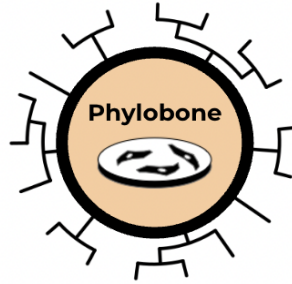




## User Manual

# Phylobone Database



<https://www.phylobone.com>

Fontcuberta-Rigo M, Nakamura M, Puigbo P. **2023**. Phylobone: a comprehensive database of bone extracellular matrix proteins in human and model organisms. **In preparation**.

\* Comments and questions to [pepuav@utu.fi](mailto:pepuav@utu.fi)

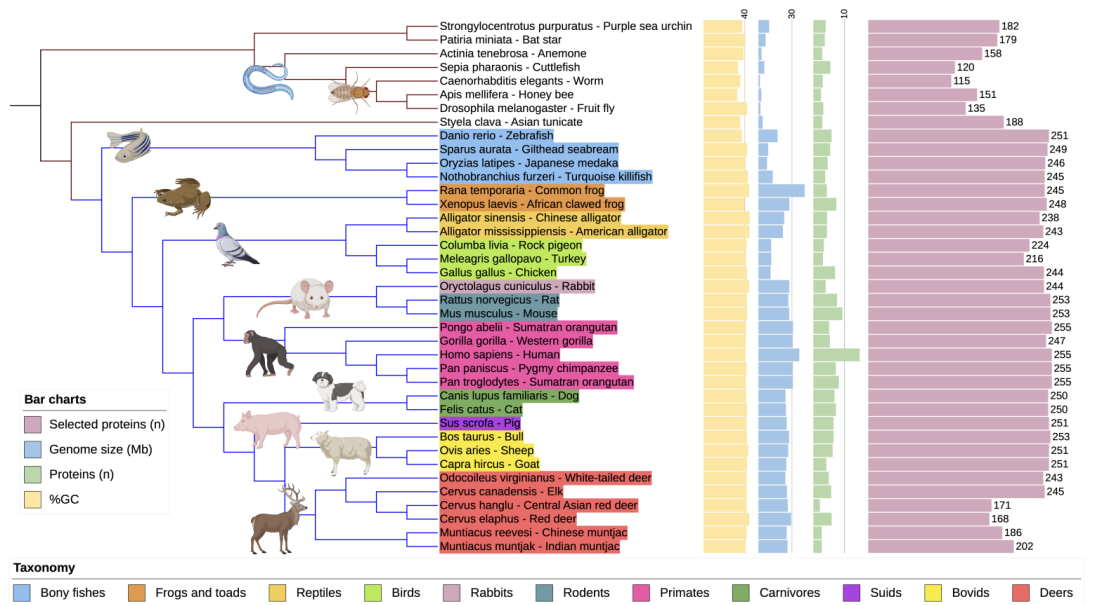
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## 1. [Phylobone database](#)

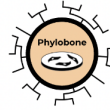
The Phylobone database is freely accessible at <https://phylobone.com>. The current version of the dataset includes 8,615 putative bone ECM proteins from 39 species of vertebrates and invertebrates, and categorized in 255 protein groups. Each protein of the database is annotated with basic information, that includes its name, organism, a general protein description, a list of gene ontologies (GO) associated, protein-protein interactions (PPI), functional domains, metabolic pathways and drugs.



## 2. [Proteins](#)

All proteins are accessible from the main web-page of the database. On the top of the page, there are links to access phyletic patterns, drugs and diseases, selected species, domains, protein protein interactions data, and proteins listed in alphabetical order. The entire phylobone database can be downloaded [here](#).

