



DIU Génétique et Reproduction

Exercices Alignements

26 Novembre 2021
Philippe Dessen
Institut Gustave Roussy, Villejuif

desse@igr.fr

<http://pdessen.free.fr/KB>

Abdelkader Heddar
Hôpital Bicêtre

abdelkader.heddar@aphp.fr

Exercices alignements

On cherche à savoir si une mutation est conservée dans l'évolution

Ex : gènes humain CLDN6

Ou gène HARS2 (Perrault)

Ou autre ...

Méthodologie

Extraction de la séquence humaine dans Uniprot

BLAST contre Uniprot ou sélection sur un terme

Sélection seulement dans SwissProt (expertisées)

Transfert des séquences en format FASTA

Alignement multiple avec seaview4

<http://pdessen.free.fr/links.html>

Site de UniProt : <http://www.uniprot.org/>

Interrogation avec CLDN6 human

UniProt

UniProtKB cldn6 human Advanced

BLAST Align Retrieve/ID mapping Peptide search

UniProtKB results

About UniProtKB

Filter byⁱ

- Reviewed (1) Swiss-Prot
- Unreviewed (6) TrEMBL

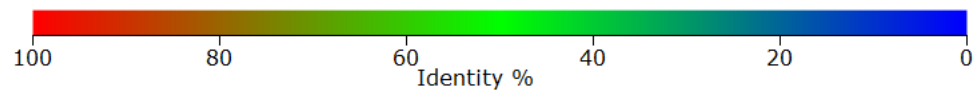
Popular

BLAST Align Download Add to basket Columns

1 to 7 of 7

☐	Entry	Entry name		Protein names	Gene names	Organism
☐	P56747	CLD6_HUMAN		Claudin-6	CLDN6 UNQ757/PRO1488	Homo sapiens (Human)
☐	Q0GH64	Q0GH64_MOUSE		Claudin	Cldn6 mCG_8070	Mus musculus (Mouse)

Selection P56747 + BLAST



Filter byⁱ

[← Edit and resubmit](#) Order by:

Reviewed (13)
Swiss-Prot

Unreviewed
(237)
TrEMBL

Proteomes (182)

Popular
organisms

Overview

[Show all 250](#)

Entry	Protein names	Match hit	
		100	2
P56747	Claudin-6 (Homo sapiens)		
G70080			

Filtrage sur 13 sequences de SwissProt

[← Edit and resubmit](#) Order by:

Overview

[Show all 13](#)

		100	200	300	
P56747	Claudin-6 (Homo sapiens)				100.0%
Q9Z262	Claudin-6 (Mus musculus)				87.7%
Q9Z0S7	Claudin-9 (Mus musculus)				71.4%
O95484	Claudin-9 (Homo sapiens)				70.9%
O35054	Claudin-4 (Mus musculus)				60.0%
O6BRI6					59.1%

BLAST Align Download Add to basket Columns 1 to 13 of 13 Show 25

Entry	Alignment	Info	Status
☐ Query: sp P5674		AECEF5153189FA788F28A46DA	
☐ P56747 CLD6	View alignment	E-value: 2.8e-156 Score: 1,142 Ident.: 100.0%	

☐ Download selected (0) ☒ Download all (13)
 Format: FASTA
☒ Compressed ☐ Uncompressed
[Preview first 10ⁱ](#) [Go](#)

Editer à l'écran en non compressé
Edition des 13 séquences complètes

>sp|P56747|CLD6_HUMAN Claudin-6 OS=Homo sapiens GN=CLDN6 PE=1
SV=2

MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTG
QMCKVYDSLLALPQDLQAARALCVIALLVALLVYLAGAKCTTCVEEKDSKARLVLT
SGIVFVISGVLTLPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGL
LCCTCPSGGSQGPSHYMARYSTSAPAISRGPSSEYPTKNYV

>sp|Q9Z262|CLD6_MOUSE Claudin-6 OS=Mus musculus GN=Cldn6 PE=1
SV=1

MASTGLQILGIVLTLLGWVNALVSCALPMWKVTAFIGNSIVVAQMVEGLWMSCVVQSTG
QMCKVYDSLLALPQDLQAARALCVVTLIVLLGLLVYLAGAKCTTCVEDRNSKSRLVLI
SGIIFVISGVLTLPVCWTAHSIIQDFYNPLVADAQKRELGASLYLGWAASGLLLLGGGL
LCCACSSGGTQGPRHYMACYSTSVPHSRGPSEYPTKNYV

>sp|Q9Z0S7|CLD9_MOUSE Claudin-9 OS=Mus musculus GN=Cldn9 PE=2
SV=2

MASTGLELLGMTLAVLGWLGTLVSCALPLWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTG
QMCKVYDSLLALPQDLQAARALCVVALLLALLGLLVAITGAQCTTCVEDEGAKARIVLT
AGVLLLLSGILVLIPVCWTAHAIIQDFYNPLVAEALKRELGASLYLGWAAAALLMLGGGL
LCCTCPPSHFERPRGPLGYSIPSRSGASGLDKRDYV

...

