

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:

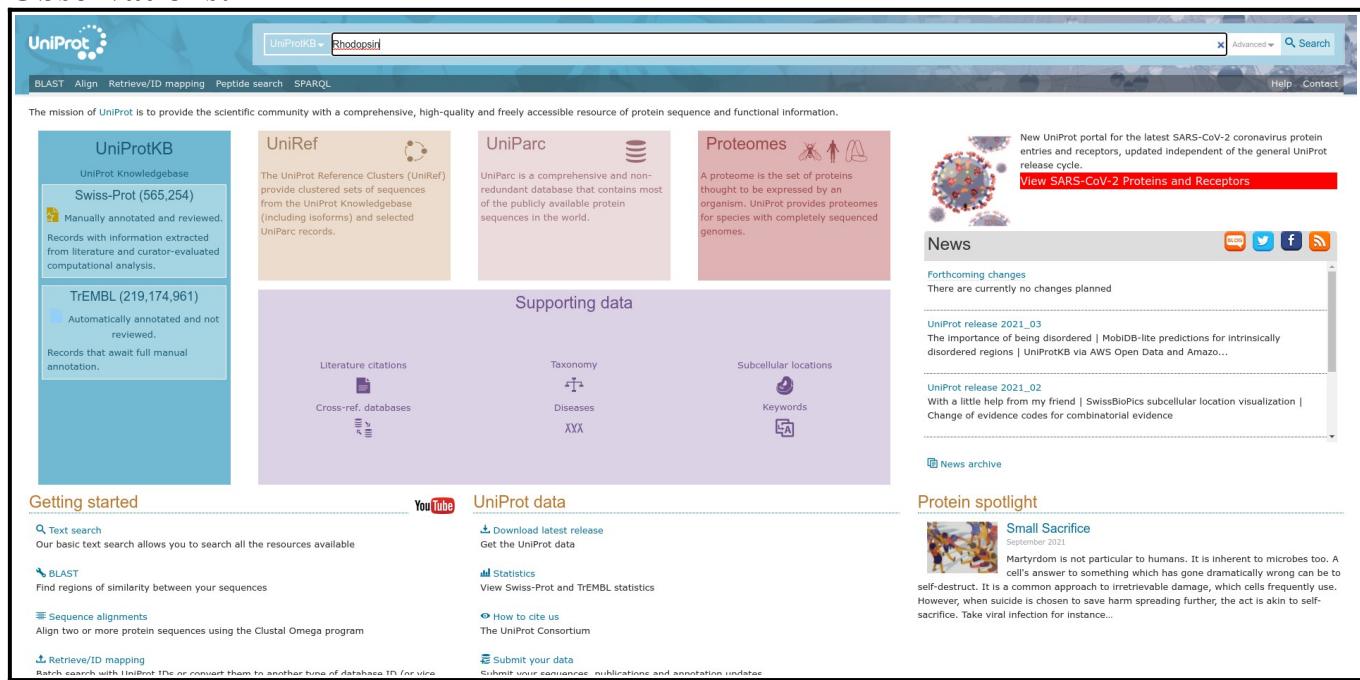
The UniProt Knowledgebase (UniProtKB) is the central hub from the collection of functional information on proteins, with accurate, consistent and rich annotation. In addition to capturing the core data mandatory for each UniProtKB entry (mainly the amino acid sequence, protein name or description, taxomic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

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 the search term 'Rhodopsin' entered in the search bar. The results are displayed in a grid format. The first result is for UniProtKB, showing 565,254 entries. Below this, there are sections for UniRef, UniParc, and Proteomes. The UniParc section describes it as a comprehensive and non-redundant database. The Proteomes section describes it as the set of proteins thought to be expressed by an organism. The Supporting data section includes links for Literature citations, Cross-ref. databases, Taxonomy, Diseases, Subcellular locations, and Keywords. On the right side, there is a news section with a COVID-19 update, a 'News' section with a 'Forthcoming changes' note, and a 'Protein spotlight' section featuring 'Small Sacrifice'.

Fig1. Homepage of Uniprot with query 'Rhodopsin'

The screenshot shows the UniProtKB 2021_03 results page for the query 'Rhodopsin'. The search bar at the top contains 'Rhodopsin'. The main content area is titled 'UniProtKB 2021_03 results'. It includes a brief description of UniProtKB and two sections: 'Reviewed (Swiss-Prot) - Manually annotated' and 'Unreviewed (TrEMBL) - Computationally analyzed'. A table below lists protein entries, including their UniProt ID, name, gene name, organism, and length. The table is filtered by 'Reviewed (511)' and shows 25 of 55,207 results.

Entry	Entry name	Protein names	Gene names	Organism	Length
P02699	OPSD_BOVIN	Rhodopsin	RHO	Bos taurus (Bovine)	348
P08100	OPSD_HUMAN	Rhodopsin	RHO OPN2	Homo sapiens (Human)	348
P28327	GRK1_BOVIN	Rhodopsin kinase GRK1	GRK1 RHOK	Bos taurus (Bovine)	561
Q15835	GRK1_HUMAN	Rhodopsin kinase GRK1	GRK1 RHOK	Homo sapiens (Human)	563
P15409	OPSD_MOUSE	Rhodopsin	Rho	Mus musculus (Mouse)	348
Q63651	GRK1_RAT	Rhodopsin kinase GRK1	Grk1 Rhok	Rattus norvegicus (Rat)	564
Q9WVL4	GRK1_MOUSE	Rhodopsin kinase GRK1	Grk1 Rhok	Mus musculus (Mouse)	564
Q8WTQ7	GRK7_HUMAN	Rhodopsin kinase GRK7	GRK7 GPRK7	Homo sapiens (Human)	553
P31356	OPSD_TODPA	Rhodopsin	RHO	Todarodes pacificus (Japanese flying squid) (Ommastrephes pacificus)	448
P22328	OPSD_CHICK	Rhodopsin	RHO	Gallus gallus (Chicken)	351
P32308	OPSD_CANLF	Rhodopsin	RHO	Canis lupus familiaris (Dog) (Canis familiaris)	348
Q49HM9	GRK7A_DANRE	Rhodopsin kinase grk7a	grk7a grk7-1, dkeyp-13a3.1	Danio rerio (Zebrafish) (Brachydanio rerio)	549

Fig2. Hit page of UniprotKB with query 'Rhodopsin'

The screenshot shows the UniProtKB header page for the protein entry P02699 (OPSD_BOVIN). The top navigation bar includes 'BLAST', 'Align', 'Retrieve/ID mapping', 'Peptide search', and 'SPARQL'. The main title is 'UniProtKB - P02699 (OPSD_BOVIN)'. The page displays detailed information about the protein, including its function (Rhodopsin), gene (RHO), organism (Bos taurus (Bovine)), and status (Reviewed). It also shows its role in the visual cycle and its interaction with 11-cis retinal. The 'Sites' section lists metal binding sites (Zinc) at positions 113, 201, and 279. The 'GO - Molecular function' section lists various biological processes, including G-protein coupled receptor activity and opsins. A 'Feedback' link is visible in the top right corner.

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

Display Help video

Function¹

Entry

Publications

Feature viewer

Feature table

By similarity 5 Publications 11 Publications

Sites

None

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 thermoception 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 Structure

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



Error Couldn't load PDB entry

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](#) **Sequence**

Sequence status¹: Complete.

Entry [P02699-1 \[UniPerc\]](#) [FASTA](#) [Add to basket](#)

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

Sequence status¹: Complete.

