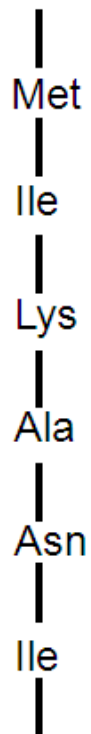


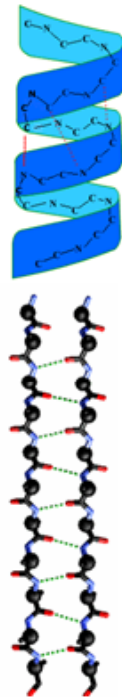
Protein Structure

Primary
structure



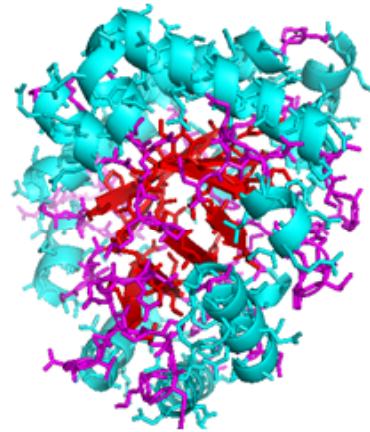
Amino acid sequence

Secondary
structure



α -helix, β -strand

Tertiary
structure



3D structure with
atomic details

Quaternary
structure



Assembled
subunits

Primary structure: human hemoglobin

```
>sp|P68871|HBB_HUMAN Hemoglobin subunit beta OS=Homo sapiens
```

```
VHLTPEEKSAVTALWGKVNVDENVGGEALGRLLVYPWTQRFFESFGDLSTPD  
AVMGNPVKKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFR  
LLGNVLVCVLAHHFG KEFTPPVQAAYQKVVAGVANALAHKYH
```

Primary structure describes the linear sequence of amino acid residues in a protein.

It includes all covalent bonds between amino acids.

The relative arrangement of the linked amino acids is not specified.

Databases for protein sequences

EXProt

Munich Information Center for Protein Sequences (MIPS)

NCBI Protein database

PIR - Protein Information Resource (Georgetown University)

PIR-NREF

PRF

SWISS-PROT (Swiss Institute of Bioinformatics)

TrEMBL

UniProt - The Universal Protein Knowledgebase

Protein Information Resource

PRO: Protein family classification

iProClass: integrated protein knowledgebase

iProLink: literature, information and knowledge

The screenshot shows the PIR website with a blue header. The header includes the PIR logo, 'A UniProt Consortium Member', and 'Protein Information Resource'. Navigation links include 'About PIR', 'Databases', 'Search/Analysis', 'Download', and 'Support'. A banner for 'INTEGRATED PROTEIN INFORMATICS RESOURCE FOR GENOMIC, PROTEOMIC AND SYSTEMS BIOLOGY RESEARCH' is present. Below this, a UniProt logo and text describe the Universal Protein Resource (UniProt) as a centralized, authoritative resource for protein sequences and functional information. It lists 'UniProtKB', 'UniRef', and 'UniParc' and notes the 'Current release: 2011_07'. Three main sections are highlighted: 'PRO Protein Ontology' with a description of protein objects and relationships, a 'Browse PRO' link, an 'Annotate with RACE-PRO' link, and a '*Sample PRO report*' link; 'iProClass Integrated Protein Knowledgebase' with 'Value-added reports for UniProtKB and unique UniParc proteins', 'Functional analysis and protein ID mapping', and a '*Sample protein report*' link; and 'iProLINK Literature Information & Knowledge' with a 'Source for text mining and ontology development', 'RLIMS-P text mining tool, BioThesaurus', 'Bibliography mapping', and a '*Sample Biblio. report*' link.

PIR A UniProt CONSORTIUM MEMBER
Protein Information Resource

About PIR Databases Search/Analysis Download Support

INTEGRATED PROTEIN INFORMATICS RESOURCE FOR GENOMIC, PROTEOMIC AND SYSTEMS BIOLOGY RESEARCH

UniProt
The Universal Protein Resource (UniProt) provides the scientific community with a single, centralized, authoritative resource for protein sequences and functional information.
UniProtKB | UniRef | UniParc
Current release: 2011_07

PRO
Protein Ontology

- Representation of protein objects with descriptions and relationships
- [Browse PRO](#)
- Annotate with [RACE-PRO](#)

Sample PRO report

iProClass
Integrated Protein Knowledgebase

- Value-added reports for [UniProtKB](#) and unique [UniParc](#) proteins
- Functional analysis and [protein ID mapping](#)

Sample protein report

iProLINK
Literature Information & Knowledge

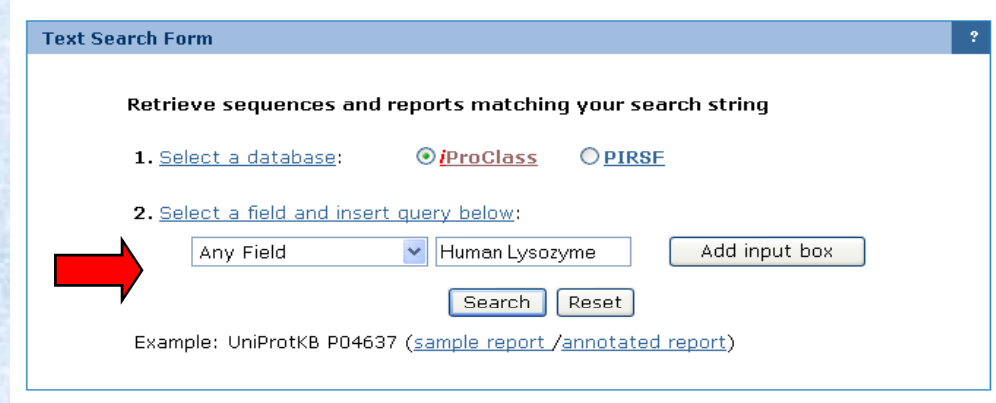
- Source for text mining and ontology development
- [RLIMS-P](#) text mining tool, [BioThesaurus](#)
- [Bibliography mapping](#)

Sample Biblio. report

<http://pir.georgetown.edu/>

Search with iProClass

The iProClass database provides value-added information reports on protein sequences, structures, families, functions, interactions, expressions and modifications.



The screenshot shows the 'Text Search Form' interface. It has a title bar with a question mark icon. Below the title bar, it says 'Retrieve sequences and reports matching your search string'. There are two steps: 1. 'Select a database:' with radio buttons for 'iProClass' (selected) and 'PIRSF'. 2. 'Select a field and insert query below:'. This step includes a dropdown menu with 'Any Field' selected, a text input box containing 'Human Lysozyme', and an 'Add input box' button. Below these are 'Search' and 'Reset' buttons. At the bottom, there is an example: 'Example: UniProtKB P04637 ([sample report](#) / [annotated report](#))'. A large red arrow points to the 'Any Field' dropdown menu.

Text Search Form ?

