

1. sp|P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1
OS=Homo sapiens OX=9606 GN=VDAC1 PE=1 SV=2

Amino acid sequence: human mitochondrial β barrel membrane protein VDAC

MAVPPTYADLGKSARDVFTKGYGFGLIKLDLTKSENGLEFTSSGSANTETTKVTGSLET
KYRWTEYGLTFTTEKWNTDNTLGTEITVEDQLARGLKLTDFDSSFSPNTGKKNAIKITGYKR
EHINLGCDMDFDIAGPSIRGALVLGYEGWLAGYQMNFFETAKSRVTQSNFAVGKYKTDEFQL
HTNVNDGTEFGGSIYQKVNKKLETAVNLAWTAGNSNTRFGIAAKYQIDPDACFSAKVNNS
SLIGLGYTQTLKPGIKLTLSALLDGKNVNAGGHKLGLGLEFQA

P21796-1 [UniParc]

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| | | | | |
|------------|------------|-------------|------------|------------|
| 10 | 20 | 30 | 40 | 50 |
| MAVPPTYADL | GKSARDVFTK | GYGFGLIKLD | LTKSENGLE | FTSSGSANTE |
| 60 | 70 | 80 | 90 | 100 |
| TTKVTGSLET | KYRWTEYGLT | FTEKWNTDNT | LGTEITVEDQ | LARGLKLTDF |
| 110 | 120 | 130 | 140 | 150 |
| SSFSPNTGKK | NAIKITGYKR | EHINLGCDMD | FDIAGPSIRG | ALVLGYEGWL |
| 160 | 170 | 180 | 190 | 200 |
| AGYQMNFFET | KSRVTQSNFA | VGKYKTDEFQL | HTNVNDGTEF | GGSIYQKVNK |
| 210 | 220 | 230 | 240 | 250 |
| KLETAVNLAW | TAGNSNTRFG | IAAKYQIDPD | ACFSAKVNNS | SLIGLGYTQT |
| 260 | 270 | 280 | | |
| LKPGIKLTLS | ALLDGKNVNA | GGHKLGLGLE | FQA | |

Procedure: Visited the Uniprot website and searched for “human mitochondrial β barrel membrane protein VDAC” in search box. Then open the [search result](#):

There were three vdac proteins namely, vdac1 , vdac 2 and vdac3. The above sequence is for vdac1.

Functions of VDAC1

- It forms a channel through the mitochondrial outer membrane along with the plasma membrane. The channel at the outer mitochondrial membrane allows diffusion of small hydrophilic molecules; on the other hand in the plasma membrane it is involved in cell volume regulation and apoptosis. (PubMed:11845315, PubMed:18755977)
- It adopts an open conformation at low or zero membrane potential and a closed conformation at potentials above 30-40 mV. The open state has a weak anion selectivity whereas the closed state is cation-selective. (PubMed:20230784, PubMed:8420959).
- Binds various signaling molecules, including the sphingolipid ceramide, the phospholipid phosphatidylcholine, and the sterol cholesterol (PubMed:31015432).

- In depolarized mitochondria, acts downstream of PRKN and PINK1 to promote mitophagy or prevent apoptosis.
- polyubiquitination by PRKN promotes mitophagy, while monoubiquitination by PRKN decreases mitochondrial calcium influx which ultimately inhibits apoptosis (PubMed:[32047033](#)).
- The VDAC1 may participate in the formation of the permeability transition pore complex (PTPC) which is responsible for the release of mitochondrial products that triggers apoptosis (PubMed:[15033708](#), PubMed:[25296756](#)).
- It may also mediate ATP export from cells (PubMed:[30061676](#)).

The Number of Transmembrane segments present in the VDAC1 protein : **19**

Topology

| Feature key | Position(s) | Description | Actions | Graphical view | Length |
|----------------------------|-------------|---------------|------------|----------------|--------|
| Transmembrane ⁱ | 26 – 35 | Beta stranded | | | 10 |
| Transmembrane ⁱ | 39 – 47 | Beta stranded | | | 9 |
| Transmembrane ⁱ | 54 – 64 | Beta stranded | Add BLAST | | 11 |
| Transmembrane ⁱ | 69 – 76 | Beta stranded | | | 8 |
| Transmembrane ⁱ | 80 – 89 | Beta stranded | | | 10 |
| Transmembrane ⁱ | 95 – 104 | Beta stranded | | | 10 |
| Transmembrane ⁱ | 111 – 120 | Beta stranded | | | 10 |
| Transmembrane ⁱ | 123 – 130 | Beta stranded | | | 8 |
| Transmembrane ⁱ | 137 – 145 | Beta stranded | | | 9 |
| Transmembrane ⁱ | 150 – 158 | Beta stranded | | | 9 |
| Transmembrane ⁱ | 163 – 175 | Beta stranded | Add BLAST | | 13 |
| Transmembrane ⁱ | 178 – 185 | Beta stranded | | | 8 |
| Transmembrane ⁱ | 189 – 198 | Beta stranded | | | 10 |
| Transmembrane ⁱ | 202 – 211 | Beta stranded | | | 10 |
| Transmembrane ⁱ | 218 – 227 | Beta stranded | | | 10 |
| Transmembrane ⁱ | 231 – 238 | Beta stranded | | | 8 |
| Transmembrane ⁱ | 242 – 251 | Beta stranded | | | 10 |
| Transmembrane ⁱ | 254 – 263 | Beta stranded | | | 10 |
| Transmembrane ⁱ | 273 – 282 | Beta stranded | | | 10 |