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

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

BLAST [GO](#)

10 20 30 40 50
MNGTEGPINIFY VPFSNKTGVV RSPFEAPQQY LAEPWQFSML AAYMFLILML
60 70 80 90 100
GFPINFLTLV VTQVHKKLRT PLNYILLNL AADLFMVF66 FTTTLYTS LH
110 120 130 140 150
GYFVFGPTGC NLEGFFATLG GEIALWSLV LAIERYVVC KPMNSRFG6E
160 170 180 190 200
NHAIMGVAFT WWMALACAAP PLVGWSRYIP EGMQCSCGID YYTPHEETNN
210 220 230 240 250
ESFVIMYMPVV HFIIPLIVTE FCYGQLVFTY KEAAAOQES ATTQAKAEV
260 270 280 290 300
TRWVIMVIA FLICLWLPYVA VAFYIFTHQD SDGPZIFMTI PAFFAKTSVA
310 320 330 340
YNPVIIYIMMN K0FRNCMVTT LCCGKNPGLGD DEASTTVSKT ET5QVAPA

Experimental Info

Feature key	Position(s)	Description	Actions	Graphical view	Length
Sequence conflict ¹	281	S → F in AA30675 (PubMed:2950966). Curated			1

Sequence databases

Select the link: [K00506](#) [K00505](#) Genomic DNA Translation: [AA30674.1](#)
destinations: [M21606](#) mRNA Translation: [AA30675.1](#)

EMBL GenBank DDBJ PIR [A90840](#), OBOO
[RefSeq](#) [NP_001014890.1](#), [NM_001014890.2](#)

Genome annotation databases

Ensembl: [ENSBTAT00000001730](#); [ENSBTAP00000001730](#); [ENSBTAG00000001310](#)
GeneID: [509933](#)

Fig6. Sequences of result for query ‘Rhodopsin’

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

Entry [P02699-1 \[UniPerc\]](#) [FASTA](#) [Add to basket](#)

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

Names & Taxonomy

Protein names: Recommended name: **Rhodopsin**
Gene names: Name: RHO
Organism: [Bos taurus \(Bovine\)](#)
Taxonomic identifier: [9913 \[NCBI\]](#)

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

Proteomes: [UP000009136](#) Component¹: Chromosome 22

Organism-specific databases: VGNC: [VGNC:33942](#), RHO

Subcellular location

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) photoreceptor cilia. [By similarity](#)

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

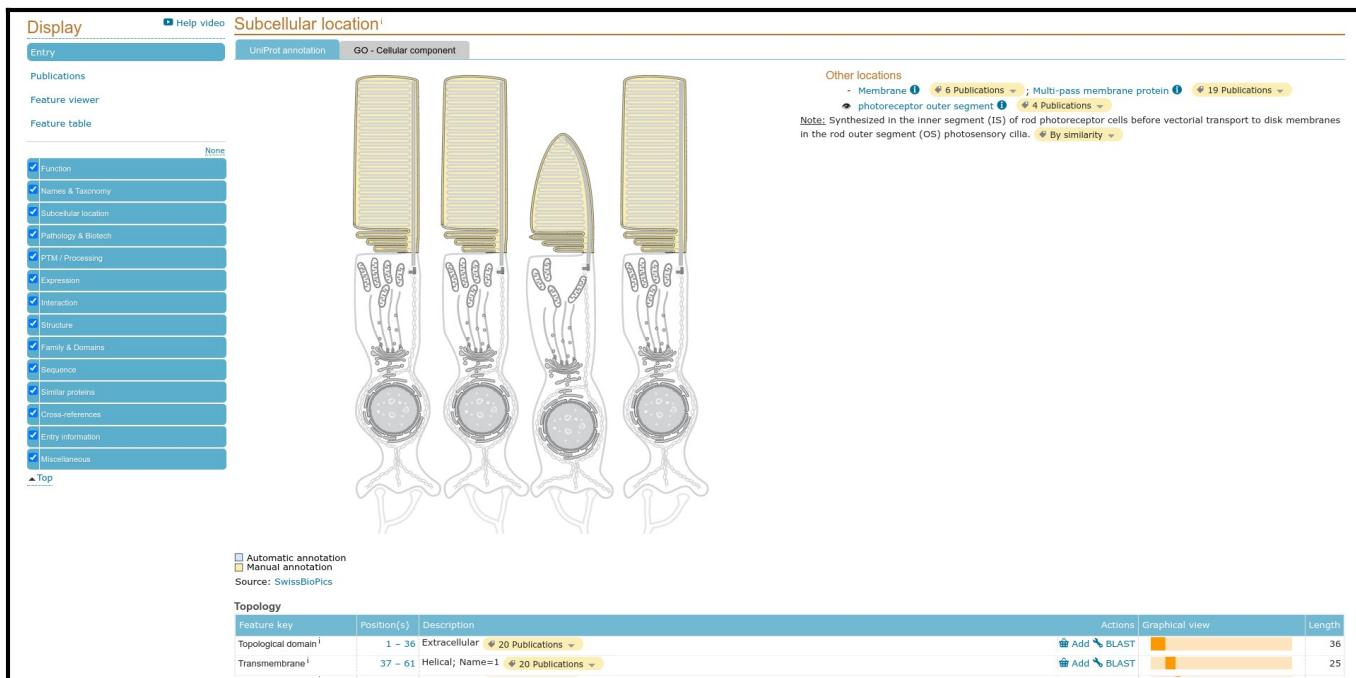


Fig8. Subcellular location of result for query 'Rhodopsin'

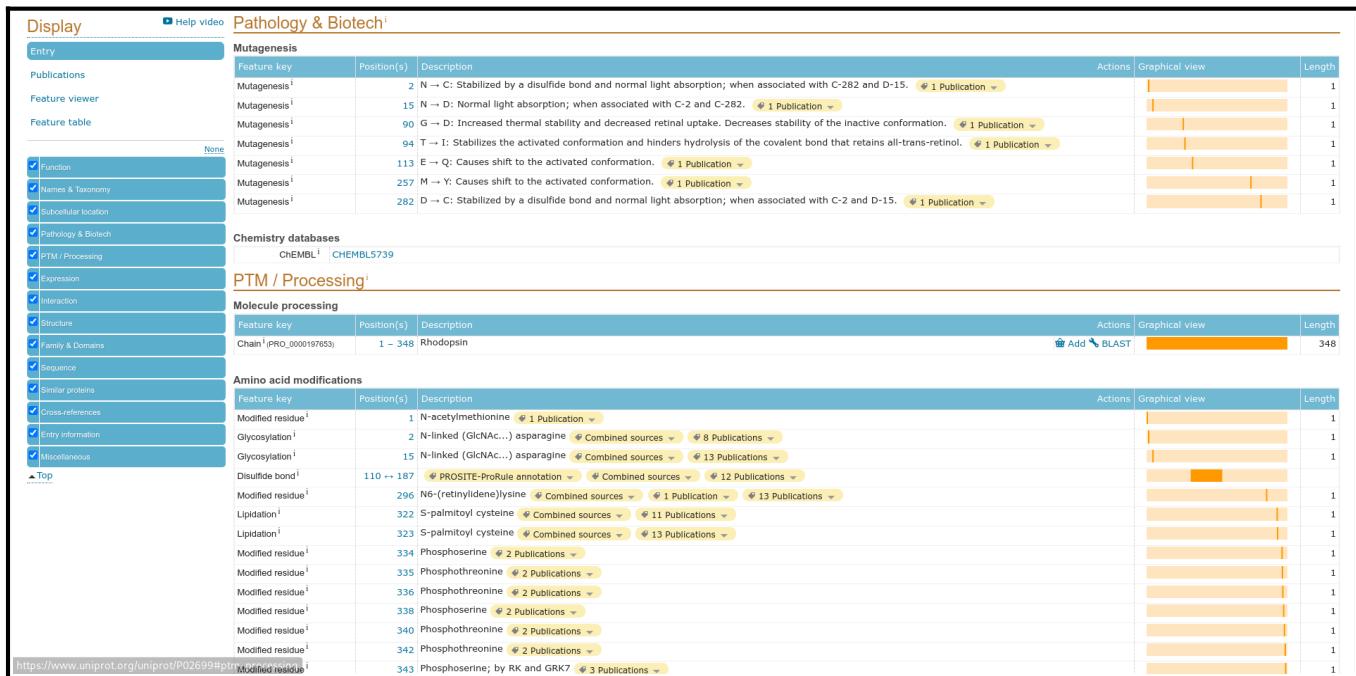


Fig9. Pathology and Biotech of result for query 'Rhodopsin'

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

Entry

Publications

Feature viewer

Feature table

None

Function

Names & Taxonomy

Subcellular location

Pathology & Biotech

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Interaction

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Family & Domains

Sequence

Similar proteins

Cross-references

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Molecule processing

Feature key	Position(s)	Description	Actions	Graphical view	Length
Chain ⁱ [Pfam0000197653]	1 – 348	Rhodopsin	Add BLAST		348

Amino acid modifications

Feature key	Position(s)	Description	Actions	Graphical view	Length
Modified residue ⁱ	1	N-acetylmethionine 1 Publication			1
Glycosylation ⁱ	2	N-linked (GlcNAc...) asparagine Combined sources 8 Publications			1
Glycosylation ⁱ	15	N-linked (GlcNAc...) asparagine Combined sources 13 Publications			1
Disulfide bond ⁱ	110 ↔ 187	PROSITE-ProRule annotation Combined sources 12 Publications			1
Modified residue ⁱ	296	66-(retinylidene)lysine Combined sources 1 Publication 13 Publications			1
Lipidation ⁱ	322	S-palmitoyl cysteine Combined sources 11 Publications			1
Lipidation ⁱ	323	S-palmitoyl cysteine Combined sources 13 Publications			1
Modified residue ⁱ	334	Phosphoserine 2 Publications			1
Modified residue ⁱ	335	Phosphothreonine 2 Publications			1
Modified residue ⁱ	336	Phosphothreonine 2 Publications			1
Modified residue ⁱ	338	Phosphoserine 2 Publications			1
Modified residue ⁱ	340	Phosphothreonine 2 Publications			1
Modified residue ⁱ	342	Phosphothreonine 2 Publications			1
Modified residue ⁱ	343	Phosphoserine; by RK and GRK7 3 Publications			1