Sauver dans un fichier texte

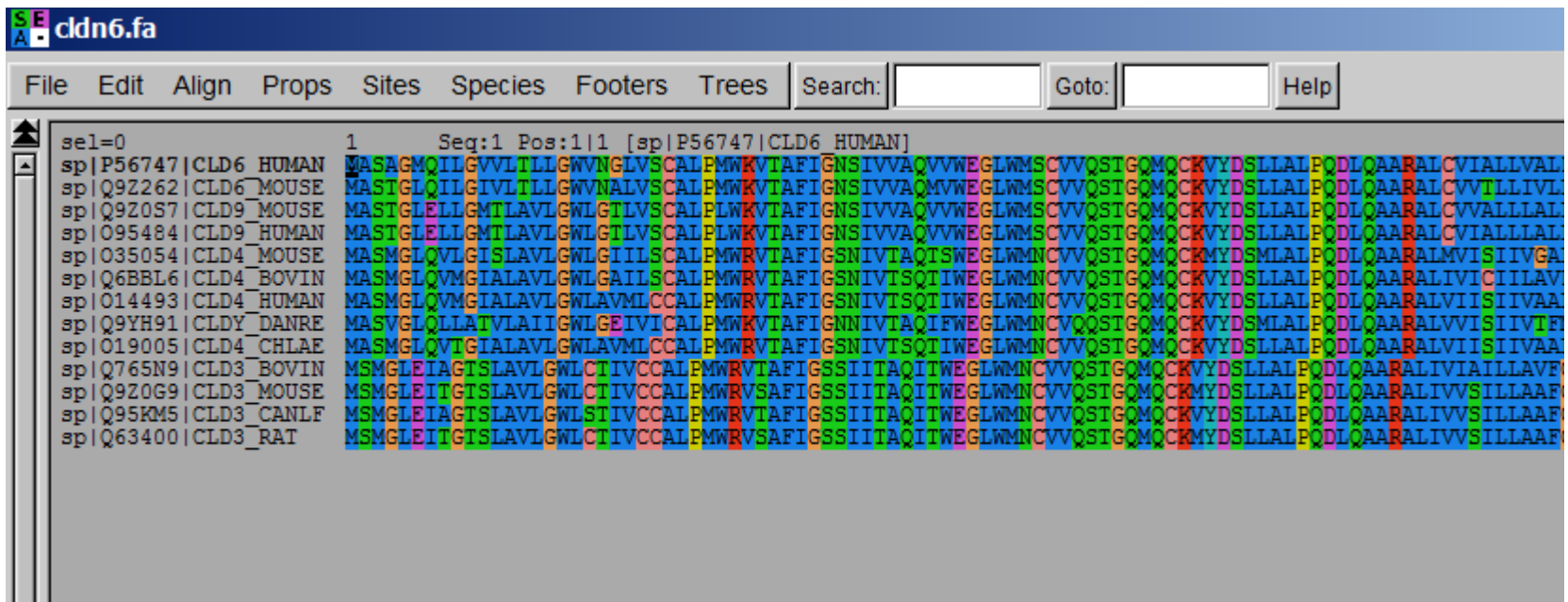
Donnez le nom de cldn6.fa

<http://doua.prabi.fr/templates/software>

Download SeaView pour Windows

Pour utiliser :

Utiliser le help pour plus d'informations



All

File Edit Align Props Sites Species Footers Trees Search: Goto: Help

sel=0 1 Seq:1 Pos:1|1 [sp|P56747|CLD6 HUMAN] 12

sp|P56747|CLD6 HUMAN MASAGMQLIGVLLTLLGWNGLVSCALPMKVTAFIGNSVVAVVVEGLWMSCVVQSTGQMCKVYDSLALFPDLQAARALCVIALLVALFGLLVYLAGAKCTTCEEEKDSKARLVLTSGVIG

sp|Q9Z262|CLD6_MOUSE MASTGLELLIGVLLTLLGWNGLVSCALPMKVTAFIGNSVVAVVVEGLWMSCVVQSTGQMCKVYDSLALFPDLQAARALCVVILLVLLGLLVYLAGAKCTTCEVEDRNSKSRVLVLTSGI