The main matrix contains: PBID (Phylobone identification code, and link to the protein's information page); Unprot (Uniprot identification code); Gene (Gene name --alternative names can be obtained by clicking on the phylobone code); Organism (in this case *Homo sapiens*, but the database includes other species); Sequences (links to download seed sequences and sequences from selected species); Alignments (multiple sequence alignments); Tree (phylogenetic trees); Views (to visualized alignments and phylogenetic trees online)



# Database

[Phyletic patterns](#) | [Drugs and diseases](#) | [Selected species](#) | [Domains&PPI](#) | [Proteins \(A-z\)](#)

[How to cite Phylobone](#)

PBID	Uniprot	Name	Gene	Organism	Sequences	Alignments	Tree	View
PB0001	<a href="#">P02765</a>	<a href="#">Alpha-2-HS-glycoprotein</a>	<a href="#">AHSG</a>	<i>Homo sapiens</i>	Seed Selected	Mafft: Aln Cleaned Aln	PhyML: Tree	Mafft: Aln Cleaned Aln PhyML: Tree
PB0002	<a href="#">P61769</a>	<a href="#">Beta-2-microglobulin</a>	<a href="#">B2M</a>	<i>Homo sapiens</i>	Seed Selected	Mafft: Aln Cleaned Aln	PhyML: Tree	Mafft: Aln Cleaned Aln PhyML: Tree
PB0003	<a href="#">P00734</a>	<a href="#">Prothrombin</a>	<a href="#">F2</a>	<i>Homo sapiens</i>	Seed Selected	Mafft: Aln Cleaned Aln	PhyML: Tree	Mafft: Aln Cleaned Aln PhyML: Tree
PB0004	<a href="#">P08493</a>	<a href="#">Matrix Gla protein</a>	<a href="#">MGP</a>	<i>Homo sapiens</i>	Seed Selected	Mafft: Aln Cleaned Aln	PhyML: Tree	Mafft: Aln Cleaned Aln PhyML: Tree
PB0005	<a href="#">P21810</a>	<a href="#">Biglycan</a>	<a href="#">BGN</a>	<i>Homo sapiens</i>	Seed Selected	Mafft: Aln Cleaned Aln	PhyML: Tree	Mafft: Aln Cleaned Aln PhyML: Tree

## [Proteins \(A-z\)](#)

List of proteins in alphabetical order, based on the name of the protein in *Homo sapiens*.

PBID	Uniprot	Name	Gene	Organism
PB0204	<a href="#">P08253</a>	72 kDa type IV collagenase	<a href="#">MMP2</a>	<i>Homo sapiens</i>
PB0072	<a href="#">Q8IUX7</a>	Adipocyte enhancer-binding protein 1	<a href="#">AEBP1</a>	<i>Homo sapiens</i>
PB0020	<a href="#">Q9BRR6</a>	ADP-dependent glucokinase	<a href="#">ADPGK</a>	<i>Homo sapiens</i>
PB0068	<a href="#">P16112</a>	Aggrecan core protein	<a href="#">ACAN</a>	<i>Homo sapiens</i>
PB0142	<a href="#">Q00468</a>	Agtrin	<a href="#">AGRN</a>	<i>Homo sapiens</i>
PB0092	<a href="#">P05186</a>	Alkaline phosphatase, tissue-nonspecific isozyme	<a href="#">ALPL</a>	<i>Homo sapiens</i>
PB0175	<a href="#">P01009</a>	Alpha-1-antitrypsin	<a href="#">SERPINA1</a>	<i>Homo sapiens</i>
PB0165	<a href="#">P08697</a>	Alpha-2-antiplasmin	<a href="#">SERPINF2</a>	<i>Homo sapiens</i>
PB0001	<a href="#">P02765</a>	Alpha-2-HS-glycoprotein	<a href="#">AHSG</a>	<i>Homo sapiens</i>
PB0222	<a href="#">P01023</a>	Alpha-2-macroglobulin	<a href="#">A2M</a>	<i>Homo sapiens</i>
PB0055	<a href="#">P12814</a>	Alpha-actinin-1	<a href="#">ACTN1</a>	<i>Homo sapiens</i>
PB0121	<a href="#">Q75443</a>	Alpha-tectorin	<a href="#">TECTA</a>	<i>Homo sapiens</i>
PB0250	<a href="#">Q99217</a>	Amelogenin, X isoform	<a href="#">AMELX</a>	<i>Homo sapiens</i>
PB0223	<a href="#">P05067</a>	Amyloid-beta precursor protein	<a href="#">APP</a>	<i>Homo sapiens</i>
PB0158	<a href="#">Q95841</a>	Angiopoietin-related protein 1	<a href="#">ANGPTL1</a>	<i>Homo sapiens</i>
PB0059	<a href="#">P04083</a>	Annexin A1	<a href="#">ANXA1</a>	<i>Homo sapiens</i>
PB0033	<a href="#">P07355</a>	Annexin A2	<a href="#">ANXA2</a>	<i>Homo sapiens</i>
PB0211	<a href="#">P08758</a>	Annexin A5	<a href="#">ANXA5</a>	<i>Homo sapiens</i>



# Proteins information

Each protein has been analyzed functionally and phylogenetically. This information is accessible by clicking on the Phylobone's Identification code (e.g. [PB0001](#)). This information contains alternative names of the protein, brief description, gene ontology information, links to main websites, sequences, multiple sequence alignments, phylogenetic trees and direct access to run blast searches for the identification of additional proteins.