Post-translational modification

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

Proteomic databases

PaxDb ⁱ	P02699
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PTM databases

GlyConnect ⁱ	523, 4 N-Linked glycans
IPTMnet ⁱ	P02699
SwissPalm ⁱ	P02699

Fig10. PTM/Processing of result for query 'Rhodopsin'

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

Entry

Publications

Feature viewer

Feature table

None

Function

Names & Taxonomy

Subcellular location

Pathology & Biotech

PTM / Processing

Expression

Interaction

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Family & Domains

Sequence

Similar proteins

Cross-references

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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

Bgee ⁱ	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 RCVRN in a Ca²⁺-dependent manner; RCVRN 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:21369983, PubMed:23579341, PubMed:26526852).
Interacts with GNAT3 (PubMed:22199838, PubMed:27458239). SAG and G-proteins compete for a common binding site (By similarity).
Interacts with PRCD; the interaction promotes PRCD stability (PubMed:27509380).
[By similarity](#) [18 Publications](#)

Binary interactionsⁱ

Subcellular location

Reset filters

P02699 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
MNGTEGPNFYVPFSNKTGVRSPFEAPQYYLAEPWQFSMLAAYMFLIMLGFPINFLTLY
VTQHKKLRTPLNYILLNLAVADLFMVFGGFTTLYTSLHGYFVFGPTGCNLEGFFATLG
GEIALWSLVVLAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMAACAPPLVGWSRYIP
EGMQCSCGIDYYTPHEETNNESFVIYMFVVFHIFIPLIVIFFCYGQLVFTVKEAAAQQQES
ATTQKAEKEVTRMVIIMVIAFLICWLWYAGVAFYIFTHQGSDFGPIFMTIPIAFFAKTSAV
YNPVIYIMMNKQFRNCMVTLCCGKNPLGDEASTTVSKTETSQVAPA
```

Fig12. Fasta Canonical for result for query ‘Rhodopsin’

Results:

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

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.

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:

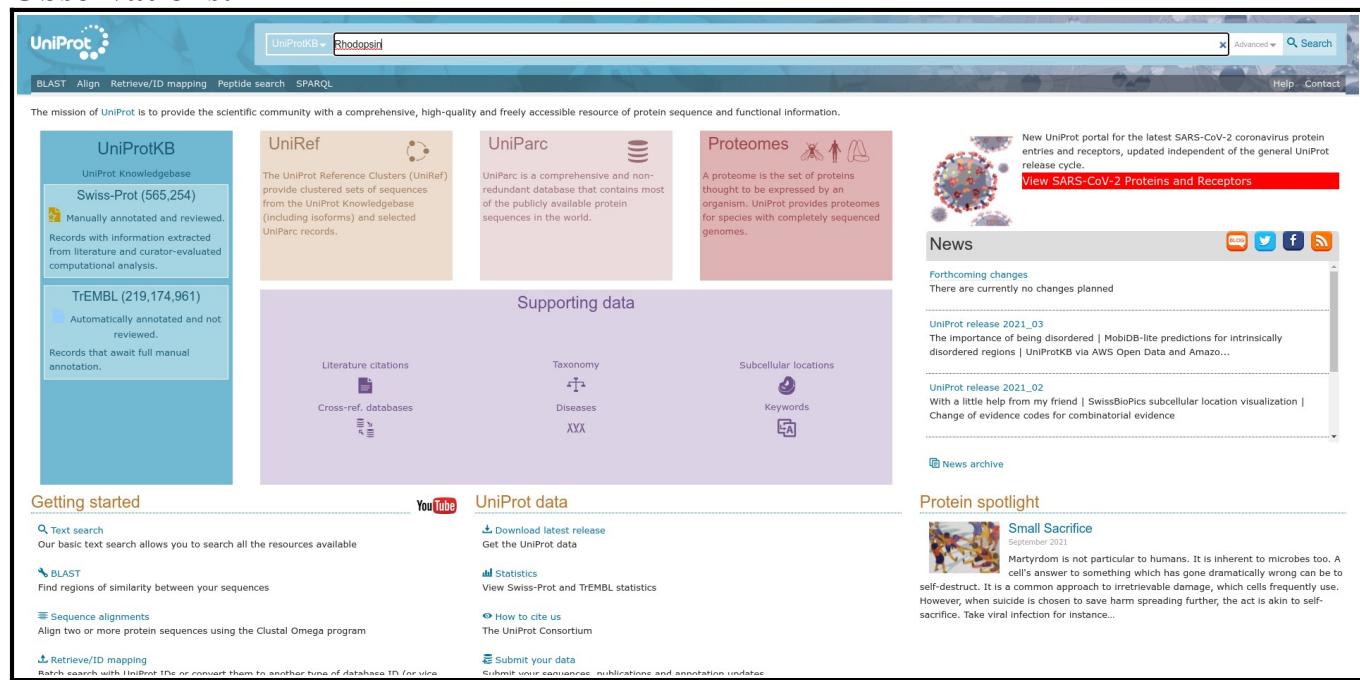
SWISS-PROT is a curated protein sequence database which strives to provide a high level of annotation (such as the description of the function of a protein, its domains structure, post-translational modifications, variants, etc.), a minimal level of redundancy and high level of integration with other 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 the search term 'Rhodopsin' entered in the search bar. The page features a navigation bar with links for BLAST, Align, Retrieve/ID mapping, Peptide search, SPARQL, Advanced, and Search. Below the navigation is a mission statement: 'The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.' The main content area is divided into several sections: 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 (SARS-CoV-2 Proteins and Receptors, Forthcoming changes, UniProt release 2021_03, UniProt release 2021_02), and Protein spotlight (Small Sacrifice, Martyrdom). The footer includes links for Text search, BLAST, Sequence alignments, Retrieve/ID mapping, and a news archive.

Fig1. Homepage of Uniprot with query 'Rhodopsin'

Fig2. Hit page of UniprotKB with query 'Rhodopsin'

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

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

Entry

Publications

Feature viewer

Feature table

None

Function

Names & Taxonomy

Subcellular location

Pathology & Biotech

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Expression

Interaction

Structure

Family & Domains

Sequence

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Cross-references

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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
Site ¹	113	Plays an important role in the conformation switch to the active conformation	3 Publications <input type="checkbox"/> 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 function

- 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 process

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- 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](#) **Structure**

Entry

Publications

Feature viewer

Feature table

None

Function

Names & Taxonomy

Subcellular location

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Error Couldn't load PDB entry

Source	Identifier	Method	Resolution	Chain	Positions	Links
PDB	1BOJ	Model		A	1-348	PDB RCSB-PDB PDB PDBsum
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PDB	1EDV	NMR		A	172-205	PDB RCSB-PDB PDB PDBsum
PDB	1EDW	NMR		A	268-293	PDB RCSB-PDB PDB PDBsum
PDB	1EDX	NMR		A	1-40	PDB RCSB-PDB PDB PDBsum
PDB	1F88	X-ray	2.80 Å	A/B	1-348	PDB RCSB-PDB PDB PDBsum

Secondary structure

Fig5. Structure of result of query 'Rhodopsin'

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

Sequence status¹: Complete.

Entry [P02699-1 \[UniPerc\]](#) [FASTA](#) [Add to basket](#)

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