sp|Q9Z0S7|CLD9_MOUSE MASTGLELLIGVLLTLLGWNGLVSCALPMKVTAFIGNSVVAVVVEGLWMSCVVQSTGQMCKVYDSLALFPDLQAARALCVVALLLALLGLLVAITGAQCTTCEVEDEGAKARIVLTAGV

sp|Q95484|CLD9_HUMAN MASTGLELLIGVLLTLLGWNGLVSCALPMKVTAFIGNSVVAVVVEGLWMSCVVQSTGQMCKVYDSLALFPDLQAARALCVIALLVALLGLLVAITGAQCTTCEVEDEGAKARIVLTAGV

sp|Q30504|CLD4_MOUSE MASMGLQVIGISLAVLGLWLGIIILSCALPMKVTAFIGNSVVIAQTSTWEGWLMNCVVQSTGQMCKMYDSLALFPDLQAARALMVISTIVGALGMLLVSVVGGKCTNCMEDETVKAKITITAGAV

sp|Q6BBL6|CLD4_BOVIN MASMGLQVVGIALAVLGLWLGAILSCALPMKVTAFIGNSVIVTSQTIWEGWLMNCVVQSTGQMCKVYDSLALFPDLQAARALVIVCIILAVFGVLLSVVGGKCTNCVDDSSKAKITIVAGV

sp|Q14493|CLD4_HUMAN MASMGLQVVGIALAVLGLWLGAILSCALPMKVTAFIGNSVIVTSQTIWEGWLMNCVVQSTGQMCKVYDSLALFPDLQAARALVISTIVVAALGVLLSVVGGKCTNCLEDESAKAKITIVAGV

sp|Q9YH91|CLDY_DANRE MASVGLLLATVLAIIIGLGEIVICALPMKVTAFIGNNVIVTAQITWEGWLMNCVVQSTGQMCKVYDSLALFPDLQAARALVVISITIVFMGVFTIAGGKCTNCIEDQDAKAKVVAAGV

sp|Q19005|CLD4_CHLAE MASMGLQVIGIALAVLGLWLGAILSCALPMKVTAFIGNSVIVTSQTIWEGWLMNCVVQSTGQMCKVYDSLALFPDLQAARALVISTIVVAALGVLLSVVGGKCTNCLEDESAKAKITIVAGV

sp|Q765N9|CLD3_BOVIN -MSMGLEIAGTSLAVLGLWLTIVCCALPMKVTAFIGNSVIITAQITWEGWLMNCVVQSTGQMCKVYDSLALFPDLQAARALVIAILLAVFGVLLVAGVQCTNCVQDDTAKAKITIVAGV

sp|Q9Z069|CLD3_MOUSE -MSMGLEIITGSLAVLGLWLTIVCCALPMKVTAFIGNSVIITAQITWEGWLMNCVVQSTGQMCKMYDSLALFPDLQAARALIVVISILLAAFGLLVALVGAQCTNCVQDETAKAKITIVAGV

sp|Q95KM5|CLD3_CANLF -MSMGLEIAGTSLAVLGLWLTIVCCALPMKVTAFIGNSVIITAQITWEGWLMNCVVQSTGQMCKVYDSLALFPDLQAARALIVVISILLAAFGLLVALVGAQCTNCVQDDTAKAKITIVAGV

sp|Q63400|CLD3_RAT -MSMGLEIITGSLAVLGLWLTIVCCALPMKVTAFIGNSVIITAQITWEGWLMNCVVQSTGQMCKMYDSLALFPDLQAARALIVVISILLAAFGLLVALVGAQCTNCVQDETAKAKITIVAGV