Retrieve sequences and reports matching your search string

1. [Select a database:](#) ☒ [iProClass](#) ☐ [PIRSF](#)

2. [Select a field and insert query below:](#)

Any Field Human Lysozyme Add input box

Search Reset

Example: UniProtKB P04637 ([sample report](#) / [annotated report](#))

1 selected (show)		GO Slim / KEGG Pathway...		BLAST FASTA Pattern Match Pairwise Alignment Multiple Alignment Domain Display		
<input type="checkbox"/> Protein AC/ID	Protein Name	Length	Organism Name	PIRSF ID	Related Seq. +	Matched Fields
<input type="checkbox"/> P79239/LYSC_PONPY <small>/ProClass UniProtKB/Swiss-Prot BioThesaurus</small>	Lysozyme C precursor	148	Pongo pygmaeus (Bornean orangutan)	PIRSF001064	300	Paper Title=>human lysozyme
<input type="checkbox"/> P61628/LYSC_PANTR <small>/ProClass UniProtKB/Swiss-Prot BioThesaurus</small>	Lysozyme C precursor	148	Pan troglodytes (Chimpanzee)	PIRSF001064	300	Paper Title=>human lysozyme
<input type="checkbox"/> P61627/LYSC_PANPA <small>/ProClass UniProtKB/Swiss-Prot BioThesaurus</small>	Lysozyme C precursor	148	Pan paniscus (Pygmy chimpanzee) (Bonobo)	PIRSF001064	300	Paper Title=>human lysozyme
<input type="checkbox"/> P61626/LYSC_HUMAN <small>/ProClass UniProtKB/Swiss-Prot BioThesaurus</small>	Lysozyme C precursor	148	Homo sapiens (Human)	PIRSF001064	300	Paper Title=>human lysozyme; Paper Title=>human
<input type="checkbox"/> P79179/LYSC_GORGO <small>/ProClass UniProtKB/Swiss-Prot BioThesaurus</small>	Lysozyme C precursor	148	Gorilla gorilla gorilla (Lowland gorilla)	PIRSF001064	300	Paper Title=>human lysozyme
<input type="checkbox"/> P02788/TRFL_HUMAN <small>/ProClass UniProtKB/Swiss-Prot BioThesaurus</small>	Lactotransferrin precursor	710	Homo sapiens (Human)	PIRSF002549; PIRSF500683	300	Paper Title=>human lysozyme
<input type="checkbox"/> Q6PCD2/Q6PCD2_HUMAN <small>/ProClass UniProtKB/TrEMBL BioThesaurus</small>	GABDE protein	365	Homo sapiens (Human)		300	Paper Title=>human lysozyme
<input type="checkbox"/> B2R4C5/B2R4C5_HUMAN <small>/ProClass UniProtKB/TrEMBL BioThesaurus</small>	Lysozyme (Renal amyloidosis), isoform CRA_a	148	Homo sapiens (Human)		300	Paper Title=>human lysozyme; Paper Title=>human
<input type="checkbox"/> Q876Z9/Q876Z9_ASPOR <small>/ProClass UniProtKB/TrEMBL BioThesaurus</small>	Predicted protein	600	Aspergillus oryzae	PIRSF037788; PIRSF500676	300	Paper Title=>human lysozyme
<input type="checkbox"/> Q4R8K7/Q4R8K7_MACFA <small>/ProClass UniProtKB/TrEMBL BioThesaurus</small>	Testis cDNA clone: QtsA-12244, similar to human lysozyme homolog (LOC57151),	109	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey)		300	Protein Name=>human lysozyme

1 selected (show)		GO Slim / KEGG Pathway...		BLAST FASTA Pattern Match Pairwise Alignment Multiple Alignment Domain Display			Save Result As: TABLE FASTA	
<input checked="" type="checkbox"/> Protein AC/ID	Protein Name	Length	Organism Name	PIRSF ID	Related Seq. +	Matched Fields		
<input checked="" type="checkbox"/> P61626/LYSC_HUMAN <small>/ProClass UniProtKB/Swiss-Prot BioThesaurus</small>	Lysozyme C precursor	148	Homo sapiens (Human)	PIRSF001064	300	UniProtKB AC=>P61626		

iProClass Summary Report for UniProtKB Entry: P61626

[Related Sequences](#)

[BioThesaurus](#)

[ID Mapping](#)

GENERAL INFORMATION

Protein Name and ID	UniProtKB ID	UniProtKB Accession	Protein Name
	LYSC_HUMAN	P61626 ; P00695; Q13170; Q9UCF8	Lysozyme C precursor
PIR-PSD: LZHU RefSeq: NP_000230.1 GenPept: AAA59535.1 ; AAC63078.1 ; FAW97222.1 ; AAA59536.1 ; CAA32175.1 ; AAH04147.1 ; FAW97221.1 ; ACQ37637.1 ; AAA36188.1 IPI: IPI00019038			
Taxonomy	<i>Source Organism:</i> Homo sapiens (Human) <i>Taxon Group:</i> Euk/mammal <i>NCBI Taxon:</i> 9606 <i>Lineage:</i> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.		
Gene Name	LYZ; LZM		
Keywords	3d-structure; amyloid; amyloidosis; antimicrobial; bacteriolytic enzyme; direct protein sequencing; disease mutation; disulfide bond; glycosidase; hydrolase; polymorphism; polysaccharide degradation; signal		
Function	Lysozymes have primarily a bacteriolytic function; those in tissues and body fluids are associated with the monocyte- macrophage system and enhance the activity of immunoagents.		
Subunit	Monomer.		

CROSS-REFERENCES

Bibliography	View Bibliography Information Submit Bibliography <i>Annotated references:</i> PMID: 8105095 ; 10350481 ; 10469827 ; 10561612 ; 11887182 ; 11927576 ; 11986950 [PDB/GeneRIF] More
	<i>Other references:</i> PMID: 11849445 ; 12675840 ; 15745733 ; 8765309 ; 9659355 ; 9745729 ; 18391951 ; 9359845 ; 8566845 ; 17353931 ; 9883972 ; 366724 ; 10534505 ; 12477932 ; 10558865 ; 18591461
DNA Sequence	GenBank/EMBL/DDBJ: M21119 ; J03801 ; M19045 ; X14008 ; U25677 ; BC004147

Structure	<div>1B5U: SCOP CATH FSSP MMDb PDBsum</div> <div>1B5V: SCOP CATH FSSP MMDb PDBsum</div> <div>1B5W: SCOP CATH FSSP MMDb PDBsum</div> <div>1B5X: SCOP CATH FSSP MMDb PDBsum</div> <div>1B5Y: SCOP CATH FSSP MMDb PDBsum</div> <div>1B5Z: SCOP CATH FSSP MMDb PDBsum</div> <div>1B7L: SCOP CATH FSSP MMDb PDBsum</div> <div>1B7M: SCOP CATH FSSP MMDb PDBsum</div> <div>1B7N: SCOP CATH FSSP MMDb PDBsum</div> <div>1B7O: SCOP CATH FSSP MMDb PDBsum</div> <div>1B7P: SCOP CATH FSSP MMDb PDBsum</div> <div>1B7Q: SCOP CATH FSSP MMDb PDBsum</div> <div>1B7R: SCOP CATH FSSP MMDb PDBsum</div> <div>1B7S: SCOP CATH FSSP MMDb PDBsum</div> <div>1B83: SCOP CATH FSSP MMDb PDBsum</div> <div>1B84: SCOP CATH FSSP MMDb PDBsum</div> <div>More</div>
PIR Feature & Post Translational Modifications	<div>FEAT1; active site: Glu, Asp (53,71) [predicted]</div> <div>FEAT2; binding site: substrate (Asp) (120) [predicted]</div> <div>FEAT3; disulfide bonds: (24-146,48-134,83-99,95-113) [experimental]</div> <div>FEAT4; domain: signal sequence (1-18) [predicted]</div> <div>FEAT5; product: lysozyme (19-148) [experimental]</div> <div>Phosphosite: P61626</div>