2. There are **116,664** sequences for “transcriptional factors” in uniprot. Out of which there are **18,085** identity clusters of 50%.

Source: [uniprot.org/uniref/?query=uniprot:\(\"transcription+factors\"\)+identity:0.5](https://uniprot.org/uniref/?query=uniprot:(\)

I searched for “transcription factors” in uniprot and then selected the cluster percentage from the left side filter menu.

3. There are **203,810** protein sequences from Homo sapiens at identity cutoff of 100%, 90% and 50%.

On searching for “homo sapiens” in uniprot, and then selecting the organism from left side menu. We got total sequences for homo sapiens. Then i selected the cluster %.

| Sequence Identity | Number of sequences |
|-------------------|---------------------|
| 50 % | 68,589 |
| 90% | 91,947 |
| 100% | 152,368 |

4. Search term used: **reviewed:yes AND organism:"Mus musculus (Mouse) [10090]"**

Search results give us 17,090 results as manually annotated protein sequences for mouse (Mus musculus).


Search term used for 3d structures : **database:(type:pdb) AND reviewed:yes AND organism:"Mus musculus (Mouse) [10090]"**

There are 2062 results for manually annotated protein sequences associated with PDB (3D structures).

5.

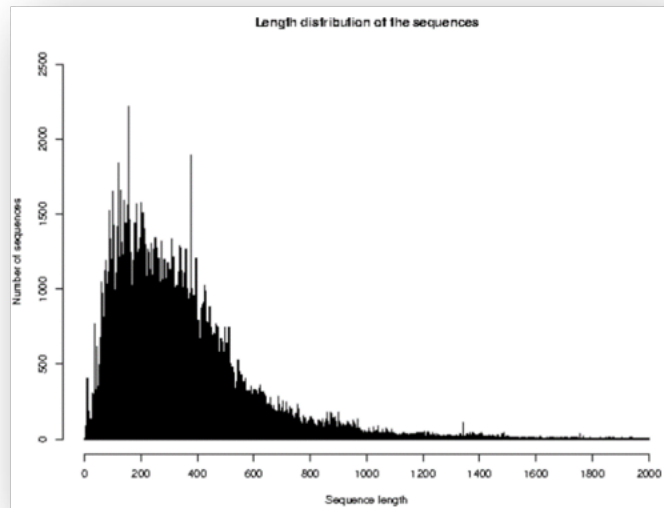
Results

1,957 out of 2,062 identifiers from UniProtKB AC/ID were successfully mapped to 1,957 STRING IDs.
[Click here to download unmapped identifier\(s\)](#)

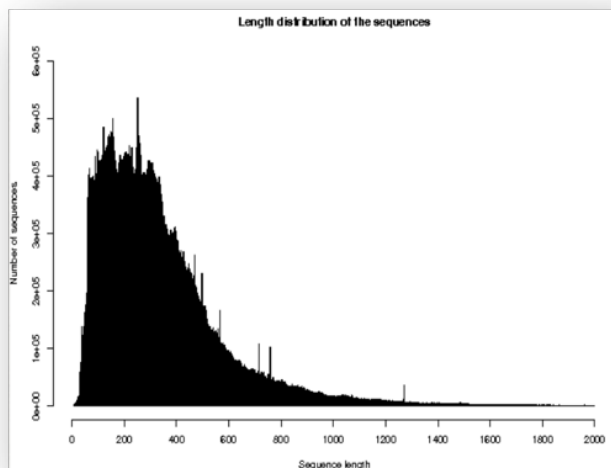
 Download

1. Search in UniProt with search query –
2. database:(type:pdb) AND reviewed:yes AND organism:"Mus musculus (Mouse) [10090]"
3. Select only the entry column and download the identifiers as a list.
4. In Retrieve/ID Mapping, paste these identifiers.
5. Under select options:
 - a. From – UniProtKB
 - b. To – STRING.... And submit.
6. a) Inference:
 - According to Swiss-Prot:
 - The average sequence length is 360 aa.
 - According to TrEMBL:
 - The average sequence length is 348 aa.

