enter Keywords (accepts Boolean operators (AND, OR, NOT))

Exclude review papers, Restrict by Organism

Fig6. Home page of iPTMnet for query Rhodopsin

PTM net Home Browse Statistics Project Info Help Result

All

1 - 20 of 21 results for **rhodopsin** in iPTMnet

<input type="checkbox"/> IPTM ID	Protein Name	Gene Name	Organism	Substrate Role	Enzyme Role	PTM-dependent PPI	Sites	Isoforms
<input type="checkbox"/> IPTM:Q15835/GRK1_HUMAN	Rhodopsin kinase GRK1 precursor	Name: GRK1 Synonyms:RHOK;	Homo sapiens	✓ 2 enzymes	✓ 4 substrates	✗	8	0
<input type="checkbox"/> IPTM:Q8WTQ7/GRK7_HUMAN	Rhodopsin kinase GRK7 precursor	Name: GRK7 Synonyms:GRK7;	Homo sapiens	✓ 3 enzymes	✓ 1 substrate	✗	8	0
<input type="checkbox"/> IPTM:Q9WVL4/GRK1_MOUSE	Rhodopsin kinase GRK1 precursor	Name: Grk1 Synonyms:RhoK;	Mus musculus (Mouse)	✓ 1 enzyme	✓ 2 substrates	✗	1	0
<input type="checkbox"/> IPTM:P28327/GRK1_BOVIN	Rhodopsin kinase GRK1 precursor	Name: GRK1 Synonyms:RHOK;	Bos taurus (Bovine)	✓ 1 enzyme	✓ 1 substrate	✗	5	0
<input type="checkbox"/> IPTM:Q63851/GRK1_RAT	Rhodopsin kinase GRK1 precursor	Name: Grk1 Synonyms:RhoK;	Rattus norvegicus (Rat)	✓ 1 enzyme	✓ 1 substrate	✗	3	0
<input type="checkbox"/> IPTM:P18549/CNRG_HUMAN	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma	Name: PDE6G Synonyms:PDG;	Homo sapiens	✓ 3 enzymes	✗	✗	4	0
<input type="checkbox"/> IPTM:P08100/OPSD_HUMAN	Rhodopsin	Name: RHO Synonyms:OPN2;	Homo sapiens	✓ 2 enzymes	✗	✗	9	0
<input type="checkbox"/> IPTM:P15409/OPSD_MOUSE	Rhodopsin	Name: Rho	Mus musculus (Mouse)	✓ 2 enzymes	✗	✗	5	0
<input type="checkbox"/> IPTM:P04972/CNRG_BOVIN	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma	Name: PDE6G Synonyms:PDG;	Bos taurus (Bovine)	✓ 2 enzymes	✗	✗	3	0
<input type="checkbox"/> IPTM:P02699/OPSD_BOVIN	Rhodopsin	Name: RHO	Bos taurus (Bovine)	✓ 1 enzyme	✗	✗	10	0
<input type="checkbox"/> IPTM:P09174/CNRG_MOUSE	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma	Name: Pde6g Synonyms:Pdeg;	Mus musculus (Mouse)	✓ 1 enzyme	✗	✗	3	0
<input type="checkbox"/> IPTM:P51489/OPSD_RAT	Rhodopsin	Name: Rho	Rattus norvegicus (Rat)	✓	✗	✗	5	0
<input type="checkbox"/> IPTM:P02700/OPSD_SHEEP	Rhodopsin	Name: RHO	Ovis aries (Sheep)	✓	✗	✗	5	0
<input type="checkbox"/> IPTM:Q13395/CNCG_HUMAN	Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma	Name: PDE6H	Homo sapiens	✓	✗	✗	3	0
<input type="checkbox"/> IPTM:Q43324/PDE6D_HUMAN	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta	Name: PDE6D Synonyms:PD6D;	Homo sapiens	✓	✗	✗	3	0
<input type="checkbox"/> IPTM:P61249/CNCG_MOUSE	Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma	Name: Pde6h	Mus musculus (Mouse)	✓	✗	✗	2	0
<input type="checkbox"/> IPTM:866C218/GRK7B_XENLA	Rhodopsin kinase grk7-b precursor	Name: grk7-b	Xenopus laevis (African clawed frog)	✓	✗	✗	1	0
<input type="checkbox"/> ProClass UnIPhox PRO								