FAMILY CLASSIFICATION	
UniRef	UniRef100_P61626 ; UniRef90_P61626 ; UniRef50_P61626
PIRSF	PIRSF001064 lysozyme c
Pfam Domain	Pfam: PF00062 : C-type lysozyme/alpha-lactalbumin family (19-146)
Prosite Motif	Prosite: PS00128 : PDOC00119 : Alpha-lactalbumin / lysozyme C signature. Prosite: PS51348 : PDOC00119 : Alpha-lactalbumin / lysozyme C family profile.
InterPro	InterPro: LYSC_HUMAN IPR001916 : Glycoside hydrolase, family 22 IPR000974 : Glycoside hydrolase, family 22, lysozyme
SCOP Fold	►Class: Alpha and beta proteins (a+b) ; Fold: Lysozyme-like ; Superfamily: Lysozyme-like ; Family: C-type lysozyme [133L:A; 134L:A; 1B5U:A; 1B5V:A; 1B5W:A; 1B5X:A; 1B5Y:A; 1B5Z:A; 1B5Z:B; 1B7L:A; 1B7M:A; 1B7N:A; 1B7O:A; 1B7P:A; 1B7Q:A; 1B7R:A; 1B7S:A; 1B83:A; 1B83:B; 1B84:A; 1B84:B; 1B85:A; 1B85:B; 1C43:A; 1C45:A; 1C46:A; 1C7P:A; 1CJ6:A; 1CJ7:A; 1CJ8:A; 1CJ9:A; 1CKC:A; 1CKD:A; 1CKF:A; 1CKG:A; 1CKG:B; 1CKH:A; 1D6P:A; 1D6Q:A; 1DI3:A; 1DI4:A; 1DI5:A; 1EQ4:A; 1EQ5:A; 1EQE:A; 1GAY:A; 1GAZ:A; 1GB0:A; 1GB2:A; More]
Other Classification	BLOCKS: IPB000974 Lysozyme signature PRINTS: PR00137 LYSOZYME PRINTS: PR00135 LYZLACT SMART: SM00263 LYZ1

FEATURE & SEQUENCE DISPLAY	
<div><div>Length = 148</div><div>P61626</div><div>PF00062</div><div>1</div><div>61</div><div>121</div></div>	<div>Click on a bar to show its sequence; to copy and paste it, press ctrl-c then ctrl-v.</div> <div><div>1</div><div>148</div></div> <div><div>1</div><div>61</div><div>121</div></div> <div><div>HKALIVLGLVLLSVTVQGGKVFERCELARTLKRLGMDGYRGISLANWMCLAKWESGYNTRA</div><div>TNYNAGDRSTDYGIPIQINSRYWCNDGKTPGAVNACHLSCSALLQDNIADAVACAKRVVRD</div><div>PQGIRAWVAWRNRCQNRDVRQYVQGGCV</div></div>

Swiss-prot/Uniprot

Annotated protein sequence database established in 1986 and maintained collaboratively, since 1987, by the Department of Medical Biochemistry of the **University of Geneva** and the **EMBL** Data Library.

It 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 domain structure, post-translational modifications and variants), a **minimal level of redundancy** and a **high level of integration** with other databases.

TrEMBL is a **computer annotated** supplement of SWISS-PROT that contains all the translations of EMBL nucleotide sequence entries not yet integrated in SWISS-PROT.

Currently, SWISS-PROT and TrEMBL have 0.53 and 79.2 million sequences, respectively.

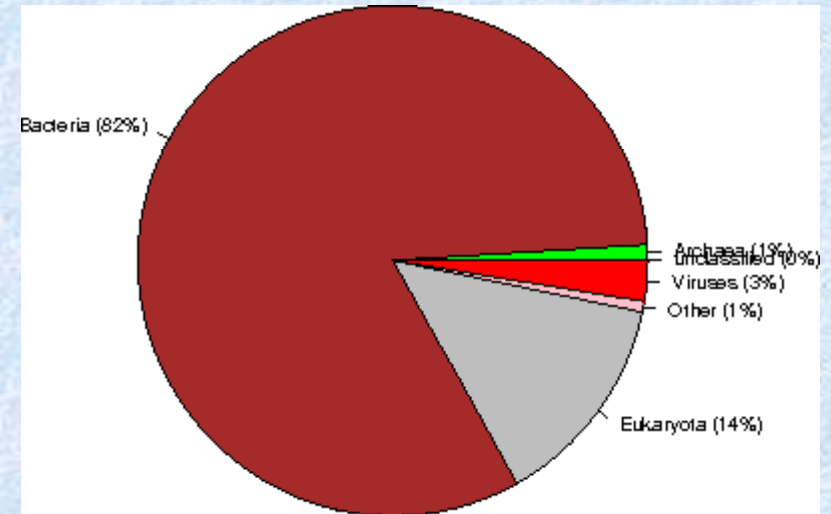
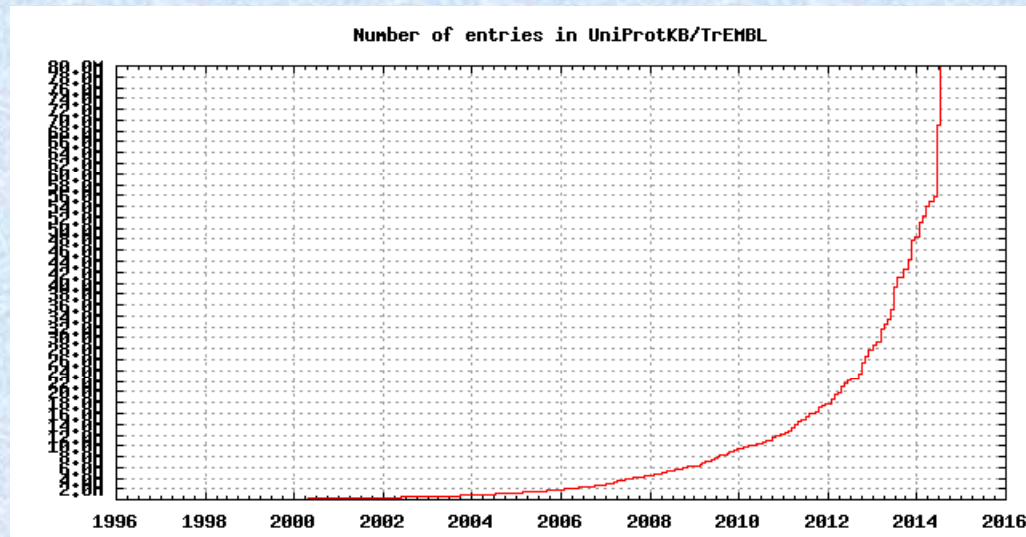
Total: 79.8 million