Sequence status¹: Complete.

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

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

BLAST [GO](#)

10 20 30 40 50
MNGTEGPINIFY VPFSNKTGVV RSPFEAPQQY LAEPWQFSML AAYMFLILML
60 70 80 90 100
GFPINFLTLV VTVQHKKLRT PLNYILLNL AVALFLMVF66 FTTTLYTS LH
110 120 130 140 150
GYFVFGPTGC NLEGFFATLG GEIALWSLV LAIERYVVC KPMNSRFRGE
160 170 180 190 200
NHAIMGVAFT WWMALACAAP PLVGWSRYIP EGMRQCSGID YTPHEETNN
210 220 230 240 250
ESFVIMPFVV HFIIPLIVTE FCYGQLVFTY KEAAAOQES ATTQAKAEV
260 270 280 290 300
TRWIIIMVIA FLICLWLPYVA VAFYIFTHQD SDGPZIFMTI PAFFAKTSVA
310 320 330 340
YNPVIIYIMMN K0FRNCMVTT LCCGKNPGLGD DEASTTVSKT ET5QVAPA

Experimental Info

Feature key	Position(s)	Description	Actions	Graphical view	Length
Sequence conflict ¹	281	S → F in AA30675 (PubMed:2950966). Curated			1

Sequence databases

Select the link: [K00506](#) [K00505](#) Genomic DNA Translation: [AA30674.1](#)
destinations: [M21606](#) mRNA Translation: [AA30675.1](#)

EMBL GenBank DDBJ PIR [A90840](#), OBOO
RefSeq [NP_001014890.1](#), [NM_001014890.2](#)

Genome annotation databases

Ensembl: [ENSBTAT00000001730](#); [ENSBTAP00000001730](#); [ENSBTAG00000001310](#)
GeneID: [509933](#)

Fig6. Sequences of result for query ‘Rhodopsin’

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

Entry [P02699-1 \[UniPerc\]](#) [FASTA](#) [Add to basket](#)

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

Names & Taxonomy

Protein names: Recommended name: **Rhodopsin**
Gene names: Name: RHO
Organism: [Bos taurus \(Bovine\)](#)
Taxonomic identifier: [9913 \[NCBI\]](#)

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

Proteomes: [UP000009136](#) Component¹: Chromosome 22

Organism-specific databases: VGNC: [VGNC:33942](#), RHO

Subcellular location

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) photoreceptor cilia. [By similarity](#)

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

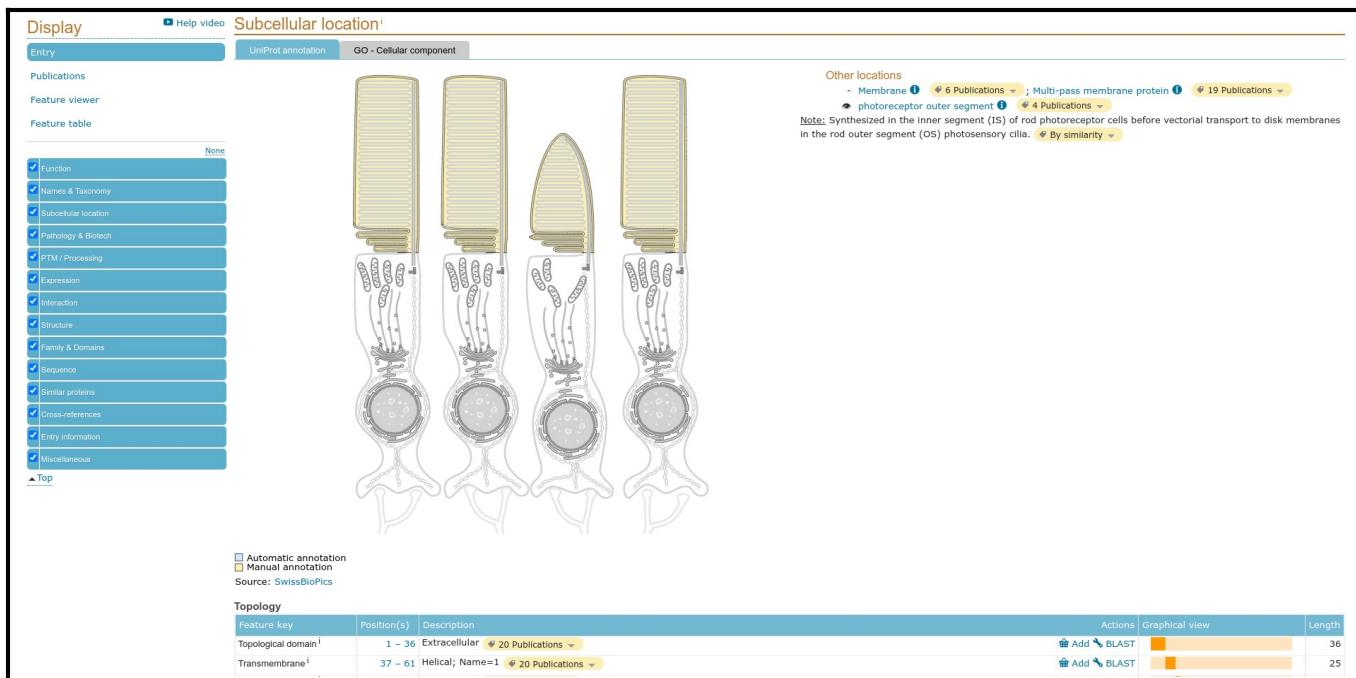


Fig8. Subcellular location of result for query 'Rhodopsin'

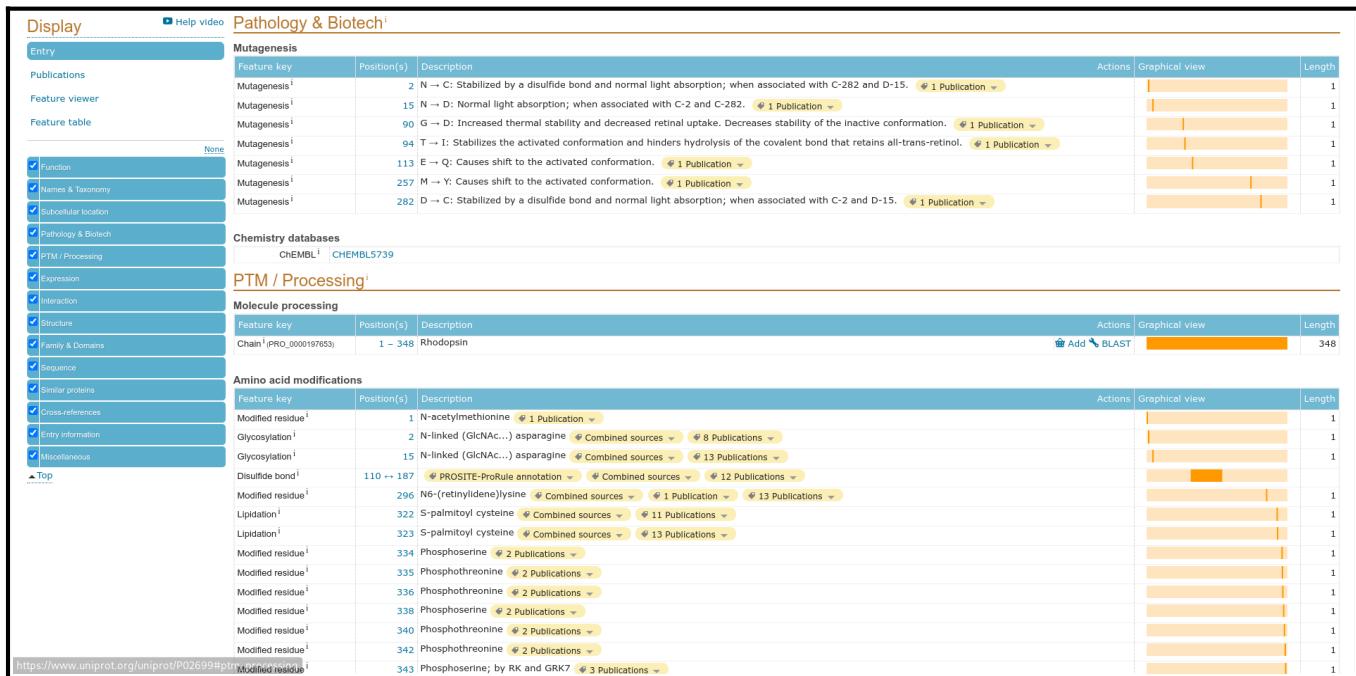


Fig9. Pathology and Biotech of result for query 'Rhodopsin'

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

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](#)

Molecule processing

Feature key	Position(s)	Description	Actions	Graphical view	Length
Chain ⁱ [Pfam0000197653]	1 – 348	Rhodopsin	Add BLAST		348

Amino acid modifications

Feature key	Position(s)	Description	Actions	Graphical view	Length
Modified residue ⁱ	1	N-acetylmethionine 1 Publication			1
Glycosylation ⁱ	2	N-linked (GlcNAc...) asparagine Combined sources 8 Publications			1
Glycosylation ⁱ	15	N-linked (GlcNAc...) asparagine Combined sources 13 Publications			1
Disulfide bond ⁱ	110 ↔ 187	PROSITE-ProRule annotation Combined sources 12 Publications			1
Modified residue ⁱ	296	66-(retinylidene)lysine Combined sources 1 Publication 13 Publications			1
Lipidation ⁱ	322	S-palmitoyl cysteine Combined sources 11 Publications			1
Lipidation ⁱ	323	S-palmitoyl cysteine Combined sources 13 Publications			1
Modified residue ⁱ	334	Phosphoserine 2 Publications			1
Modified residue ⁱ	335	Phosphothreonine 2 Publications			1
Modified residue ⁱ	336	Phosphothreonine 2 Publications			1
Modified residue ⁱ	338	Phosphoserine 2 Publications			1
Modified residue ⁱ	340	Phosphothreonine 2 Publications			1
Modified residue ⁱ	342	Phosphothreonine 2 Publications			1
Modified residue ⁱ	343	Phosphoserine; by RK and GRK7 3 Publications			1

Post-translational modification

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

Proteomic databases

PaxDb ⁱ	P02699
--------------------	--------

PTM databases

GlyConnect ⁱ	523, 4 N-Linked glycans
IPTMnet ⁱ	P02699
SwissPalm ⁱ	P02699

Fig10. PTM/Processing of result for query 'Rhodopsin'

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

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](#)

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

Bgee ⁱ	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 RCVRN in a Ca²⁺-dependent manner; RCVRN 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:21369983, PubMed:23579341, PubMed:26526852).
Interacts with GNAT3 (PubMed:22199838, PubMed:27458239). SAG and G-proteins compete for a common binding site (By similarity).
Interacts with PRCD; the interaction promotes PRCD stability (PubMed:27509380).
[By similarity](#) [18 Publications](#)

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
MNGTEGPNFYVPFSNKTGVVRSPFEAPQYYLAEPWQFSMLAAYMFLLIMLGFPINFLTLY
VTVQHKKLRTPLNYILLNLAVADLFMVFGGFTTLYTSLHGYFVFGPTGCNLEGFFATLG
GEIALWSLVVLAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIP
EGMQCSCGIDYYTPHEETNNESFVIYMFVVFHIFIPLIVIFFCYGQLVFTVKEAAAQQQES
ATTQKAKEVTRMVIIMVIAFLICWLWYAGVAFYIFTHQGSDFGPIFMTIPIAFFAKTSAV
YNPVIYIMMNKQFRNCMVTLCCGKNPLGDEASTTVSKTETSQVAPA
```