Mutation R209Q sur CLDN6

```

sel=0
sp|P56747|CLD6_HUMAN 144 Seq:1 Pos:211|209 [sp|P56747|CLD6_HUMAN] 22
sp|Q9Z262|CLD6_MOUSE IQDFYNPLVDAQKRELGASLYLGWAASGLLLLGGGLLCCACSSGGTQGP RHMACYST--SVPH--SRGPSEYPTKNYV
sp|Q9Z0S7|CLD9_MOUSE IQDFYNPLVAEALKRELGASLYLGWAAAALLMLGGGLLCCTCPPSHFERPRGPRLGYSI--PS---RSGASGLDKRDYV
sp|O95484|CLD9_HUMAN IQDFYNPLVAEALKRELGASLYLGWAAAALLMLGGGLLCCTCPPPQVERPRGPRLGYSI--PS---RSGASGLDKRDYV
sp|O35054|CLD4_MOUSE IRDFYNPMVASGQKREMGASLYVGWAAASGLLLLGGGLLCCSCPPRSNDK--PYSAKYSAARSVPASN-----YV
sp|Q6BBL6|CLD4_BOVIN IRDFYNPLVASGQKREMGASLYVGWAAAGLLILGGALLCFNCPPR--NDK--PYSAKYSAARSAPASN-----YV
sp|O14493|CLD4_HUMAN IQDFYNPLVASGQKREMGASLYVGWAAASGLLLLGGGLLCCNCPPR--TDK--PYSAKYSAARSAAASN-----YV
sp|Q9YH91|CLDY_DANRE IKDFYNPTLSDAQKRELGASLFIWGCASGLLLLGGALLCCQCPKNE--G--RAYSVKYSAAPRSAPGAYV-----YV
sp|O19005|CLD4_CHLAE IQDFYNPLVASGQKREMGASLYVGWAAASGLLLLGGGLLCCNCPPR--TDK--PYSAKYSAARSAAASN-----YV
sp|Q765N9|CLD3_BOVIN IRDFYNPLVPEAQKREMGAAALYVGWAAASALQLLGGALLCCSCPPRD--NY--ARTKIVYSAPRSTGPGVTSTGTAYDRKDYV
sp|Q9Z0G9|CLD3_MOUSE IRDFYNPLVPEAQKREMGAGLYVGWAAAALQLLGGALLCCSCPPRD--KY--APTKILYSAPRSTGPGTGTGTAYDRKDYV
sp|Q95KM5|CLD3_CANLF IRDFYNPLVPDAQKREMGAGLYVGWAAAALQLLGGALLCCSCPPRD--KKY--APTKIVYSAPRSAGPGTS--TAYDRKDYV
sp|Q63400|CLD3_RAT IRDFYNPLVPEAQKREMG TGLYVGWAAAALQLLGGALLCCSCPPRE--KY--APTKILYSAPRSTGPGTGTGTAYDRKDYV

```

Séquences plus exhaustives de UniProt (39)

UniProtKB results

filter byⁱ

Unreviewed (39)
TrEMBL

Popular organisms

- Mouse (2)
- Bovine (1)
- Human (1)

BLAST Align Download Add to basket Columns

Entry Entry

Q6PBE4

Download selected (39)
Download all (39)

Format: FASTA (canonical)