<http://www.ebi.ac.uk/swissprot/>

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

Uniprot: statistics

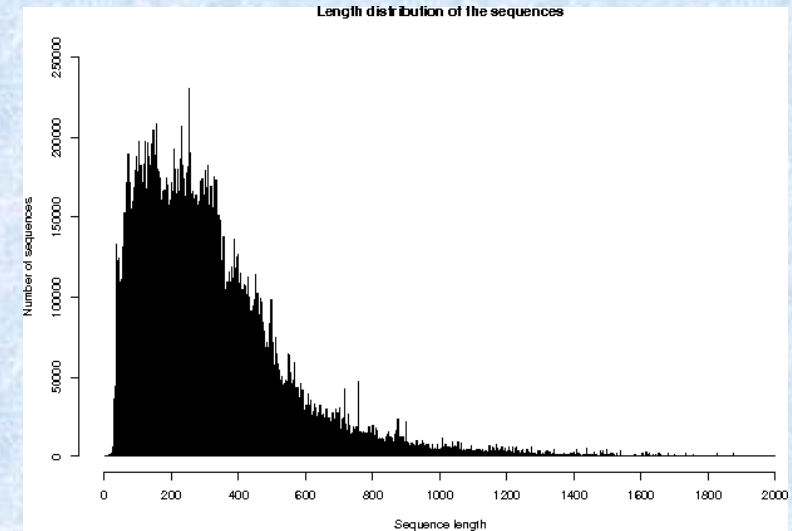
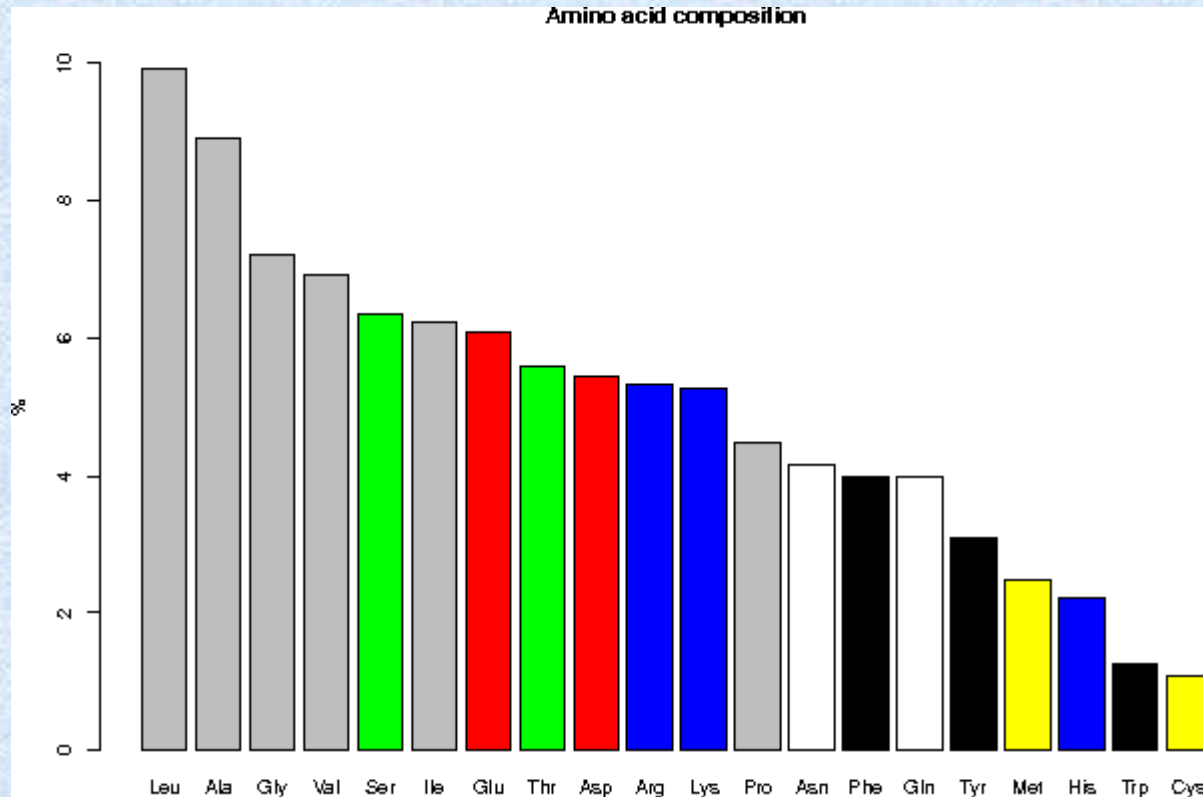
Number of entries: ~79.8 million



Kingdom	sequences (% of the database)
Archaea	796882 (1%)
Bacteria	65532440 (82%)
Eukaryota	10896348 (14%)
Viruses	2058511 (3%)
Other	540061 (<1%)

Uniprot: statistics

Average sequence length:
315 amino acids



Uniprot: contents

Name and origin of the protein

protein attributes

general information

Ontologies

sequence annotation

amino acid sequence

bibliographic references

cross-references with sequence, structure and interaction databases

entry information.

Uniprot: search results

UniProt > UniProtKB

Search Blast Align Retrieve ID Mapping *

Search in Protein Knowledgebase (UniProtKB) ☒ Query hemoglobin B chain Search Advanced Search » Clear

1 - 25 of 1,243 results for **hemoglobin** AND **B** AND **chain** in UniProtKB sorted by **score** descending

Browse by [taxonomy](#), [keyword](#), [gene ontology](#), [enzyme class](#) or [pathway](#) | Reduce sequence redundancy to [100%](#), [90%](#) or [50%](#) |

[Download](#)

Page 1 of 50 | [Next](#) »

Results [Customize](#)

- > Show only [reviewed \(825\)](#) ★ (UniProtKB/Swiss-Prot) or [unreviewed \(418\)](#) ☆ (UniProtKB/TrEMBL) entries
- > Quote terms: "hemoglobin b"
- > Restrict term "hemoglobin" to [protein family \(24\)](#), [gene name \(3\)](#), [gene ontology \(883\)](#), [keyword \(9\)](#), [protein name \(970\)](#), [web resource \(5\)](#)
- > Restrict term "b" to [author \(608\)](#), [domain \(4\)](#), [gene name \(15\)](#), [gene ontology \(5\)](#), [keyword \(4\)](#), [protein name \(58\)](#), [organism \(1\)](#), [source \(7\)](#), [strain \(5\)](#), [taxonomy \(6\)](#), [tissue \(2\)](#)
- > Restrict term "chain" to [author \(48\)](#), [gene name \(2\)](#), [gene ontology \(7\)](#), [keyword \(7\)](#), [protein name \(740\)](#), [annotation topic \(943\)](#)
- > Restrict term "chain" to [pathway](#)

Accession	Entry name	Status	Protein names	Gene names	Organism	Length
P68871	HBB_HUMAN	★	Hemoglobin subunit beta	HBB	Homo sapiens (Human)	147
<input type="checkbox"/> P69905	HBA_HUMAN	★	Hemoglobin subunit alpha	HBA1 HBA2	Homo sapiens (Human)	142
<input type="checkbox"/> P69892	HBG2_HUMAN	★	Hemoglobin subunit gamma-2	HBG2	Homo sapiens (Human)	147
<input type="checkbox"/> P69891	HBG1_HUMAN	★	Hemoglobin subunit gamma-1	HBG1 PRO2979	Homo sapiens (Human)	147
<input type="checkbox"/> P0A592	TRHBN_MYCTU	★	Group 1 truncated hemoglobin glbN	glbN Rv1542c MT1594 MTCY48.23	Mycobacterium tuberculosis	136
<input type="checkbox"/> P02042	HBD_HUMAN	★	Hemoglobin subunit delta	HBD	Homo sapiens (Human)	147

Uniprot: contents

Names and origin

Protein names	<i>Recommended name:</i> Hemoglobin subunit beta <i>Alternative name(s):</i> Beta-globin Hemoglobin beta chain <i>Cleaved into the following chain:</i> 1. LVV-hemorphin-7
Gene names	Name: HBB
Organism	Homo sapiens (Human) [Complete proteome]
Taxonomic identifier	9606 [NCBI]
Taxonomic lineage	Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Mammalia > Eutheria > Euarchontoglires > Primates > Haplorrhini > Catarrhini > Hominidae > Homo

Protein attributes

Sequence length	147 AA.
Sequence status	Complete.
Sequence processing	The displayed sequence is further processed into a mature form.
Protein existence	Evidence at protein level.