Fig12. Fasta Canonical for result for query ‘Rhodopsin’

Results:

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

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.

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>

Date: 29-09-21

WEBLEM 4c

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

Aim:

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

Introduction:

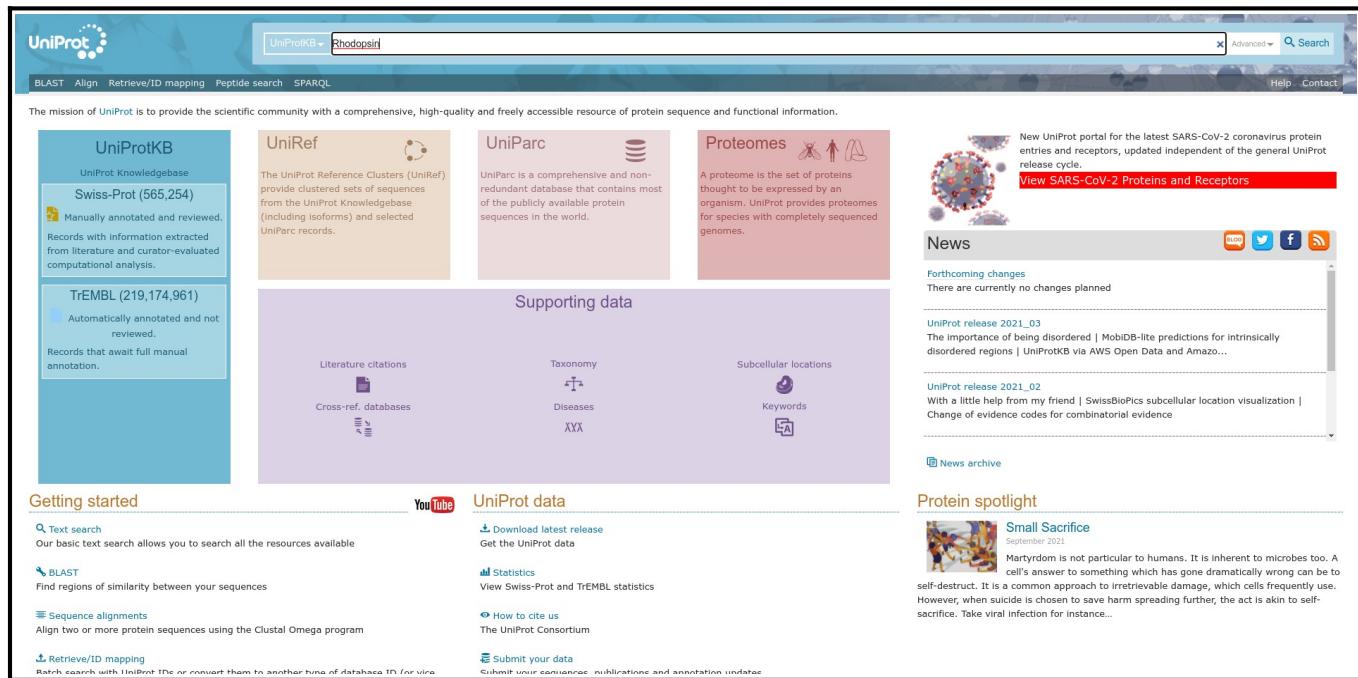
UniProtKB/TrEMBL is a computer-annotated protein sequence database complementing UniProtKB/TrEMBL contains the translations of all coding sequences (CDS) present in the EMBL/GenBank/DDBJ Nucleotide Sequence Databases and also protein sequences extracted. The database is enriched with automated classification 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 main content area displays various protein databases and supporting data. On the right side, there are news items and a protein spotlight. The 'UniProt data' section includes links for download, statistics, and submission.

UniProtKB

UniProt Knowledgebase

Swiss-Prot (565,254)

Manually annotated and reviewed. Records with information extracted from literature and curator-evaluated computational analysis.

TrEMBL (219,174,961)

Automatically annotated and not reviewed. Records 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.

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

News archive

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 for Uniprot with query Rhodopsin

UniProtKB - rhodopsin AND reviewed.no

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.

Filter by: Unreviewed (54,696) TrEMBL

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)

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	<i>Gallus gallus</i> (Chicken)	351
<input type="checkbox"/> Q9VTU7	Q9VTU7_DROME	Rhodopsin	Rh7	<i>Drosophila melanogaster</i> (Fruit fly)	483
<input type="checkbox"/> U3KGW6	U3KGW6_FICAL	Rhodopsin	RHO	<i>Ficedula albicollis</i> (Collared flycatcher) (<i>Muscicapa albicollis</i>)	351
<input type="checkbox"/> Q9IA36	Q9IA36_TAEGU	Rhodopsin	RHO	<i>Taenioptygia guttata</i> (Zebra finch) (<i>Poephila guttata</i>)	351
<input type="checkbox"/> G1ND14	G1ND14_MELGA	Rhodopsin	RHO	<i>Meleagris gallopavo</i> (Wild turkey)	351
<input type="checkbox"/> U3IB29	U3IB29_ANAPP	Rhodopsin	RHO	<i>Anas platyrhynchos</i> (Northern mallard)	351
<input type="checkbox"/> A0A093Q1T7	A0A093Q1T7_9PASS	Rhodopsin	N305_14752	<i>Manacus vitellinus</i> (golden-collared manakin)	351
<input type="checkbox"/> Q9VDS3	Q9VDS3_DROME	Exit protein of rhodopsin and TRP A	Xport-A	<i>Drosophila melanogaster</i> (Fruit fly)	116
<input type="checkbox"/> A4ZIS8	A4ZIS8_ORNAN	Rhodopsin	RHO	<i>Ornithorhynchus anatinus</i> (Duckbill platypus)	353
<input type="checkbox"/> Q9PTX9	Q9PTX9_DANRE	Rhodopsin	exorh exo-rod	<i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)	354
<input type="checkbox"/> H2QNC5	H2QNC5_PANTR	Rhodopsin	RHO	<i>Pan troglodytes</i> (Chimpanzee)	348
<input type="checkbox"/> G3R589	G3R589_GORGO	Rhodopsin	RHO	<i>Gorilla gorilla gorilla</i> (Western lowland gorilla)	348

Fig2. Hit page for Unreviewed for query Rhodopsin

UniProtKB - F1P3Y2 (F1P3Y2_CHICK)

Display Help video BLAST Align Format Add to basket History Add a publication Feedback

Entry

Protein Rhodopsin
Gene RHO
Organism *Gallus gallus* (Chicken)
Status Unreviewed - Annotation score: - Protein inferred from homology¹

Function¹

GO - Molecular 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 - Biological process¹

- 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 ...