Compressed Uncompressed

Preview first 10ⁱ

Go

Gene names Org

by the results on this page

cldn6.1 cldn6, Xen
TEgg067d18.1-001, trop
TGas124n16.1-001 (We
frog trop

```

sel=0      108      Seq:1 Pos:211|209 [sp|P56747|CLD6_HUMAN]
sp|P56747|CLD6_HUMAN VEEKDSKARLVLTSGIVFVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGGSGQPSHYMARYSTSAFA--ISRGPSEYPTKNYV
sp|Q92262|CLD6_MOUSE VEDRNSKSRLVLTSGIIFVISGVLTLIPVCWTAHSIIQDFYNPLVADAQKRELGAASLYLGWAASGLLLLGGGLLCCACSSGGTQGPFRHYMACYSTSV--F-HSRGPSEYPTKNYV
sp|Q920S7|CLD9_MOUSE VEDEGAKARIVLTAGVLLLLSGILVLIIVCWTAHAIIRDFYNPLVAEALKRELGAASLYLGWAAAALLMLGGGLLCCTCPPSHFERPRGPRGLGYSI----F-SRSGASGLDKRDYV
sp|Q95484|CLD9_HUMAN VEDEGAKARIVLTAGVILLLAGILVLIIVCWTAHAIIRDFYNPLVAEALKRELGAASLYLGWAAAALLMLGGGLLCCTCPPFPQVERPRGPRGLGYSI----F-SRSGASGLDKRDYV
sp|O35054|CLD4_MOUSE MEDETVKAKIMITAGAVFIVASMLIMVPSWTAHNVIIRDFYNPMVASGQKREMGASLYVGWAASGLLLLGGGLLCCSCPPRSN-DK-PYSAKYSAARSVPASN-----YV
sp|Q6BBL6|CLD4_BOVIN VDDESSKAKIMIVAGVVFLLAGLLVMVPSWTANNVIIRDFYNPLVASGQKREMGASLYVGWAAAGLLILGGALLCFNCPPR-N-DK-PYSAKYSAARSAPASN-----YV
sp|O14493|CLD4_HUMAN LEDESAKAKTMIVAGVVFLLAGLMVIVPSWTAHNIIQDFYNPLVASGQKREMGASLYVGWAASGLLLLGGGLLCCNCPPR-T-DK-PYSAKYSAARSAAAASN-----YV
sp|Q9YH91|CLDY_DANRE IEDQDAKAKVVAAGVFFLVGGILCLIPVCWSANSVIIRDFYNPLVDAQKRELGAALYIGWAASTLMLLGGALLCCQCPKNE---GRAYSVKYSAPRSPAGAY---V-----
sp|O19005|CLD4_CHLAE LEDESAKAKTMIVAGVVFLLAGLLVIVPSWTAHNIIQDFYNPLVASGQKREMGASLYVGWAASGLLLLGGGLLCCNCPPR-T-DK-PYSAKYSAARSAAAASN-----YV
sp|Q765N9|CLD3_BOVIN VQDDTAKAKITIVAGVLFLLAALLTLVPVSWSANTIIIRDFYNPLVPEAQKREMGALYVGWAAASALQLLGGALLCCSCPPRD--NYARTKIVYSAPRSTGFPVTSTGTAYDRKDYV
sp|Q920G9|CLD3_MOUSE VQDDTAKAKITIVAGVLFLLAALLTLVPVSWSANTIIIRDFYNPLVPEAQKREMGALYVGWAAASALQLLGGALLCCSCPPRD--KYAPTILYYSAPRSTGPGTGTGTAYDRKDYV
sp|Q95KM5|CLD3_CANLF VQDDTAKAKITIVAGVLFLLAALLTLVPVSWSANTIIIRDFYNPLVPEAQKREMGALYVGWAAASALQLLGGALLCCSCPPRD--KYAPTILYYSAPRSTGPGTGTGTAYDRKDYV
sp|Q63400|CLD3_RAT VQDDTAKAKITIVAGVLFLLAALLTLVPVSWSANTIIIRDFYNPLVPEAQKREMGALYVGWAAASALQLLGGALLCCSCPPRE--KYAPTILYYSAPRSTGPGTGTGTAYDRKDYV
tr|Q6PBE4|Q6PBE4_XEN IEDENTKAKVSMISGIVFVSGILMLIPVCWSANSIIIRDFYNPLVPEAQKRELGAALYIGWAAASGLLLMGGALLCCSCPKKD---DNHYSARYTAATSNPRSD----YPSKNYV
tr|Q0GH64|Q0GH64_MOU VEDRNSKSRLVLTSGIIFVISGVLTLIPVCWTAHSIIQDFYNPLVADAQKRELGAASLYLGWAASGLLLLGGGLLCCACSSGGTQGPFRHYMACYSTSV--F-HSRGPSEYPTKNYV
tr|H2QAE9|H2QAE9_XEN IEDENTKAKVSMISGIVFVSGILMLIPVCWSANSIIIRDFYNPLVPEAQKRELGAALYIGWAAASGLLLMGGALLCCSCPKKD---DNHYSARYTAATSNPRSD----YPSKDYV
tr|B4F7F0|B4F7F0_RAT VEDRNSKSRLVLTSGIIFVISGVLTLIPICWTAHAIIRDFYNPLVADAQKRELGAASLYLGWAASGLLLIIGGLLCCACSSGGTQGPFRHYVARYSSFPV--F-HSRGPSEYPTKNYV
tr|Q810I9|Q810I9_MOU VEDRNSKSRLVLTSGIIFVISGVLTLIPVCWTAHSIIQDFYNPLVADAQKRELGAASLYLGWAASGLLLLGGGLLCCACSSGGTQGPFRHYMACYSTSV--F-HSRGPSEYPTKNYV
tr|C3VML2|C3VML2_PIG VEDKDKTAKRLVLTSGIIFVLSGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGRSGQSSHYMARYSASAPHT--ASRGPSEYPTKNYV
tr|H2NPW9|H2NPW9_PON VEEKDSKARLVLTSGIVFVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCPLGGRSGPSHYMARYSTSAFA--ISRGPSEYPTKNYV
tr|L7N0I6|L7N0I6_CAN VEDKDSKARLVLTSGIIFVISGVLTLIPVCWTAHAIIRDFYNPLVSDAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGGGRSSSHYMARYSASAAHG--TSQGPSEYPTKNYV
tr|M3W2L0|M3W2L0_FEL VEDKDSKARLVLTSGIIFVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGGARGSNHYMARYSASAAHG--TSQGPSEYPTKNYV
tr|H0WYS4|H0WYS4_OTO VEDKDSKARLVLTSGIIFVISGVLTLIPICWTAHAIIRDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGGSGQPSHYMARYSASAPHT--TSRGPSEYPTKNYV
tr|G1QD87|G1QD87_MY VEDKDSKARLVLTSGIIFVISGVLTLIPICWTAHAIIRDFYNPLVAEPQKRELGAASLYLGWAASGLLLLGGGLLCCYTCFSGGSRGSSHYMARYSASAPHT--ISRGPSEYPTKNYV
tr|A0A096ND68|A0A096 VEEKDSKARLVLTSGIVFVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGVSRGSPHYMARYSTSAFA--ISRGPSEYPTKNYV
tr|F7DSA3|F7DSA3_MAC VEEKDSKARLVLTSGIVFVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGGSRGSPHYMARYSTSAFA--ISRGPSEYPTKNYV
tr|G1TD67|G1TD67_RAB VEDKDSKARLVLTSGITFIISGILTLIPVCWTAHTIIQDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGGSRGSSHYMARYSASGPNA--ASRGPSEYPTKNYV
tr|G3QR09|G3QR09_GOR VEEKDSKARLVLTSGIVFVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGGSGQPSHYMARYSTSAFA--ISRGPSEYPTKNYV
tr|G1REE3|G1REE3_NOM VEEKDSKARLVLTSGIVFVFSGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGRSGRSPHYMARYSTSAFA--ISRGPSEYPTKNYV
tr|A0A0D9SBX5|A0A0D9 VEEKDSKARLVLTSGIVFVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGGSRGSSHYMARYSTSAFA--ISRGPSEYPTKNYV
tr|F6SPI8|F6SPI8_HOR VEDKDSKARLVLTSGIIFGISAVLTLPICWTAHAIIRDFYNPLVAEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGGSRSSSHYMARYSASAPHT--TSRGPSEYPTKNYV
tr|G3N0D8|G3N0D8_BOV VEDKDSKARLVLTSGIIFVISGVLTLIPVCWTAHTIIQDFYNPLVPEAQKRELGAASLYLGWAASGLLLLGGGLLCCTCFSGGSRSSSHYMARYSVSAPHT--ASRGPSEYPTKNYV
tr|A0A151PDY9|A0A151 VEDEASKARVAVGSGALFAFAGLLCLVPVCWTAHAIIRDFYNPLVDAQKRELGAALYVGWAAAGLLGLGGGLLCCSCPKAD----RTYSAHYTAAASHPRSD----YPSKNYV
tr|H0W7W3|H0W7W3_CAV VEDKDSKARLVLTSGIIFVISGVLTLIPVCWTAHTIIQDFYNPLVPEAQKRELGAASLYLGWAASGLLLLGGGLLCCYTCFSGGSRGSSHYMARYSTSAFA--ISRGPSEYPTKNYV
tr|I3MSG6|I3MSG6_ICT VEDQDSKARLVLTSGIIFVISGVLTLIPVCWTAHTIIQDFYNPLVAEAQKRELGAASLYLGWAACGLLMLGGGLLCCTCFSGEARSSSHYMARYSASAPHT--PSRGPSEYPTKNYV