Uniprot: contents

General annotation (Comments)

Function	Involved in oxygen transport from the lung to the various peripheral tissues. Ref.35 LVV-hemorphin-7 potentiates the activity of bradykinin, causing a decrease in blood pressure. Ref.35
Subunit structure	Heterotetramer of two alpha chains and two beta chains in adult hemoglobin A (HbA).
Tissue specificity	Red blood cells.
Post-translational modification	Glucose reacts non-enzymatically with the N-terminus of the beta chain to form a stable ketoamine linkage. This takes place slowly and continuously throughout the 120-day life span of the red blood cell. The rate of glycation is increased in patients with diabetes mellitus. S-nitrosylated; a nitric oxide group is first bound to Fe ²⁺ and then transferred to Cys-94 to allow capture of O ₂ . Acetylated on Lys-60, Lys-83 and Lys-145 upon aspirin exposure. Ref.34 reports the identification of HBB acetylated on Lys-145 in the cytosolic fraction of HeLa cells. This may have resulted from contamination of the sample.
Involvement in disease	Defects in HBB may be a cause of Heinz body anemias (HEIBAN) [MIM:140700]. This is a form of non-spherocytic hemolytic anemia of Dacie type 1. After splenectomy, which has little benefit, basophilic inclusions called Heinz bodies are demonstrable in the erythrocytes. Before splenectomy, diffuse or punctate basophilia may be evident. Most of these cases are probably instances of hemoglobinopathy. The hemoglobin demonstrates heat lability. Heinz bodies are observed also with the Ivemark syndrome (asplenia with cardiovascular anomalies) and with glutathione peroxidase deficiency. Ref.51 Ref.125 Ref.126 Ref.129 Defects in HBB are the cause of beta-thalassemia (B-THAL) [MIM:604131]. A form of thalassemia. Thalassemias are common monogenic diseases occurring mostly in Mediterranean and Southeast Asian populations. The hallmark of beta-thalassemia is an imbalance in globin-chain production in the adult HbA molecule. Absence of beta chain causes beta(0)-thalassemia, while reduced amounts of detectable beta globin causes beta ⁺ -thalassemia. In the severe forms of beta-thalassemia, the excess alpha globin chains accumulate in the developing erythroid precursors in the marrow. Their deposition leads to a vast increase in erythroid apoptosis that in turn causes ineffective erythropoiesis and severe microcytic hypochromic anemia. Clinically, beta-thalassemia is divided into thalassemia major which is transfusion dependent, thalassemia intermedia (of intermediate severity), and thalassemia minor that is asymptomatic. Ref.52 Defects in HBB are the cause of sickle cell anemia (SKCA) [MIM:603903]; also known as sickle cell disease. Sickle cell anemia is characterized by abnormally shaped red cells resulting in chronic anemia and periodic episodes of pain, serious infections and damage to vital organs. Normal red blood cells are round and flexible and flow easily through blood vessels, but in sickle cell anemia, the abnormal hemoglobin (called Hb S) causes red blood cells to become stiff. They are C-shaped and resembles a sickle. These stiffer red blood cells can lead to microvascular occlusion thus cutting off the blood supply to nearby tissues. Defects in HBB are the cause of beta-thalassemia dominant inclusion body type (B-THALIB) [MIM:603902]. An autosomal dominant form of beta thalassemia characterized by moderate anemia, lifelong jaundice, cholelithiasis and splenomegaly, marked morphologic changes in the red cells, erythroid hyperplasia of the bone marrow with increased numbers of multinucleate red cell precursors, and the presence of large inclusion bodies in the normoblasts, both in the marrow and in the peripheral blood after splenectomy. Ref.52
Miscellaneous	One molecule of 2,3-bisphosphoglycerate can bind to two beta chains per hemoglobin tetramer.

Uniprot: contents

Ontologies

Keywords

Biological process	Oxygen transport Transport
Coding sequence diversity	Polymorphism
Disease	Congenital dyserythropoietic anemia Disease mutation Hereditary hemolytic anemia
Ligand	Heme Iron Metal-binding Pyruvate
Molecular function	Hypotensive agent Vasoactive
PTM	Acetylation Glycation Glycoprotein Phosphoprotein S-nitrosylation
Technical term	3D-structure Complete proteome Direct protein sequencing

Gene Ontology (GO)

Biological process	<p>blood coagulation Traceable author statement. Source: Reactome</p> <p>hydrogen peroxide catabolic process Inferred from direct assay. Source: BHF-UCL</p> <p>nitric oxide transport Non-traceable author statement. Source: UniProtKB</p> <p>positive regulation of cell death Inferred from direct assay. Source: BHF-UCL</p> <p>positive regulation of nitric oxide biosynthetic process Non-traceable author statement. Source: UniProtKB</p> <p>protein heterooligomerization Inferred from direct assay. Source: BHF-UCL</p> <p>regulation of blood pressure Inferred from electronic annotation. Source: UniProtKB-KW</p> <p>regulation of blood vessel size Inferred from electronic annotation. Source: UniProtKB-KW</p>
Cellular component	<p>haptoglobin-hemoglobin complex Inferred from direct assay. Source: BHF-UCL</p> <p>hemoglobin complex Non-traceable author statement Ref.33 Ref.71. Source: UniProtKB</p>
Molecular function	<p>heme binding Inferred from electronic annotation. Source: InterPro</p> <p>hemoglobin binding Inferred from direct assay. Source: UniProtKB</p> <p>oxygen binding Inferred from direct assay. Source: UniProtKB</p> <p>oxygen transporter activity Non-traceable author statement Ref.71. Source: UniProtKB</p>

Uniprot: contents

Binary interactions

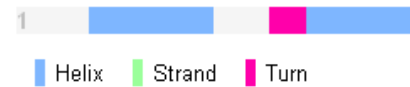
With	Entry	#Exp.	IntAct	Not	Natural variations			
HBA1	P69905	1	EBI-715554,EBI-714680		<input type="checkbox"/>	Natural variant	21	V → A in Raleigh; O(2) affinity down. [dbSNP:rs33949930]
					<input type="checkbox"/>	Natural variant	31	H → L in Graz. [dbSNP:rs35906307] Ref.76
					<input type="checkbox"/>	Natural variant	31	H → Q in Okayama; O(2) affinity up. [dbSNP:rs713040]
					<input type="checkbox"/>	Natural variant	31	H → R in Deer Lodge; O(2) affinity up. [dbSNP:rs33983205]
					<input type="checkbox"/>	Natural variant	31	H → Y in Fukuoka. [dbSNP:rs35906307]
					<input type="checkbox"/>	Natural variant	61	P → R in Warwickshire. [dbSNP:rs34769005]
					<input type="checkbox"/>	Natural variant	71	E → A in G-Makassar.
					<input type="checkbox"/>	Natural variant	71	E → K in C. Ref.3 Ref.49
					<input type="checkbox"/>	Natural variant	71	E → Q in Machida. [dbSNP:rs33930165]
					<input type="checkbox"/>	Natural variant	71	E → V in S; sickle cell anemia. [dbSNP:rs334] Ref.10 Ref.39
					<input type="checkbox"/>	Natural variant	81	E → G in G-San Jose; mildly unstable. [dbSNP:rs34948328]
					<input type="checkbox"/>	Natural variant	81	E → K in G-Siriraj. [dbSNP:rs34948328]
					<input type="checkbox"/>	Natural variant	91	K → E in N-Timone. [dbSNP:rs33932981] Ref.101
					<input type="checkbox"/>	Natural variant	91	K → Q in J-Luhe. [dbSNP:rs33926764]
					<input type="checkbox"/>	Natural variant	91	K → T in Rio Grande. Ref.114
					<input type="checkbox"/>	Natural variant	101	S → C in Porto Alegre; O(2) affinity up. [dbSNP:rs33918131]
					<input type="checkbox"/>	Natural variant	111	A → D in Ankara. [dbSNP:rs33947457] Ref.55

Sequence annotation (Features)			
Feature key	Position(s)	Length	Descrip
Molecule processing			
<input type="checkbox"/> Initiator methionine	1	1	Remov
<input checked="" type="checkbox"/> Chain	2 – 147	146	Hemog
<input type="checkbox"/> Peptide	33 – 42	10	LVV-he
Sites			
<input type="checkbox"/> Metal binding	64	1	Iron (he
<input type="checkbox"/> Metal binding	93	1	Iron (he
<input type="checkbox"/> Binding site	2	1	2,3-bisj
<input type="checkbox"/> Binding site	3	1	2,3-bisj
<input type="checkbox"/> Binding site	83	1	2,3-bisj
<input type="checkbox"/> Binding site	144	1	2,3-bisj

Interpro content

Cross-references

Secondary structure



Details...