The majority of sequences are between 200 and 400 amino acids long. It's also clear that sequences of longer length have a lower frequency.



Swiss-Prot



TrEMBL

b)

As per given in **TrEMBL**:

The shortest sequence in UniProtKB = **7 AAs**, with sequence ID = A0A1Y7VI41

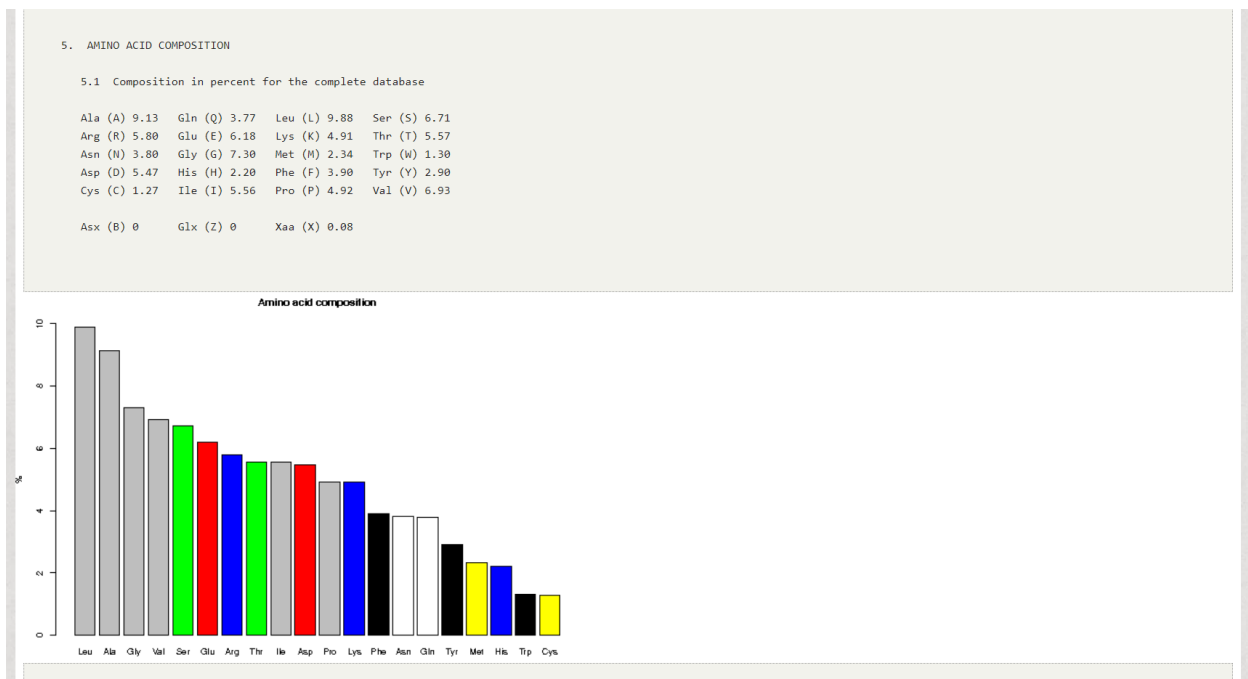
The longest sequence in UniProtKB = **45,354 AAs** with sequence ID = A0A5A9P0L4

As per given in Swiss_Prot:

The shortest sequence in UniProtKB = **2 AAs**, which sequence ID = P0DPR3

The longest sequence in UniProtKB = **35,213 AAs** with sequence ID = A2ASS6

C) in TrEMBL



In Swiss-prot

6.1 Composition in percent for the complete database

| | | | | | | | |
|---------|------|---------|------|---------|------|---------|------|
| Ala (A) | 8.25 | Gln (Q) | 3.93 | Leu (L) | 9.65 | Ser (S) | 6.64 |
| Arg (R) | 5.53 | Glu (E) | 6.72 | Lys (K) | 5.80 | Thr (T) | 5.35 |
| Asn (N) | 4.06 | Gly (G) | 7.07 | Met (M) | 2.41 | Trp (W) | 1.10 |
| Asp (D) | 5.46 | His (H) | 2.27 | Phe (F) | 3.86 | Tyr (Y) | 2.92 |
| Cys (C) | 1.38 | Ile (I) | 5.91 | Pro (P) | 4.74 | Val (V) | 6.86 |

| | | | | | |
|---------|-------|---------|-------|---------|------|
| Asx (B) | 0.000 | Glx (Z) | 0.000 | Xaa (X) | 0.00 |
|---------|-------|---------|-------|---------|------|