```

Exemple de HARS2

The screenshot shows the UniProtKB search results for the query 'hars2'. The browser address bar shows the URL 'www.uniprot.org/uniprot/?query=HARS2&sort=score'. The search bar contains 'hars2' and a 'Search' button. Below the search bar, there are navigation links: 'BLAST', 'Align', 'Retrieve/ID mapping', 'Peptide search', 'Help', and 'Contact'. The main heading is 'UniProtKB results'. To the right of the heading are links for 'About UniProtKB' and a 'Basket' icon. Below the heading, there are filter options: 'Filter by' with 'Reviewed (8) Swiss-Prot' and 'Unreviewed (64) TrEMBL'. There are also action buttons: 'BLAST', 'Align', 'Download', and 'Add to basket'. A pagination bar shows '1 to 25 of 72' and a 'Show 25' dropdown. A message box says 'Did you mean ars2 (1,749) ?'. Below this is a table of results.

Entry	Entry name	Protein names	Gene names	Orga
☐ P49590	SYHM_HUMAN	Probable histidine--tRNA ligase, mi...	HARS2 HARSL, HARSR, HO3	Homoc... (Hum...

Sauvegarde des 8 sequences de SwissProt

UniProtKB results

[? About UniProtKB](#)

[Basket](#)

Filter byⁱ

 Reviewed^x
(8)
Swiss-Prot

Popular organisms

Human (3)

Bovine (2)

Mouse (2)

PONAB (1)

Search terms

Filter "hars2" as:

[gene name \(7\)](#)

[BLAST](#)

[Align](#)

[Download](#)

[Add to basket](#)

[Columns](#)

1 to 8 of 8

Show 25

Did you mean

Entry Entry

Entry Entry

☒ P49590 SYHM

☐ Q8TEA8 DTD1_HUMAN

☐ Q9DD18 DTD1_MOUSE

☐ Q2T9V8 DTD1_BOVIN

☒ Download selected (4)

☐ Download all (8)

Format: FASTA (canonical)

☐ Compressed ☒ Uncompressed

[Preview first 10ⁱ](#)

Go

names Organism Le

4 result(s) selected. (Clear select)

2 HARSL, Homo sapiens (Human)

ligase, mi...