Sequence databases

- ☒ EMBL
- ☐ GenBank
- ☐ DDBJ

3D structure databases

- ☒ PDBe
- ☐ RCSB PDB
- ☐ PDBj

Entry	Method	Resol
1A00	X-ray	2.5
1A01	X-ray	1.5
1A0U	X-ray	2.5
1A0Z	X-ray	2.5
1A3N	X-ray	1.5
1A3O	X-ray	1.5
1ABW	X-ray	2.5
1ABY	X-ray	2.5
1AJ9	X-ray	2.5
1B86	X-ray	2.5
1BAB	X-ray	1.5
1BBB	X-ray	1.5
1BIJ	X-ray	2.5
1BUW	X-ray	1.5
1BZD	X-ray	1.5
1BZ1	X-ray	1.5
1BZZ	X-ray	1.5
1C7B	X-ray	1.5
1C7C	X-ray	1.5
1C7D	X-ray	1.5
1CBL	X-ray	1.5
1CBM	X-ray	1.74
1CH4	X-ray	2.50

ProteinModelPortal	P68871.
SMR	P68871. Positions 2-147.
ModBase	Search...

Protein-protein interaction databases

IntAct	P68871. 24 interactions.
MINT	MINT-5000306.
STRING	P68871.

PTM databases

PhosphoSite	P68871.
-------------	---------

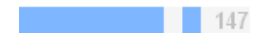
2-D gel databases

SWISS-2DPAGE	P68871.
PMMA-2DPAGE	P68871.
REPRODUCTION-2DPAGE	IP100654755. P68871.
Siena-2DPAGE	P68871.
UCD-2DPAGE	P02023. P68871.

Proteomic databases

PeptideAtlas	P68871.
PRIDE	P68871.

AB/C/D	1-147	[2]
AB/C/D	2-147	[1]



iding resistance to malaria."

Uniprot: contents

Genome annotation databases		Enzyme and pathway databases	
Ensembl	ENST00000335295 ; ENSP	Reactome	REACT_604 . Hemostasis.
GeneID	3043 .	Gene expression databases	
KEGG	hsa:3043 .	ArrayExpress	P68871 .
UCSC	uc001mae.1 . human.		
Organism-specific		Entry information	
CTD		Entry name	HBB_HUMAN
GeneCards		Accession	Primary (citable) accession number: P68871 Secondary accession number(s): A4GX73 ↔ Q9UCP9
H-InvDB		Entry history	Integrated into UniProtKB/Swiss-Prot: July 21, 1986 Last sequence update: January 23, 2007 Last modified: June 28, 2011 This is version 97 of the entry and version 2 of the sequence. [Complete history]
HGNC		Entry status	Reviewed (UniProtKB/Swiss-Prot)
HPA		Annotation program	Chordata Protein Annotation Program 1 hit.
MIM		Disclaimer	Any medical or genetic information present in this entry is provided for research, and is not intended to be used as a substitute for professional medical advice, diagnosis, treatment or care
neXtProt		Relevant documents	
Orphanet		Human chromosome 11 Human chromosome 11: entries, gene names and cross-references to MIM	
PharmGKB		Human entries with polymorphisms or disease mutations List of human entries with polymorphisms or disease mutations	
GenAtlas			
Phylogenomic databases		DrugBank	DB00893 . Iron Dextran.
HOVERGEN	HBG009709 .	NextBio	12048 .
		PMAP-CutDB	P68871 .

Uniprot: search results

UniProt > UniProtKB

Search Blast Align Retrieve ID Mapping *

Search in Protein Knowledgebase (UniProtKB) ☒ Query **hemoglobin B chain** Search Advanced Search » Clear

1 - 25 of 1,243 results for **hemoglobin** AND **B** AND **chain** in UniProtKB sorted by **score** descending

Browse by [taxonomy](#), [keyword](#), [gene ontology](#), [enzyme class](#) or [pathway](#) | Reduce sequence redundancy to **100%, 90% or 50%** | Download

Page 1 of 50 | Next »

Results Customize

- > Show only [reviewed \(825\)](#) ★ (UniProtKB/Swiss-Prot) or [unreviewed \(418\)](#) ★ (UniProtKB/TrEMBL) entries
- > Quote terms: "hemoglobin b"
- > Restrict term "hemoglobin" to [protein family \(24\)](#), [gene name \(3\)](#), [gene ontology \(883\)](#), [keyword \(9\)](#), [protein name \(970\)](#), [web resource \(5\)](#)
- > Restrict term "b" to [author \(608\)](#), [domain \(4\)](#), [gene name \(15\)](#), [gene ontology \(5\)](#), [keyword \(4\)](#), [protein name \(58\)](#), [organism \(1\)](#), [source \(7\)](#), [strain \(5\)](#), [taxonomy \(6\)](#), [tissue \(2\)](#)
- > Restrict term "chain" to [author \(48\)](#), [gene name \(2\)](#), [gene ontology \(7\)](#), [keyword \(7\)](#), [protein name \(740\)](#), [annotation topic \(943\)](#)
- > Restrict term "chain" to [pathway](#)

Accession	Entry name	Status	Protein names	Gene names	Organism	Length
<input type="checkbox"/> P68871	HBB_HUMAN	★	Hemoglobin subunit beta	HBB	Homo sapiens (Human)	147
<input type="checkbox"/> P69905	HBA_HUMAN	★	Hemoglobin subunit alpha	HBA1 HBA2	Homo sapiens (Human)	142
<input type="checkbox"/> P69892	HBG2_HUMAN	★	Hemoglobin subunit gamma-2	HBG2	Homo sapiens (Human)	147
<input type="checkbox"/> P69891	HBG1_HUMAN	★	Hemoglobin subunit gamma-1	HBG1 PRO2979	Homo sapiens (Human)	147
<input type="checkbox"/> P0A592	TRHBN_MYCTU	★	Group 1 truncated hemoglobin glbN	glbN Rv1542c MT1594 MTCY48.23	Mycobacterium tuberculosis	136
<input type="checkbox"/> P02042	HBD_HUMAN	★	Hemoglobin subunit delta	HBD	Homo sapiens (Human)	147

Search in Sequence Clusters (UniRef) **Query** uniprot:(hemoglobin B chain) identity:0.5 Search Advanced Search » Clear

1 - 25 of 240 results for **uniprot:(hemoglobin AND B AND chain) AND identity:0.5** in UniRef

[Browse by taxonomy](#) | [Map to UniProtKB](#) or [UniParc](#) Download

Page 1 of 10

Results Customize

Accession	Status	UniRefCluster name	Size	Members	Organisms	Length	Identity
<input type="checkbox"/> UniRef50_A1B9S1	★	Cluster: TonB-dependent heme/hemoglobin receptor family protein	1	A1B9S1	Paracoccus denitrificans (strain Pd 1222)	686	50%
<input type="checkbox"/> UniRef50_A1U6I3	★	Cluster: TonB-dependent heme/hemoglobin receptor family protein	4	A1U6I3 F2N3G5 C0N4R6 A4XQE8	Marinobacter aquaeolei (strain ATCC 700491 / DSM 11845 / VT8) (Marinobacter hydrocarbonoclasticus (strain DSM 11845)) Pseudomonas stutzeri DSM 4166 Methylophaga thiooxydans DMS010 Pseudomonas mendocina (strain ymp)	657	50%
<input type="checkbox"/> UniRef50_A1WVF8	★	Cluster: TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	1	A1WVF8	Verminephrobacter eiseniae (strain EF01-2)	730	50%
<input type="checkbox"/> UniRef50_A6QC57	★	Cluster: Globin	4	A6QC57 E6WZ29 A6Q1V1 Q30RW0	Sulfurovum sp. (strain NBC37-1) Nitratiraptor salsuginis (strain DSM 16511 / JCM 12458 / E9I37-1) Nitratiraptor sp. (strain SB155-2) Sulfurimonas denitrificans (strain ATCC 33889 / DSM 1251) (Thiomicrospira denitrificans (strain ATCC 33889 / DSM 1251))	173	50%
<input type="checkbox"/> UniRef50_A6UBU8	★	Cluster: TonB-dependent hemoglobin/transferrin/lactoferrin family receptor	3	A6UBU8 A9D265 B9JZN4	Sinorhizobium medicae (strain WSM419) (Ensifer medicae) Hoeftia phototrophica DFL-43 Agrobacterium vitis (strain S4 / ATCC BAA-846) (Rhizobium vitis (strain S4))	734	50%

240 results for uniprot:(hemoglobin AND B AND chain) AND identity:0.5 in UniRef

> Download data [compressed](#) or [uncompressed](#)

Tab-Delimited

Summary information from the result view.