## PB0001 DATABASE

[Click here to access PB0001 phyletic profile](#)

PBID	Uniprot	Name	Gene	Alternative	Organism	Uniprot Description
PB0001	P02765	Alpha-2-HS-glycoprotein	A2HS, AHS, AHPRI, FETUA, HSGA	A2HS, AHS, AHPRI, FETUA, HSGA	<i>Homo sapiens</i>	Promotes endocytosis, possesses opsonic and influences the mineral phase of bone. It affinity for calcium and barium ions.

Domains	Gene Ontology
	GO:0004864 (enables) endopeptidase inhibitor activity
	GO:0004862 (enables) cysteine-type endopeptidase inhibitor activity
	GO:0019210 (enables) kinase inhibitor activity
	GO:0001501 (involved in) skeletal system development
	GO:0001503 (involved in) ossification
	GO:0006907 (involved in) pinocytosis
	GO:0006953 (involved in) acute-phase response
	GO:0010921 (involved in) negative regulation of endopeptidase activity
	GO:0030500 (involved in) regulation of bone mineralization
	GO:0030502 (involved in) negative regulation of bone mineralization
	GO:0046642 (involved in) negative regulation of insulin receptor signaling pathway
	GO:0050727 (involved in) regulation of inflammatory response
	GO:0050766 (involved in) positive regulation of phagocytosis
	GO:0031012 (is active in) extracellular matrix
	GO:0005578 (located in) extracellular region
	GO:0005615 (located in) extracellular space
	GO:0005788 (located in) endoplasmic reticulum lumen
	GO:0005794 (located in) Golgi apparatus
	GO:0031032 (located in) platelet alpha granule lumen
	GO:0034724 (located in) secretory granule lumen
	GO:0062023 (located in) collagen-containing extracellular matrix
	GO:0073062 (located in) extracellular exosome
	GO:0072662 (located in) blood microparticle

External Links	Description
Intact	Open source database system and analysis tools for molecular interaction data.
Protein Atlas	An open access resource for human proteins
InterPro (new plan)	InterPro provides functional analysis of proteins by classifying them into families and predicting domains an important sites.

**Seed proteins (Human and Zebrafish)**

```
>sp|P02765|FETUA_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens OX=9606 GN=AHS2 PE
SV=2
MKSLLVLLCLAQMGCHSAHPGGLIYQPCDDPTEEAALVAIDYINQMLFNGVKHTL
NQIDEVWVQPSGELFEEIDLETTCVLDLTPFVAVCSVQLKEAVEDGDFQQLK
LDRKSVYAKCSSESSAEEDVYVQCDPLADLNDVTVAAKALAAAFAGNNSGF
QLERISRAQVLPFFVFTVFTVSGTCKAKETAAKLLAEQYGFCAFLSEELGG
AEAVVTCVFTVQPSVQSGEGEAVVFPVVDPAFFPFLGAPLFAAGSPDSEHLV
LAAPFQHLRAHDIYLRFTFNGVLSGSEVSPKRTKTVVQVGVAAAVVFPVPCFG
RIRHFV
>tr|A5MW15|A5MW15_DABNE Alpha-2-HS-glycoprotein 2 OS=Danio rerio OX=7955 GN=ahsg2
SV=1
MTEVQHTYIIQQTKLHSLHSLVHSLQBYRFLFLSMQLMATSIVLGLLITGSMAGQVQTV
NLACDFPEAEALAAQDYLNAQHTHGVYILNRIDGNVVSFPHEDDTLHEDLPLET
TCVLDLTPFVAVCSVQLKEAVEDGDFQQLKLEKLVVAVCSVQLKEAVEDGDFQQLK
LMDTDLGLLEALDIFQNTLTKTALPEIGRHTSQTIVSGVQFAYATLITGCSYV
VDGDSIQHTVAIHLGLLSSAGLIDVDCDFIFNPTQVTHESNATHVQQLLHAFTF
GFQHTFVHSLRHKLTAHLEPAGSLISSESTSEAFVAVLQDAVYKREVAAPFEPA
VDARVETPTLVDFIALSCPKKHFH
```