DTD1 C20orf88, Homo sapiens (Human)

Dtd1 Hars2 Mus musculus (Mouse)

DTD1 HARS2 Bos taurus (Bovine)

Selection des sequences SYHM et sauvegarde en format FASTA

Natural
variantⁱVAR_069532

200

L → V in PRLTS2;

Natural
variantⁱVAR_069533

368

V → L in PRLTS2;

>sp|P49590|SYHM_HUMAN Probable histidine--tRNA ligase, mitochondrial OS=Homo sapiens GN=HARS2 PE=1 SV=1
MPLLGLLPRRAWASLLSQLLRPPCASCTGAVRCQSQVAEAVLTSQLKAHQEKPNFIIKTP
KGTRDLSPOQHMVVREKILDVLISCFKRHGAKGMDTPAFELKETLTEKYGEDSGLMYDLKD
QGGELLSLRYDLTVPPFARYLAMNKVKMKRYHVGKVRRESPTIVQGRYREFCQCDFDIA
GQFDPMIPDAECLKIMCEILSGLQLGDFLIKVNDRRIVDGMFAVCGVPESKFRAICSSID
KLDKMAWKDVRHEMVVKKGLAPEVADRIGDYVQCHGGVSLVEQMFQDPRLSQNKQALEGL
GDLKLLFEYLTTLFGIADKISFDLSLARGLDYYTGVIYEAVLLQTPTQAGEEPLNVGSVAA
GGRYDGLVGMFDPKGHKVPCVGLSIGVERIFYIVEQRMKTKGEKVRTTETQVFVATPQKN
FLQERLKLIAELWDSGIKAEMLYKNNPKLLTQLHYCESTGIPLVVIIGEQLKEGVKIR
SVASREEVAIKRENFVAEIQKRLSES

>sp|Q99KK9|SYHM_MOUSE Probable histidine--tRNA ligase, mitochondrial OS=Mus musculus GN=Hars2 PE=1 SV=1
MPHLGPLRRRAWAALLGQLLRPPSTVCTRGCQSQVAKAVLTSEQLKSHQEKPNFVIKVPK
GTRDLSPOQHMVVREKILDKIISCFKRHGAKGLDTPAFELKEMLTEKYEDNFGLMYDLKDQ
GGELLSLRYDLTVPPFARYLAMNKLKMKRYQVGKVRRESPTIVQGRYREFCQCDFDIAG
EFDPMIPDAECLRIMCEILSGLQLGDFLIKVNDRRVVDGIFAVCGVPESKLRTICSSMDK
LDKMSWEGVRHEMVAKKGLAPEVADRIGDFVQYHGGISLVEDLFDKDPRLSQSQLALQGLG
DLKLLFEYLRLLFGIADKISLDLSLARGLDYYTGVIYEAVLLESQAQKETLSVGSVAA
GRYDNLVAQFDPKGHHVPCVGLSIGVERIFYLVEQKMKMSGEKVRTTETQVFVATPQKNF
LQERLKLIAELWDAGIKAEMLYKNNPKLLTQLHYCEKADIPLMVIIGEQRNEGVKILRS
VASREEVTINRESLVAEIQKRLSES

>sp|Q5R5E5|SYHM_PONAB Probable histidine--tRNA ligase, mitochondrial OS=Pongo abelii GN=HARS2 PE=2 SV=1
MHLLGLLPRRAWASLLSQLLRPPWASCTGAVRCQSQVAEAVLTSQLKAHQEKPNFIIKTP
KGTRDLSPOQHMVVREKILDVLISCFKRHGAKGMDTPAFELKETLTEKYGEDSGLMYDLKD
QGGELLSLRYDLTVPPFARYLAMNKVKMKRYHVGKVRRESPTIVQGRYREFCQCDFDIA
GQFDPMIPDAECLKIMCEILSGLQLGDFLIKVNDRRIVDGMFAVCGVPESKFRAICSSID
KLDKMAWKDVRHEMVVKKGLAPEVADRIGDYVQCHGGVSLVEQMFQDPRLSQNKQALEGL
GDLKLLFEYLTTLFGIADKISFDLSLARGLDYYTGVIYEAVLLQTPTQAGEEPLNVGSVAA
GGRYDGLVGMFDPKGHKVPCVGLSIGVERIFYIVEQRMKTKGEKVRTTETQVFVATPQKN
FLQERLKLIAELWNSGIKAEMLYKNNPKLLTQLHYCESTGIPLVVIIGEQLKEGVKIR
SVASREEVAIKRENLVAEIQKRLSES