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

Fig3. Header page for query Rhodopsin

Display  Function¹

Entry

Publications

Feature viewer

Feature table

None

GO - Molecular 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 - Biological process¹

- cellular response to light stimulus  Source: GO_Central
- detection of temperature stimulus involved in thermotropism  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 ...

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

Recommended name: **Rhodopsin**  UniRule annotation

Gene names

Name: **RHO**  Imported

Organism

Gallus 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
GEIALWSLVLAVERYVVVCKPMSNFRFGENHAIMGVAFSWIMAMACAAPPLFGWSRYIP
EGMQCSCGIDYYTLKPEINNESFVIYMFVVHFMIPALAVIFFCYGNLVCTVKEAAAQQQES
ATTQKAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTNQGSDFGPIFMТИPAFFAKSSAI
YNPVIYIVMNKQFRNCMITTLCGKNPLGDEDTSAGKTETSSVSTSQVSPA
```

Fig5. FASTA Canonical for result page of query Rhodopsin

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

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 names: Recommended name: **Rhodopsin** [UniRule annotation](#)

Gene names: Name: **RHO** [Imported](#)

Organism: **Gallus gallus (Chicken)** [Imported](#)

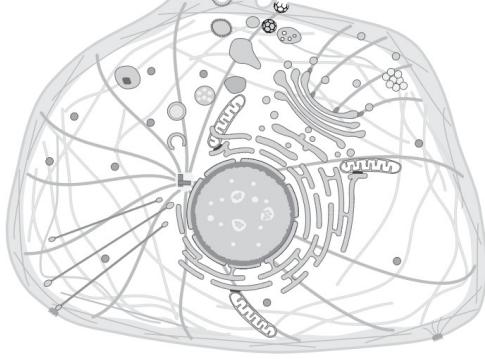
Taxonomic identifier: **9031 [NCBI]**

Taxonomic lineage: Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Archelosauria > Archosauria > Dinosauria > Saurischia > Theropoda > Coelurosauria > Aves > Neognathae > Galloanserae > Galliformes > Phasianidae > Phasianinae > Gallus

Proteomes: UP000000539 Component¹: Chromosome 12

Subcellular location

[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

Fig6. Names and Taxonomy of result page for query Rhodopsin

Display [Help video](#) **Subcellular location**

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](#)

Automatic annotation

Manual annotation

Source: [SwissBioPics](#)

Topology

Feature key	Position(s)	Description	Actions	Graphical view	Length
Transmembrane ⁱ	40 – 63	Helical UniRule annotation	Add BLAST		24
Transmembrane ⁱ	75 – 96	Helical UniRule annotation	Add BLAST		22
Transmembrane ⁱ	102 – 133	Helical UniRule annotation	Add BLAST		32
Transmembrane ⁱ	153 – 173	Helical UniRule annotation	Add BLAST		21
Transmembrane ⁱ	203 – 223	Helical UniRule annotation	Add BLAST		21
Transmembrane ⁱ	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 **PTM / Processing**

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

Keywords - PTM: 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 function:

- 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 (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 similarities

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

Keywords - Domain: 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 **Expression**

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

Keywords - Domain: Transmembrane, Transmembrane helix (UniRule annotation, ARBA annotation)

Expression

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

Interaction

GO - Molecular function:

- 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 (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 similarities

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

Keywords - Domain: Transmembrane, Transmembrane helix (UniRule annotation, ARBA annotation)

Phylogenomic databases

GeneTree	ENSGT01030000234549
HOGENOM	CLU_009579_3_0_1
InParanoid	F1P3Y2
OMA	ENRKYI

Fig9. Expression for result of query Rhodopsin

Display [Help video](#)

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	ENSGT01030000234549
HOGENOM	CLU_009579_3_0_1
InParanoid	F1P3Y2
OMA	EQQQYLY
TreeFam	TF324998

Family and domain databases

InterPro [View protein in InterPro](#)

Fig10. Interaction for result of query Rhodopsin

Display [Help video](#)

Similar proteins¹

100% Identity 90% Identity 50% Identity

Protein	Similar proteins	Species	Score	Length	Source
F1P3Y2	Rhodopsin			351	UniRef100_F1P3Y2

[Full view](#)

Cross-references¹

Sequence databases

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

EMBL GenBank DDBJ

3D structure databases

ModBase [Search...](#) SWISS-MODEL-Workspace [Submit a new modelling project...](#)

Protein family/group databases

GPCRDB [Search...](#)

Genome annotation databases

Ensembl [ENSGALT00000033236](#); [ENSGALP00000032596](#); [ENSGALG00000020745](#)

Phylogenomic databases

GeneTree	ENSGT01030000234549
HOGENOM	CLU_009579_3_0_1
InParanoid	F1P3Y2
OMA	EQQQYLY
TreeFam	TF324998

Enzyme and pathway databases

Reactome [R-GGA-2453002](#), 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](#), Vpx cargo-targeting to cilium

Fig11. Similar proteins for result of query Rhodopsin

Results:

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

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.

References:

1. <https://www.uniprot.org/>
2. <https://www.uniprot.org/uniprot/?query=rhodopsin&fil=reviewed%3A1&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

Text Search Result						
Display Options		Help				
42785 proteins 856 pages 50 / page K << 1 2 3 4 5 >>>		Save Result As: <input type="checkbox"/> TABLE <input type="checkbox"/> FASTA				
<input type="checkbox"/> analyze <input type="checkbox"/> GO Slim / Pathway						
Protein AC/ID	Protein Name	Length	Organism Name	PRO ID	PIRSF ID	UniRef50
<input type="checkbox"/> A3KFT3/QR2MS_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 2M5	312	Homo sapiens (Human)	PR:000011781; PR:A3KFT3	PIRSF003152; PIRSF800006	UniRef50_Q8NH8C
<input type="checkbox"/> A4D2G3/02A2S_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 2A2S	310	Homo sapiens (Human)	PR:000011746; PR:A4D2G3	PIRSF003152; PIRSF800006	UniRef50_A4D2G3