Fig7. Hit page for query Rhodopsin in iPTMnet

iPTMnet Report for Q15835 (GRK1)

Display

Protein Information

Q15835 (GRK1) as Substrate

Q15835 (GRK1) as PTM Enzyme

PTM sites affected in variants

[Back to top](#)

[Cytoscape View](#) [Clear](#) [Submit](#)

Protein Information

UniProt AC / UniProt ID: Q15835 / GRK1_HUMAN

Protein Name: Rhodopsin kinase GRK1 precursor

Gene Name: GRK1

Synonyms: RHOK;

Organism: Homo sapiens (Human)

[Cytoscape View](#)

[DAG View](#)

Interactive Sequence View

Show PRO entries Modification site affected in variant

Number of sequence: 1 • Alignment length: 563 • Scale: "—" = 7 amino acids

IPTM:Q15835_hGRK1

Q15835 (GRK1) as Substrate

[Expanded View](#)

[Search](#) [Display Overlay PTM](#)

Site **PTM Type** **PTM Enzyme** **Score** **Source** **PMID**

Q15835

Fig8. Result page for query Rhodopsin in iPTMnet

PIR UnIProt CONSORTIUM MEMBER
Protein Information Resource

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HOME / iProLINK

iProLINK

iProLINK (Integrated Protein Literature, INformation and Knowledge) is a resource with access to text mining tools and annotated corpora developed in house. The collection of data sources can be utilized by computational and biological researchers to explore literature information on proteins and their features or properties.

Text Mining Tools

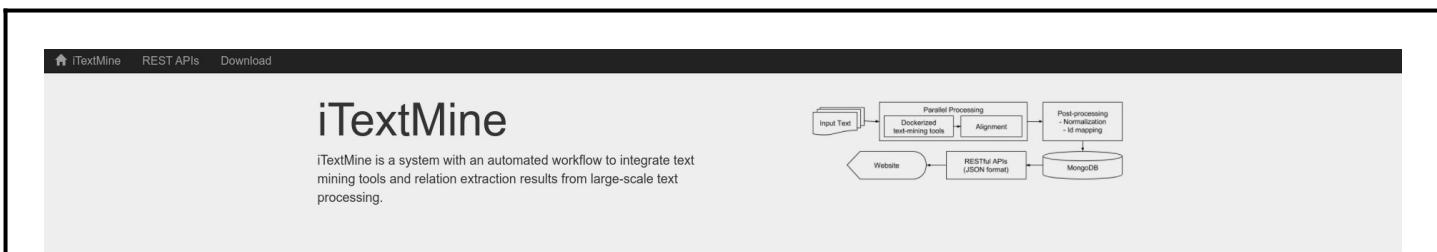
- iTextMine**: integrated text mining tools and relation extraction results from large-scale text processing
- pGenN**: a gene normalization tool tailored for plants
- miRTeX**: a relation extraction tool that identifies miRNA-target relations as well as miRNA-gene and gene-miRNA regulation relations
- eFIP**: a relation extraction tool that identifies information relevant to phosphorylated proteins and phosphorylation-dependent protein-protein interactions
- emIRIT**: an integrative text mining system collecting miRNA information from the literature
- RLIMS-P**: a relation extraction tool that identifies information relevant to protein phosphorylation
- IXtractR**: a generalizable relation extraction system (*for developers*)
- iSimp**: a sentence simplification system (*for developers*)

Literature Corpora **Publications**

University of Delaware
15 Innovation Way, Suite 205
Newark, DE 19711, USA

Georgetown University Medical Center
3300 Whitehaven Street, NW, Suite 1200
Washington, DC 20007, USA

Fig9. Home page for iProLINK



Enter keywords or PMIDs
(one or multiple PMIDs per line, separated by commas or spaces)

Medline PMC
 RLIMS-P eFIP miRTex eGARD

[Search](#) [Visualize](#)

You can search various types of queries

- Keywords accepts Boolean operators (AND, OR, NOT)
- One PubMed ID
- Examples:
 - PMID:27665963
 - bub1 Network
 - search "SATB1" OR "Special AT-rich sequence-binding protein 1"

- Available text mining tools
- RLIMS-P: mining protein phosphorylation (kinase-substrate-site)
 - eFIP: phosphorylation-dependent protein-protein interactions (PPIs)
 - miRTex: miRNA-gene relations
 - eGARD: targeted therapy information from the scientific literature
 - PubTator: entity normalization

Fig10. ItextMine page for iProLINK with PMID.