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Excel

Summary information from the result view for MS Excel™.

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FASTA

Sequence data in FASTA format.

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XML

Complete data in XML format.

[[Download](#) (400 KB*) | [Open](#) | [Open first 10](#)]

RDF/XML

Complete data in RDF format.

[[Download](#) (500 KB*) | [Open](#) | [Open first 10](#)]

List

List of accession numbers.

[[Download](#) (5 KB*) | [Open](#) | [Open first 10](#)]

```
>UniRef50_A1B9S1 TonB-dependent heme/hemoglobin receptor family :
MPRHSIRGALLAGTACLTALTFTAPLLAQERAGADSAQSTYVLDQIVLRAGKPKVASEVP
QSVSVVDSRQLEDIAPIHIGEVLATVPGVAGVGSGSFFGQGFNIRFGSSGAAASESGIV
QLIDGEEKYYESYRQGALFVEPDFLRQVEVLRGPGSSTLYGSGALGGVIAMETIEAGDLI
AEGQTFGGRTKLGYASNPDTVLGSAVGWRPAEDFEALAAFAWRKLGDTKADGNTTVRA
NSKTPNLLLKAKKTFGDQYVAFSYQHLEAKGDDQDFNQLEGAQVGLFPGFPGWVGVDITT
RDQATARFIWGNPEDNRYVDLTATLSYTNLTKDVRQGDDEPIMDSLLGERDYRLWKFK
LSNVADLSGAGYDHLTTGAEVLKQDRSSSVSSSHPEAYTRAUAAAYALSELTWGDLTIN
SGLRYEKQORTEPKSSVTVTDDTYDADSVEPQVAAIYRLNDSLVSFVSVAFVNRMPVTDEL
YDSFMGGAPSGDLKDEKGNIELGLSYHSGILTASDEAVVKLTFRNHIDDMIVRTNAP
APMPAYVNIIDRAYLRGGELEATYSVAAWFEFGAASVNVGVDQDGADLDTLPNNRVTLQAI
WQASDALRLGLRSTLADGRDKPNGTHRAGYGVHDVVFATWVPQGGAAAGIEVHVGVNDVTD
RDYTPATWLSGPAPGRNFKLSVSRSF
>UniRef50_A1U6I3 TonB-dependent heme/hemoglobin receptor family :
MANSSPMKQPRRFRNTLWLALMAAPLAHAQPVSLDPIQVTADREADADTVVDAETIERF
QADDLEDVFAQPDVSVGGSNSIAQKVYVRGFDPLLNVSVDGATQAGALFHHSGRLSVE
PELLKQVEVNAGAGRATEGAGALGGSIRFVTKDPDDLRLPGESAGALVKFGSFSNTDGYK
ASGTAFGRLSDNWSTLVSVSQSDHEPFDGSGDRIAGSDARQQLGFAKLVGQLPADQTIK
LSHEVRTDEGERPQRPQWVVSFNRLYELDGRDRTTTLNYGYAPAGNALVDLEATVYHTE
SDIEQNVEDRWGRYFGFSRNIGDLRNTSRFGGHSLTYGVDYREDKVNAGYQEDKRAEQQ
TGEVLGVYLQGDWLWTSRLLFSAGARYDDYRLKDNDQRFSEDEVSPNANLAWEVVDGLT
LKAGYAEAFRGPTTQDAFKLEGSENDPDLEGEKARNTEVGFDYRYETFRLSAEVYRSEIK
DAIADPLLPFRESIYKNIGDLES DGYLISAGYQWQALSAGLSFHSNDAEVDGQPLTVYEH
NLLGNTMGDTWIADLAYRWDRNLEFGWQGRFVEGIDNLDTSVGTIDKPGYGVHDLYLHWL
PTGMEDLRLSLTIKNVGDKQYLAHASNADYQHIEDYEGIVGMPEPGRDIRVGLAMRF
```

Question

Obtain the sequences of “transcription factors” with less than 50% sequence identity.

Find the amino acid sequence of human mitochondrial beta barrel membrane protein VDAC

Dataset for transcription factors

UniProt > UniProtKB

Search in: Protein Knowledgebase (UniProtKB) **Query** transcription factors Search Clear Fields »

Search Blast Align Retrieve ID Mapping *

1 - 25 of 10,963 results for **transcription** AND **factors** in UniProtKB sorted by **score** descending

Browse by taxonomy, keyword, gene ontology, enzyme class or pathway | Reduce sequence redundancy to 100%, 90% or 50% | Customize display **Download...**

> Show only reviewed ★ (UniProtKB/Swiss-Prot) or unreviewed ★ (UniProtKB/TrEMBL) entries
 > Quote terms: "transcription factors"
 > Restrict term "transcription" to protein family, gene ontology, keyword, protein name
 > Restrict term "factors" to protein family, gene ontology, protein name, web resource