**Selected proteins from model organisms**

```
>NP_001613.2 alpha-2-HS-glycoprotein isoform 2 preproprotein (Homo sapiens)
MKSLLVLLCLAQMGCHSAHPGGLIYQPCDDPTEEAALVAIDYINQMLFNGVKHTLNDKVKWV
QPSGELFEEIDLETTCVLDLTPFVAVCSVQLKEAVEDGDFQQLKLEKLVVAVCSVQLKEAVEDGDFQ
DVRVSCDCLLALNDVTVAAKALAAAFAGNNSGFQLERISRAQVLPFFVFTVFTVSGTCKAKETAAK
KEATEAKCNLLAEQYGFCAFLSEELGGAEAVVTCVFTVQPSVQSGEGEAVVFPVVDPAFFPFLGAPL
FAGSPDSEHLVLAAPFQHLRAHDIYLRFTFNGVLSGSEVSPKRTKTVVQVGVAAAVVFPVPCFGA
AGVFPVPCGIRIRHFV
>XP_030257367.1 alpha-2-HS-glycoprotein-like (Sparus aurata)
MKSLLVLLCLAQMGCHSAHPGGLIYQPCDDPTEEAALVAIDYINQMLFNGVKHTLNDKVKWV
QPSGELFEEIDLETTCVLDLTPFVAVCSVQLKEAVEDGDFQQLKLEKLVVAVCSVQLKEAVEDGDFQ
DVRVSCDCLLALNDVTVAAKALAAAFAGNNSGFQLERISRAQVLPFFVFTVFTVSGTCKAKETAAK
KEATEAKCNLLAEQYGFCAFLSEELGGAEAVVTCVFTVQPSVQSGEGEAVVFPVVDPAFFPFLGAPL
FAGSPDSEHLVLAAPFQHLRAHDIYLRFTFNGVLSGSEVSPKRTKTVVQVGVAAAVVFPVPCFGA
AGVFPVPCGIRIRHFV
>XP_004978952.1 alpha-2-HS-glycoprotein (Oryzias latipes)
MKSLLVLLCLAQMGCHSAHPGGLIYQPCDDPTEEAALVAIDYINQMLFNGVKHTLNDKVKWV
QPSGELFEEIDLETTCVLDLTPFVAVCSVQLKEAVEDGDFQQLKLEKLVVAVCSVQLKEAVEDGDFQ
DVRVSCDCLLALNDVTVAAKALAAAFAGNNSGFQLERISRAQVLPFFVFTVFTVSGTCKAKETAAK
KEATEAKCNLLAEQYGFCAFLSEELGGAEAVVTCVFTVQPSVQSGEGEAVVFPVVDPAFFPFLGAPL
FAGSPDSEHLVLAAPFQHLRAHDIYLRFTFNGVLSGSEVSPKRTKTVVQVGVAAAVVFPVPCFGA
AGVFPVPCGIRIRHFV
```

**Mafft alignment of selected proteins**

```
-----MNFLLG-----
-----FALVLLGLLGMAGQSN
VL-----RLCGDFVEEALVAGDFLNGQHHGYTALNRIDVHLLTPFVAVCS
TYFLELLETTCVHVDLTPFVAVCSVQLKEAVEDGDFQQLKLEKLVVAVCSVQLKEAVEDGDFQ
-ESEED--LCLGCPPELLNHTAALDFVHSLSKLNNETE-NVTTLVQVGRMSQVVE
GGHYIVETVVEANCLN-----DTCTFLNHTMARGICIAFGQT-----DPVAVC
KMFYSLIPVDSNST--VAEAFALP-----PLVHVHSGG-----AVKV
DAVAVDELPALPTPTESSAGDSAVVFLSVKRAAE--APAPAPAGTDLV-----A
VYFPCGIRIRF--
>XP_422764.2 alpha-2-HS-glycoprotein [Gallus gallus]
-----MKSLLV-----
-----AFLLVQLPIHRAAPA
APFP-----PLGCDPFEIAAAEFVYINGSHHDTFALNRIDVHLLTPFVAVCS
LLELLELLETTCVHVDLTPFVAVCSVQLKEAVEDGDFQQLKLEKLVVAVCSVQLKEAVEDGDFQ
```