>sp|A5D7V9|SYHM_BOVIN Probable histidine--tRNA ligase, mitochondrial OS=Bos taurus GN=HARS2 PE=2 SV=1
MPQLGLLPGRAWTVLLGLLRPPPGALCIRAVRSHSQVAEALFASQLKPHQEKSNFTIKTP
KGTRDLSPOQHMVVREKILDVVVSCFKRHGAKGLDTPAFELKEILTEKYGEDSGLIYDLKD
QGGELLSLRYDLTVPPFARYLAMNKVKMKRYHVGKVRRESPTIVQGRYREFYQCDFDIA
GQFDPMIPDAECLKIMCEILSGLHLGDFLIKVSDRRILDGIFAVCGVPESKFHAICSSVD
KLDKISWKDVRHEMVVKKGLAPEVADRIGDYVQCHGGISLVEQMFQDPRLSQNKQALEGL
GDLKLLFEYLTTLFGVAEKVSFDLSLARGLDYYTGVIYEAVLLQTPVHAEELPLNMGSVAA
GGRYDGLVGMFDPRGHKVPCVGLSIGVERIFSIVEQRIKTFGEKIRTTETQVFVATPQKN
FLQERLKLIAELWDAGIKAELMYKNNPKLLPQLHYCENMGIPLVVIIGEQLKEGVKILR
SVASREEVAIKRENLVAEIQKRLSES

Position 200 L-> V

hars2.fa

File Edit Align Props Sites Species Footers Trees Search: Goto: Help

sel=0 199 Seq:1 Pos:201|200 [sp|P49590|SYHM HUMAN]

sp P49590 SYHM_HUMAN	E	I	L	S	G	L	Q	L	G	D	F	L	I	K	V	N	D	R	R	I	V	D	G	M	F	A	V	C	G	V	P	E	S	K	F	R	A	I	C	S	S	I	D	K	L	D	K	N
sp Q99KK9 SYHM_MOUSE	E	I	L	S	G	L	Q	L	G	D	F	L	I	K	V	N	D	R	R	V	V	D	G	I	F	A	V	C	G	V	P	E	S	K	L	R	T	I	C	S	S	M	D	K	L	D	K	N
sp Q5R5E5 SYHM_PONAB	E	I	L	S	G	L	Q	L	G	D	F	L	I	K	V	N	D	R	R	I	V	D	G	M	F	A	V	C	G	V	P	E	S	K	F	R	A	I	C	S	S	I	D	K	L	D	K	N
sp A5D7V9 SYHM_BOVIN	E	I	L	S	G	L	H	L	G	D	F	L	I	K	V	S	D	R	R	I	L	D	G	I	F	A	V	C	G	V	P	E	S	K	F	H	A	I	C	S	S	V	D	K	L	D	K	N

Position 368 V > L

hars2.fa

File Edit Align Props Sites Species Footers Trees Search: Goto: Help

sel=0 358 Seq:1 Pos:369|368 [sp|P49590|SYHM HUMAN]

sp P49590 SYHM_HUMAN	S	V	A	A	G	G	R	Y	D	G	L	V	G	M	F	D	P	K	G	H	K	V	P	C	V	G	L	S	I	G	V	E	R	I	F	Y	I	V	E	Q	R	M	K	T	K	G	E	K	V	R	T
sp Q99KK9 SYHM_MOUSE	S	V	A	A	G	G	R	Y	D	N	L	V	A	Q	F	D	P	K	G	H	H	V	P	C	V	G	L	S	I	G	V	E	R	I	F	Y	L	V	E	Q	K	M	K	S	G	E	K	V	R	T	
sp Q5R5E5 SYHM_PONAB	S	V	A	A	G	G	R	Y	D	G	L	V	G	M	F	D	P	K	G	H	K	V	P	C	V	G	L	S	I	G	V	E	R	I	F	Y	I	V	E	Q	R	M	K	T	K	G	E	K	V	R	T
sp A5D7V9 SYHM_BOVIN	S	V	A	A	G	G	R	Y	D	G	L	V	G	M	F	D	P	R	G	H	K	V	P	C	V	G	L	S	I	G	V	E	R	I	F	S	I	V	E	Q	R	I	K	T	F	G	E	K	I	R	T