The search results page shows a table with the following data:

Search 27665963 in		All	rlims	eFIP	miRTex	eGARD	Issue Report
Find 1 document (1 page)							
Visualize selected documents 1 25 rows per page ▾							
PMID	Gene Mention	miRNA Mention	Disease Mention	Drug Mention	Score		
<input type="checkbox"/> 27665963	CFL1, LIMK1				12		
Visualize selected documents 1 25 rows per page ▾							

Hold "Shift" and click header for multi-sort.

Fig11. Hit page for query Rhodopsin with PMID

PMID: 27665963 [RLIMS-P](#) [eFIP](#) [miRTex](#) [aGARD](#)

Abstract

1. **MicroRNA-138** inhibits migration and invasion of non-small cell lung cancer cells by targeting **LIMK1**.
 ...
 3. **LIM domain kinase 1 (LIMK1)** is a **serine/threonine kinase** that regulates **actin** **polymerization** via **phosphorylation** and inactivation of **cofilin**.
 ...

Entity: 6, Relation: 4 [Show legend](#)

Legend: SUBSTRATE KINASE INTERACTANT SITE GENE MIRNA ANOMALY EXPRESSION DISEASE OUTCOME/RESPONSE SR_DRUG DRUG CELL_TRIGGER Normalized

Tool: RLIMS-P

PTM enzyme	Substrate	Site	Sentence
LIM domain kinase 1 (LIMK1)	cofilin (P23528)	Thr, Ser	3

Tool: eFIP

PTM enzyme	Substrate	Site	Interactant	Sentence
LIM domain kinase 1 (LIMK1)	cofilin (P23528)	Ser, Thr	actin	3

Tool: miRTex

miRNA	Gene	Relation Type	Direct	Sentence
MicroRNA-138	LIMK1 (P03667)	MIRNA→TARGET	yes	1

Fig12. Result of query Rhodopsin in iTextMine with PMID

Conclusion:

The PIR(Protein Information Resources) maintains several databases about proteins. Its integrated public bioinformatics resources to support genomic and proteomic research , and scientific studies.

Results:

PIR has similar database but from different resources and integrated resources . In one domain can read all resources and it can be use as a cross references . In PRO entring the PRO ID can search the paper and from iProLink in iTextMine can search the paper by entring the PubMed ID .

References:

- [https://proteininformationresource.org/cgi-bin/textsearch.pl?
submit.x=0&submit.y=0&query0=rhodopsin&field0=ALL&search=1](https://proteininformationresource.org/cgi-bin/textsearch.pl?submit.x=0&submit.y=0&query0=rhodopsin&field0=ALL&search=1)
- <https://proteininformationresource.org/cgi-bin/ ipcEntry?id=A3KFT3>
- <https://proconsortium.org/pro.shtml>
- [https://proconsortium.org/cgi-bin/textsearch_pro?
search=search&field0=ALLFLDS&query0=rhodopsin&search.x=0&search.y=0](https://proconsortium.org/cgi-bin/textsearch_pro?search=search&field0=ALLFLDS&query0=rhodopsin&search.x=0&search.y=0)
- <https://proconsortium.org/app/entry/PR:P15409/>
- <https://research.bioinformatics.udel.edu/iptmnet/>
- <https://research.bioinformatics.udel.edu/iptmnet/search/all/rhodopsin/mod-ac%2Cgn%2Cgo%2Cgc%2Cgs%2Cme%2Cmy%2Cp%2Csu%2Cub%2Csno/>
- <https://research.bioinformatics.udel.edu/iptmnet/entry/Q15835/>
- <https://research.bioinformatics.udel.edu/iprolink/>
- <https://proteininformationresource.org/itextmine/>
- [https://research.bioinformatics.udel.edu/itextmine/integrate/doc/rlims-efip-mirtex-egard/
medline/27665963](https://research.bioinformatics.udel.edu/itextmine/integrate/doc/rlims-efip-mirtex-egard/medline/27665963)