**BMGE Cleaned alignment of selected proteins**

```
>NP_001613.2 alpha-2-HS-glycoprotein isoform 2 preproprotein (Homo sapiens)
MKSLLVLLCLAQMGCHSAHPGGLIYQPCDDPTEEAALVAIDYINQMLFNGVKHTLNDKVKWV
QPSGELFEEIDLETTCVLDLTPFVAVCSVQLKEAVEDGDFQQLKLEKLVVAVCSVQLKEAVEDGDFQ
DVRVSCDCLLALNDVTVAAKALAAAFAGNNSGFQLERISRAQVLPFFVFTVFTVSGTCKAKETAAK
KEATEAKCNLLAEQYGFCAFLSEELGGAEAVVTCVFTVQPSVQSGEGEAVVFPVVDPAFFPFLGAPL
FAGSPDSEHLVLAAPFQHLRAHDIYLRFTFNGVLSGSEVSPKRTKTVVQVGVAAAVVFPVPCFGA
AGVFPVPCGIRIRHFV
>XP_030257367.1 alpha-2-HS-glycoprotein-like (Sparus aurata)
MKSLLVLLCLAQMGCHSAHPGGLIYQPCDDPTEEAALVAIDYINQMLFNGVKHTLNDKVKWV
QPSGELFEEIDLETTCVLDLTPFVAVCSVQLKEAVEDGDFQQLKLEKLVVAVCSVQLKEAVEDGDFQ
DVRVSCDCLLALNDVTVAAKALAAAFAGNNSGFQLERISRAQVLPFFVFTVFTVSGTCKAKETAAK
KEATEAKCNLLAEQYGFCAFLSEELGGAEAVVTCVFTVQPSVQSGEGEAVVFPVVDPAFFPFLGAPL
FAGSPDSEHLVLAAPFQHLRAHDIYLRFTFNGVLSGSEVSPKRTKTVVQVGVAAAVVFPVPCFGA
AGVFPVPCGIRIRHFV
>XP_004978952.1 alpha-2-HS-glycoprotein (Oryzias latipes)
MKSLLVLLCLAQMGCHSAHPGGLIYQPCDDPTEEAALVAIDYINQMLFNGVKHTLNDKVKWV
QPSGELFEEIDLETTCVLDLTPFVAVCSVQLKEAVEDGDFQQLKLEKLVVAVCSVQLKEAVEDGDFQ
DVRVSCDCLLALNDVTVAAKALAAAFAGNNSGFQLERISRAQVLPFFVFTVFTVSGTCKAKETAAK
KEATEAKCNLLAEQYGFCAFLSEELGGAEAVVTCVFTVQPSVQSGEGEAVVFPVVDPAFFPFLGAPL
FAGSPDSEHLVLAAPFQHLRAHDIYLRFTFNGVLSGSEVSPKRTKTVVQVGVAAAVVFPVPCFGA
AGVFPVPCGIRIRHFV
```