<input type="checkbox"/> A6NCV1/06C7A_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 6C7A	312	Homo sapiens (Human)	PR:000011968; PR:A6NCV1	PIRSF003152; PIRSF800006	UniRef50_A6NCV1
<input type="checkbox"/> A6ND48/01A11_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 1A11	311	Homo sapiens (Human)	PR:000011712; PR:A6ND48	PIRSF003152; PIRSF800006	UniRef50_A6ND48
<input type="checkbox"/> A6NDH6/05H15_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 5H15	313	Homo sapiens (Human)	PR:000011931; PR:A6NDH6	PIRSF003152; PIRSF800006	UniRef50_A6NDH6
<input type="checkbox"/> A6NDL8/06C68_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 6C68	312	Homo sapiens (Human)	PR:000011966; PR:A6NDL8	PIRSF003152; PIRSF800006	UniRef50_A6NDL8
<input type="checkbox"/> A6NET4/0R5K3_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 5K3	321	Homo sapiens (Human)	PR:000011938; PR:A6NET4	PIRSF003152; PIRSF800006	UniRef50_Q8VGQZ
<input type="checkbox"/> A6NFB9/0R6C6_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 6C6	314	Homo sapiens (Human)	PR:000011964; PR:A6NFB9	PIRSF003152; PIRSF800006	UniRef50_A6NFB9
<input type="checkbox"/> A6NGY5/051F1_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 5F1	319	Homo sapiens (Human)	PR:000011867; PR:A6NGY5	PIRSF038651; PIRSF800006	UniRef50_A6NGY5
<input type="checkbox"/> A6NH00/0R2T8_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 2T8	312	Homo sapiens (Human)	PR:000011798; PR:A6NH00	PIRSF003152; PIRSF800006	UniRef50_A6NH00
<input type="checkbox"/> A6NH9A9/0C4C46_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 4C46	309	Homo sapiens (Human)	PR:000011820; PR:A6NH9A	PIRSF003152; PIRSF800006	UniRef50_Q8NGL6
<input type="checkbox"/> A6NHG9/0S1H4_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 5H14	310	Homo sapiens (Human)	PR:000011930; PR:A6NHG9	PIRSF003152; PIRSF800006	UniRef50_A6NHG9
<input type="checkbox"/> A6N1J9/06C70_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 6C70	312	Homo sapiens (Human)	PR:000011967; PR:A6N1J9	PIRSF003152; PIRSF800006	UniRef50_Q96RD1
<input type="checkbox"/> A6N2Z3/06C65_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 6C65	312	Homo sapiens (Human)	PR:000011965; PR:A6N2Z3	PIRSF003152; PIRSF800006	UniRef50_Q96RD1
<input type="checkbox"/> A6NKK0/0R5H1_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 5H1	313	Homo sapiens (Human)	PR:000011929; PR:A6NKK0	PIRSF003152; PIRSF800006	UniRef50_A6NKK0
<input type="checkbox"/> A6NL08/06C75_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 6C75	312	Homo sapiens (Human)	PR:000011969; PR:A6NL08	PIRSF003152; PIRSF800006	UniRef50_A6NL08
<input type="checkbox"/> A6NI76/0R5R1_HUMAN UniProtKB/Swiss-Prot	olfactory receptor 5R1	306	Homo sapiens (Human)	PR:000011921; PR:A6NI76	PIRSF003152; PIRSF800006	UniRef50_A6NI76

Fig2. Hit page for PIR for query Rhodopsin

ProClass Summary Report for UniProtKB Entry: A3KFT3				ID Mapping	
GENERAL INFORMATION					
Protein Name and ID	UniProtKB ID: QR2MS_HUMAN	UniProtKB Accession: A3KFT3	Protein Name: Olfactory receptor 2M5		
	RefSeq: NP_001004690.1 GenPept: EAW72716.1 CCDS: CCDS31105.1				
Taxonomy	Source Organism: Homo sapiens (Human) Taxon Group: Eukaryota NCBI Taxon: 9606 Lineage: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Earchontoglires; Primates; Haplorhini; Catarrhini; Hominidae; Homo.				
Gene Name	OR2MS; 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	View Bibliography Information Annotated references: PMID: 16710414 ; 21248752 [UniProt] Other references: PMID: 14983052 ; 21873635				
DNA Sequence	EMBL: AL592313 DDBJ: M36213 GenBank: AL592313				
Genome/Gene	Gene Name: OR2MS; olfactory receptor family 2 subfamily M member 5 Synonyms: OR2M5P; Map Location: 1q44 Entrez Gene: 12709 UniGene: Hs.55358 RefSeq: NM_001004690.1 NP_001004690.1 [Map Viewer] Ensembl: ENSG0000010366476 ; ENSP00000355432; ENSG00000162727 UCSC: uc010m000.2 human KEGG: hsa127059				
Gene Expression	CleanPx SOURCE Bge: ENSG00000162727				
Genetic Variation/Disease	HapMap: OR2MS				
	Protein Ontology: PRO: PR_2000011781				

Fig3. Result page for query Rhodopsin

PRO
Protein Ontology

[Home](#) | [Linked Open Data](#) | [Browse](#) | [Search](#) | [Statistics](#) | [Download](#)

PR:000025934_smad

RACE-PRO
PRO tracker
Community

PRO Consortium
Publications
Documentation

NIH grant:
5R01GM06546-09

Special feature: Protein Ontology terms for SARS-CoV-2 proteins (View/Download)

NEWS
• PRO recognized for work on SARS-CoV-2 proteoforms
• Linked Open Data pages and accompanying services launched

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 (e.g. the entity representing all protein products of the human SMAD2 gene is described in PR:Q15796; one particular human SMAD2 protein form, phosphorylated on the last two serines of a conserved C-terminal SxxS motif is defined by PR:300025934). Current release: 24.0, September 3, 2021.

Browse PRO

... Quick Browse Example: methylated (sample output)

Retrieve a PRO entry (enter a PRO ID): Example: PR:000025934 (sample output)

Search PRO (enter text or ID): Example: smad (sample output)

Annotation:RACE-PRO PRO tracker

PRO SPARQL

PRO encompasses three sub-ontologies: proteins based on evolutionary relatedness (ProEvo); protein forms produced from a given gene locus (ProForm); and protein-containing complexes (ProComp).

(Explanation of the figure)

PRO

The diagram illustrates the three sub-ontologies of PRO:

- ProEvo:** Root Level - protein. This is further divided into:
 - Family-Level Distinction:** In common, specific isoform. Example: translation product of an evolutionarily-related gene.
 - Gene-Level Distinction:** In common, specific gene. Example: translation product of a specific gene.
 - Sequence-Level Distinction:** In common, specific allele or splice variant. Example: translation product of a specific mRNA.