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All	Accession	Entry name	Status	Protein names	Gene names	Organism	Length
<input checked="" type="checkbox"/>	P0A4H2	BVGA_BORPE	★	Virulence factors putative positive transcription regulator bvgA	bvgA (BP1878)	Bordetella pertussis	209
<input checked="" type="checkbox"/>	P0A4H3	BVGA_BORBR	★	Virulence factors putative positive transcription regulator bvgA	bvgA (BB2994)	Bordetella bronchiseptica (Alcaligenes bronchisepticus)	209
<input checked="" type="checkbox"/>	P0A4H4	BVGA_BORPA	★	Virulence factors putative positive transcription regulator bvgA	bvgA (BPP3028)	Bordetella parapertussis	209
<input checked="" type="checkbox"/>	P18850	ATF6A_HUMAN	★	Cyclic AMP-dependent transcription factor ATF-6 alpha (cAMP-dependent transcription factor ATF-6 alpha) (Activating transcription factor 6 alpha) (ATF6-alpha) [Cleaved into: Processed cyclic AMP-dependent transcription factor ATF-6 alpha]	ATF6	Homo sapiens (Human)	670
<input checked="" type="checkbox"/>	A6H8Y1	BDP1_HUMAN	★	Transcription factor TFIIIB component B'' homolog (Transcription factor IIIB 150) (TFIIIB150) (Transcription factor-like nuclear regulator)	BDP1 (KIAA1241) (KIAA1689) (TFNR)	Homo sapiens (Human)	2,624
<input checked="" type="checkbox"/>	Q04636	POB3_YEAST	★	FACT complex subunit POB3 (Facilitates chromatin transcription complex subunit POB3)	POB3 (YML069W)	Saccharomyces cerevisiae (Baker's yeast)	552


```

>sp|P18485|1A12_SOLLC 1-aminocyclopropane-1-carboxylate synthase 2 OS=Solanum lycopersicum GN=ACS2 PE=1 SV=2
MGFEIAKTNSILSKLATNEEHGENSPYFDGWKAYDSDPFHPLKNPNQVIMGLAENQLCL
DLIEDWIKRNPKGSIKSEGIKSFKAIANFQDYHGLPEFRKAIKFMKTRGGRVRFDPER
VVMAGGATGANETIIFCLADPGDAFLVPSPIYPFNRDLRWRTGVQLIPIHCESNNFKI
TSKAVKEAYENAQKSNIKVKGLILTNPSNPLGTTLDKDTLKSVLSTNQHNHILVCDEIY
AATVFDTPQFVSAEILDEQEMTYCNKDLVHIVYSLSKDMGLPGFRVGGIYSFNDDVUNC
ARKMSSFGVLSTQTYFLAAMLSDEKFDVDFLRESAMRLGKRHKHFTNGLEVVGKCLKN
NAGLFCWMDLRPLLRETFDSEMSLWRVIINDVKLVNVPSPGSSFECEPGWFRVCFANMDD
GTVDIALARIRRFVGVGKSGDKSSSMEKKQWKKNNLRLSFSKRMVDESVLSPSSPIPP
SPLVR
>sp|P16375|7UP1_DROME Steroid receptor seven-up, isoforms B/C OS=Drosophila melanogaster GN=svp PE=1 SV=1
MCASPSTAPGFFNPRPQSGAELSAFDIGLSRSMGLGVPPHSAWHEPPASLGGLHAASAG
PGTTTGSVATGGGGTTPSSVASQQSAVIKQDLSCPSLNQAGSGHHPGIKEDLSSSLPSAN
GGSAGGHHSGSGSGSGSVNPGHSDMLPLIKGHGQDMLTSIKGQPTGCGSTTPSSQANS
SHSQSSNSGSQIDSKQNIQECVVCQDKSSGKHGQFTCEGCKSFFKRSVRRNLTYSCRGSR
NCPIDQHHRNQCCYCRLLKKCLKMGMRREAVQGRVPPTQPLAGMHGQYQIANGDPMGIA
GFNGHSYLSSYISLLLRAPYPTSTRYGQCMQPNNIMGIDNICELAAARLLFSAVEWAKNIP
FFPELQVTDQVALLRLVWSELVFLNASQCSMPLHVAPLLAAAGLHASPMAADRVAFMH
IRIFQEQVEKLKALHVDSEAESCLKAIVLFTTDACGLSDVTHIESLQEKSOCALEEYCRT
QYPNQPTRFGKLLRLPSLRTVSSQVIEQLFFVRLVGKTPIETLIRDMLLSGNSFSWPYL
PSM
>sp|P16376|7UP2_DROME Steroid receptor seven-up, isoform A OS=Drosophila melanogaster GN=svp PE=2 SV=3
MCASPSTAPGFFNPRPQSGAELSAFDIGLSRSMGLGVPPHSAWHEPPASLGGLHAASAG
PGTTTGSVATGGGGTTPSSVASQQSAVIKQDLSCPSLNQAGSGHHPGIKEDLSSSLPSAN
GGSAGGHHSGSGSGSGSVNPGHSDMLPLIKGHGQDMLTSIKGQPTGCGSTTPSSQANS
SHSQSSNSGSQIDSKQNIQECVVCQDKSSGKHGQFTCEGCKSFFKRSVRRNLTYSCRGSR
NCPIDQHHRNQCCYCRLLKKCLKMGMRREAVQGRVPPTQPLAGMHGQYQIANGDPMGIA
GFNGHSYLSSYISLLLRAPYPTSTRYGQCMQPNNIMGIDNICELAAARLLFSAVEWAKNIP
FFPELQVTDQVALLRLVWSELVFLNASQCSMPLHVAPLLAAAGLHASPMAADRVAFMH
IRIFQEQVEKLKALHVDSEAESCLKAIVLFTTGKLLDILYKDVPAALLTKVSALLGKGSTA
SNDDVLAVVRDHLDELNRQEQESQAQQQAPLHLAAFMNCVAGVEAAVQQAQEQVPTSSA
SASVSAPLVPSAGSAFSSCQAKSAGSEMDLLASLYAQATTPSSGGGDASGHNNSSGLG
ASLPTQSQSGSSSRNLASPLSTSLATAPAPASASAPVPTSSVAQVPVPAPVPTSSA
SSSSLGGGAYQTPSAAAAAAMFHYQTPPRAAFGSAFDMFHHSTPFGVGVGHAHALAHSS
GSGSASFGSPSYRSPYSLAGSRWQL

```

Search in

Protein Knowledgebase (UniProtKB) ▼

Query

mitochondrial beta barrel membrane protein
AND human and VDAC

Search

Advanced Search »

Clear

3 results for **mitochondrial** AND **beta** AND **barrel** AND **membrane** AND **protein** AND **human** AND **VDAC** in UniProtKB sorted by **score** descending

Browse by [taxonomy](#), [keyword](#), [gene ontology](#), [enzyme class](#) or [pathway](#) | Reduce sequence redundancy to [100%](#), [90%](#) or [50%](#) |

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Results [Customize](#)

- > Restrict term "mitochondrion" to [protein family](#) (3), [gene ontology](#) (3), [keyword](#) (3), [location](#) (3), [protein name](#) (3)
- > Restrict term "beta" to [keyword](#) (3), [annotation topic](#) (1)
- > Restrict term "membrane" to [gene ontology](#) (3), [keyword](#) (3), [location](#) (3), [protein name](#) (3)
- > Restrict term "protein" to [gene ontology](#) (3), [keyword](#) (2), [protein name](#) (3)
- > Restrict term "mitochondrion" to [pathway](#)
- > Restrict term "beta" to [pathway](#)
- > Restrict term "membrane" to [pathway](#)
- > Restrict term "protein" to [pathway](#)

	Accession	Entry name	Status	Protein names	Gene names	Organism	Length
<input type="checkbox"/>	P21796	VDAC1_HUMAN	★	Voltage-dependent anion-selective channel pro...	VDAC1 VDAC	Homo sapiens (Human)	283
<input type="checkbox"/>	P45880	VDAC2_HUMAN	★	Voltage-dependent anion-selective channel pro...	VDAC2	Homo sapiens (Human)	294
<input type="checkbox"/>	Q9Y277	VDAC3_HUMAN	★	Voltage-dependent anion-selective channel pro...	VDAC3	Homo sapiens (Human)	283

Sequences

Sequence	Length	Mass (Da)	Tools
<input type="checkbox"/> P21796 [UniParc].	FASTA	283	30,773

Last modified January 23, 2007. Version 2.
Checksum: 89BA3378B04020D5

```

      10      20      30      40      50      60
MAVPPTYADL GKSARDVFTK GYGFGGLIKLD LKTKSENGLE FTSSGSANTE TTKVTGSLET

      70      80      90     100     110     120
KYRWTEYGLT FTEKWNTDNT LGTEITVEDQ LARGLKLTFD SSFSPNTGKK NAKIKTGYKR

     130     140     150     160     170     180
EHINLGCDMD FDIAGPSIRG ALVLGYEGWL AGYQMNFFETA KSRVTQSNFA VGYKTDEFQL

     190     200     210     220     230     240
HTNVNDGTEF GGSIIYQKVNK KLETAVNLAW TAGNSNTRFG IAAKYQIDPD ACFSAKVNNS

     250     260     270     280
SLIGLGYTQT LKPGIKLTLS ALLDGKNVNA GGHKLGLGLE FQA

```

```

>sp|P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2
MAVPPTYADL GKSARDVFTK GYGFGGLIKLD LKTKSENGLE FTSSGSANTE TTKVTGSLET
KYRWTEYGLT FTEKWNTDNT LGTEITVEDQ LARGLKLTFD SSFSPNTGKK NAKIKTGYKR
EHINLGCDMD FDIAGPSIRG ALVLGYEGWL AGYQMNFFETA KSRVTQSNFA VGYKTDEFQL
HTNVNDGTEF GGSIIYQKVNK KLETAVNLAW TAGNSNTRFG IAAKYQIDPD ACFSAKVNNS
SLIGLGYTQT LKPGIKLTLS ALLDGKNVNA GGHKLGLGLE FQA

```