 - Modification-Level Distinction:** In common, specific translation product. Example: cleaved/modified translation product.
- ProForm:** Root Level - protein. This is further divided into:
 - Modification Level:** Sequence Level, Gene Level, Family Level, Root Level.
 - ProEvo:** Root Level - protein.
- ProComp:** Root Level - protein complex. This is further divided into:
 - Root Level:** protein complex.
 - Modification Level:** Subunit Level, Organism Level, Complex Level.
 - ProEvo:** Root Level - protein.

Relationships between entities are indicated by arrows labeled with PRO terms such as *is_a*, *part_of*, *has_part*, and *has_function*.

Fig4. Home page of PRO with PR ID

PRO Protein Ontology

Home | Linked Open Data | Browse | Search | Statistics | Download

PR:000025934, smad

RACE-PRO
PRO tracker
Community

PRO Consortium
Publications
Documentation

Protein Ontology Report - mRHO

PR:P15409 - http://purl.obolibrary.org/obo/PR_P15409

This page represents a class of proteins encompassing all the protein products of the **Rho** gene in **mouse**.

Ontology Information

PRO ID	PR:P15409	Show OBO stanza
PRO name	rhodopsin (mouse)	
Synonyms	PRO-short-label: EXACT: mRHO Gene-based, RELATED: Rho	
Definition	A rhodopsin that is encoded in the genome of mouse. [OMA:P15409, PRO:Dnx] organism-gene	
PRO Category	PR:000001245 rhodopsin	
Parent	MGI:97914 Rh	
Gene Template	NCBITaxon:10090 Mus musculus	
Taxon		Retrieve All terms OBO Stanza / PAF
Terms by PRO Category		

Organism-Specific

Category	Number of Terms
organism-gene	1
organism-sequence	1
organism-modification	0

Term Hierarchy Visualization: [DAG](#) [OLS](#) [Cytoscape](#)

Related Cross References

DB identifiers	UniProtKB:P15409
----------------	------------------

Interactive Sequence View

Modification ▾

- Number of sequence: 2 • Alignment length: 348 • Scale: "-" = 4 amino acids

PR:P15409 mRHO
PR:P15409-1 mRHOiso1

40 80 120 160 200 240 280 320

Select/align proteoforms across species [🔍](#)

[top](#)

Fig5. Result page of PRO for query rhodopsin

PIR A UniProt Consortium Member
Protein Information Resource

About PIR Resources Search/Analysis Download Support

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

(NSF grants ABI-1062520)
NIH/NIGMS grants U01GM120953

iPTMnet

Search for proteins in iPTMnet database

Search phosphorylation information in the literature

RLIMS-P

University of Delaware Georgetown University Medical Center

Fig6. Home page of iPTMnet for query Rhodopsin

PTMnet Home Browse Statistics Project Info Help Result

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

<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 (Human)	✓ 2 enzymes	✓ 4 substrates	✗	8	0
<input type="checkbox"/> IPTM:Q8WTQ7/GRK7_HUMAN	Rhodopsin kinase GRK7 precursor	Name: GRK7 Synonyms:GPRK7;	Homo sapiens (Human)	✓ 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:Q63651/GRK1_RAT	Rhodopsin kinase GRK1 precursor	Name: Grk1 Synonyms:Rhok;	Rattus norvegicus (Rat)	✓ 1 enzyme	✓ 1 substrate	✗	3	0
<input type="checkbox"/> IPTM:P18545/CNRG_HUMAN	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma	Name: PDE6G Synonyms:PDE6;	Homo sapiens (Human)	✓ 3 enzymes	✗	✗	4	0
<input type="checkbox"/> IPTM:P08100/OPSD_HUMAN	Rhodopsin	Name: RHO Synonyms:OPN2;	Homo sapiens (Human)	✓ 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:PDE6;	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:Q13956/CNCG_HUMAN	Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma	Name: PDE6H	Homo sapiens (Human)	✓	✗	✗	3	0
<input type="checkbox"/> IPTM:Q43924/PDE6D_HUMAN	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta	Name: PDE6D Synonyms:PDED;	Homo sapiens (Human)	✓	✗	✗	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:B6C218/GRK7B_XENLA	Rhodopsin kinase grk7-b precursor	Name: grk7-b	Xenopus laevis (African clawed frog)	✓	✗	✗	1	0

Fig7. Hit page for query Rhodopsin in iPTMnet

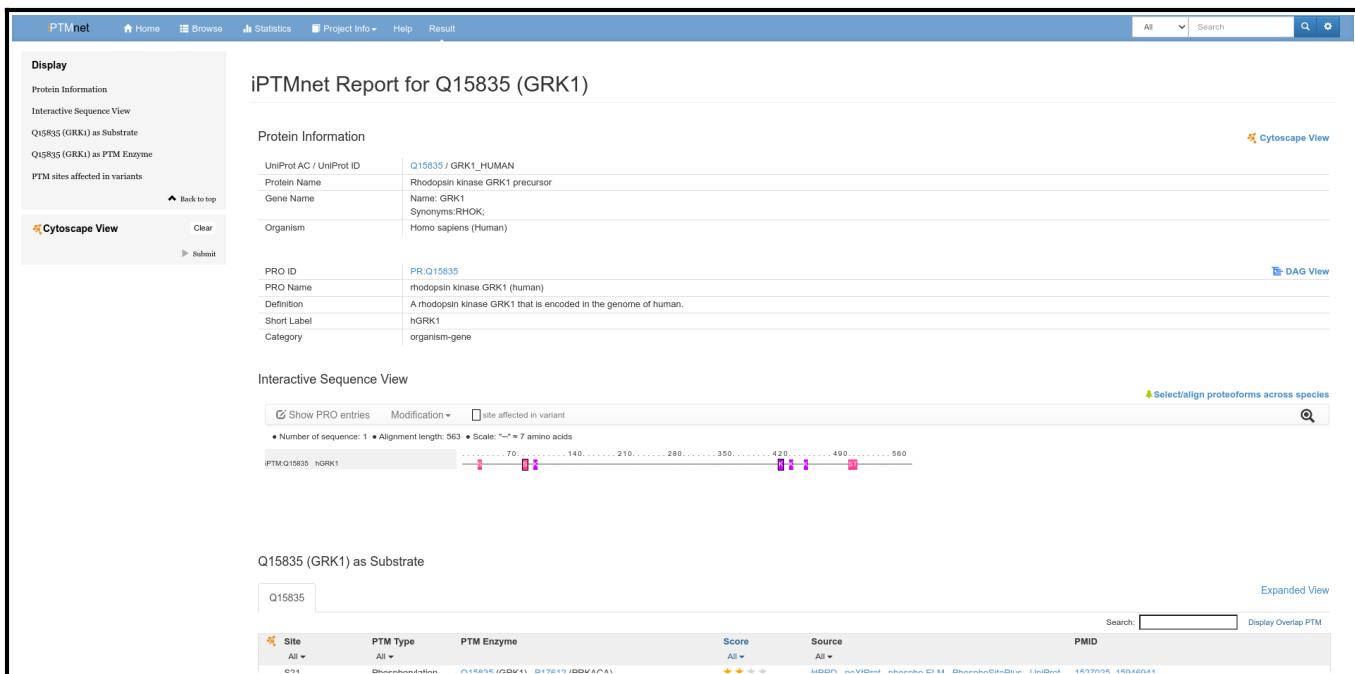


Fig8. Result page for query Rhodopsin in iPTMnet

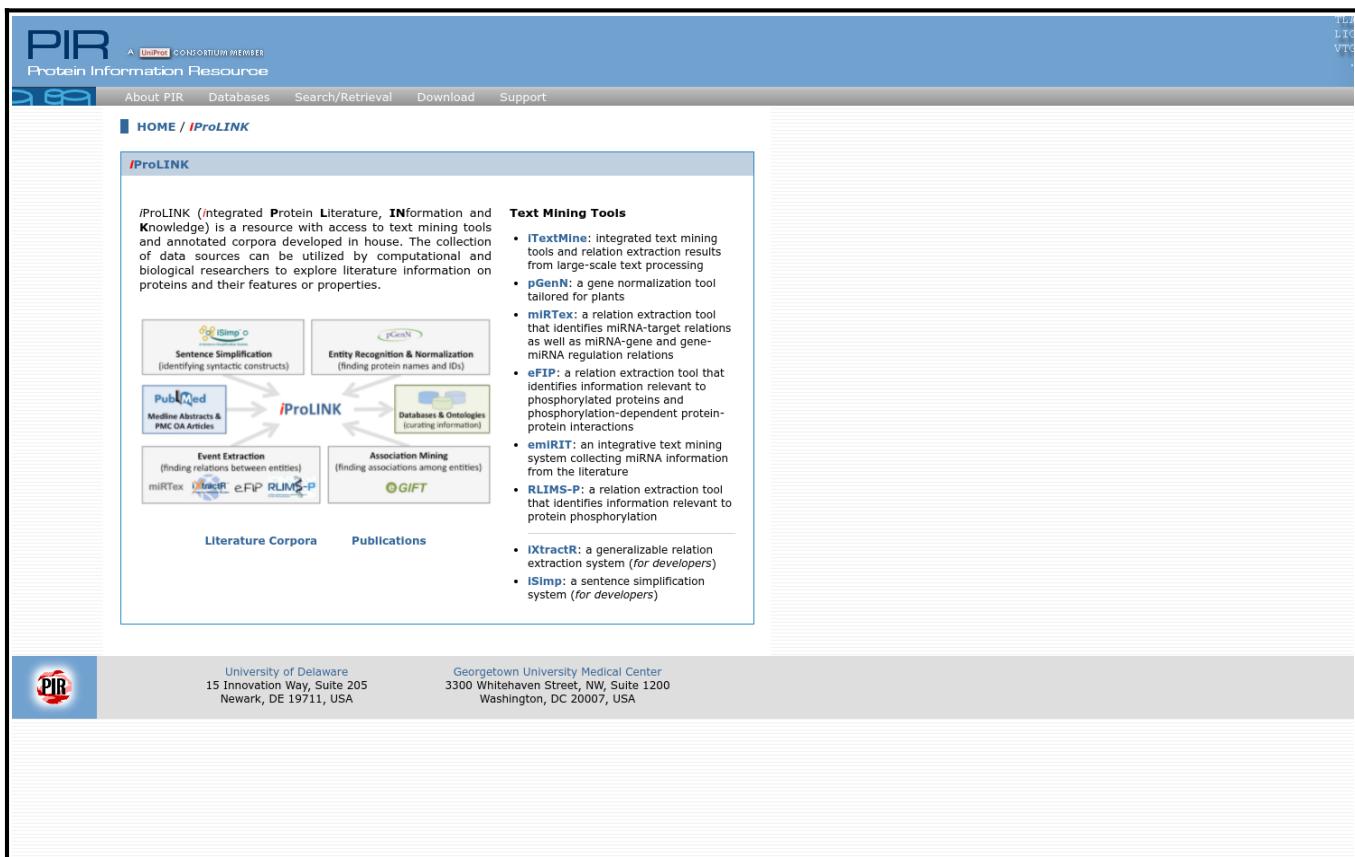


Fig9. Home page for iProLINK

iTexMine REST APIs Download

iTextMine

iTextMine is a system with an automated workflow to integrate text mining tools and relation extraction results from large-scale text processing.

```

graph LR
    Input[Input Text] --> Parallel[Parallel Processing  
Dockerized text-mining tools]
    Parallel --> Alignment[Alignment]
    Alignment --> Post[Post-processing  
- Normalization  
- ID mapping]
    Post --> MongoDB[MongoDB]
    Website[Website] --> REST[REST APIs (JSON format)]
    REST --> MongoDB
  
```

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

27665963

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.

iTexMine REST APIs Download

Search 27665963 in All rlims eFIP miRTex eGARD Issue Report

Find 1 document (1 page)

<input type="checkbox"/> PMID	Gene Mention	miRNA Mention	Disease Mention	Drug Mention	<u>Score</u>
<input type="checkbox"/> 27665963	CFL1, LIMK1				12

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

Fig11. Hit page for query Rhodopsin with PMID

TextMine REST APIs Download

PMID: 27665963 RLiMS-P 1 eFIP 1 miRTex 1 eGARD 0 Issue Report

Abstract

- MicroRNA-138 inhibits migration and invasion of non-small cell lung cancer cells by targeting LIMK1.
- ...
- 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 (P53687)	MIRNA→TARGET	yes	1

Fig12. Result of query Rhodopsin in iTextMine with PMID

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 .

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.

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/ 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/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>