**PhyML tree of selected proteins**

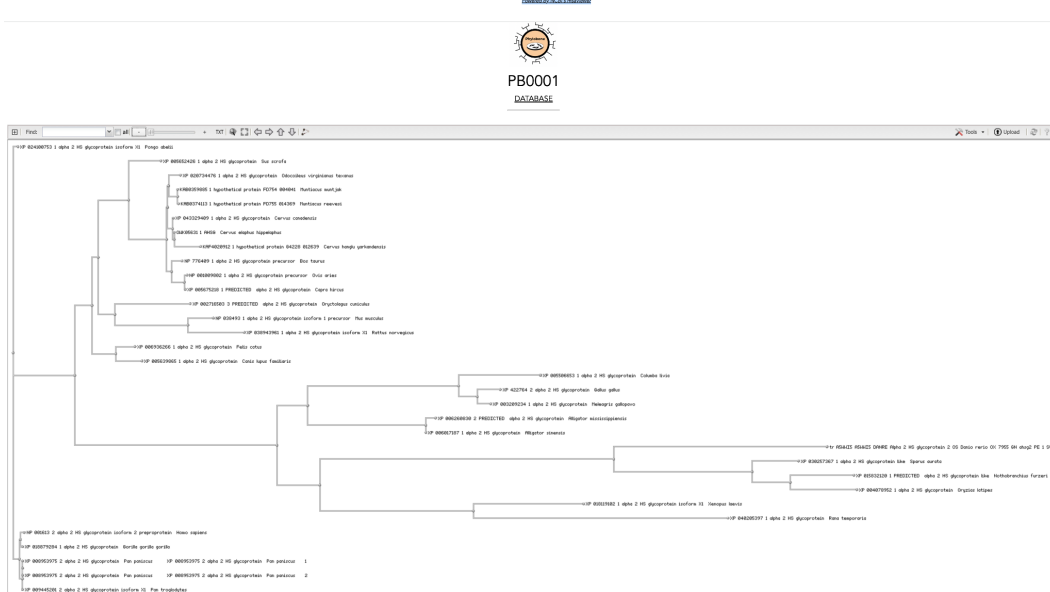
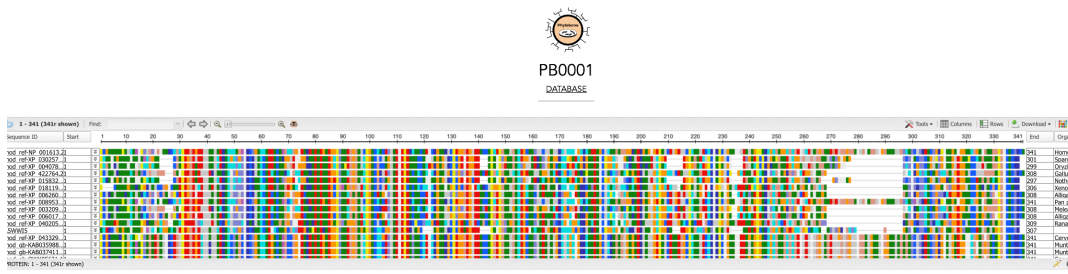
```
(XP_024100753.1_alpha_2_HS_glycoprotein_isoform_X1_Fongo_abelii:0.01552672,
(((XP_005652426.1_alpha_2_HS_glycoprotein_Sus_acrofa:0.1633711,
(((XP_020734476.1_alpha_2_HS_glycoprotein_Odocoileus_virginianus_texasus:0.03830429,
(KAB0359885.1_hypothetical_protein_FD704_04041_Muntiacus_muntjak:0.00000001,KAB0374
113.1_hypothetical_protein_FD755_01436_Muntiacus_reevesi:0.00301664):0.02882942):0.
00137481,(XP_043329409.1_alpha_2_HS_glycoprotein_Cervus_canadensis:0.0039539,
(OMX05631.1_AMS0_Cervus_elaphus_hippelaphus:0.00000001,KAF4020912.1_hypothetical_pro
tein_04228_012639_Cervus_hanglu_yarkandensis:0.0841243):0.00599127):0.01574857):0.00
319384,(NF_0784009.1_alpha_2_HS_glycoprotein_precursor_Bos_taurus:0.03415369,
(NF_001009802.1_alpha_2_HS_glycoprotein_precursor_Ovis_aries:0.00924531,XP_005675218
1_PREDICTED_alpha_2_HS_glycoprotein_Capra_hircus:0.00322999):0.04126299):0.0157392
3):0.12135288):0.09735347,
(XP_002116503.3_PREDICTED_alpha_2_HS_glycoprotein_Oryctolagus_cuniculus:0.24120103,
(NF_038493.1_alpha_2_HS_glycoprotein_isoform_1_precursor_Mus_musculus:0.08139858,XP_
03849361.1_alpha_2_HS_glycoprotein_isoform_X1_Rattus_norvegicus:0.18085352):0.23375
627):0.05334284):0.01948621,
(XP_006936266.1_alpha_2_HS_glycoprotein_Felis_catus:0.06142035,XP_005639865.1_alpha
_2_HS_glycoprotein_Canis_lupus_familiaris:0.00354966):0.07570811):0.05538136,
(((XP_005506653.1_alpha_2_HS_glycoprotein_Columba_livia:0.26248893,
(XP_422764.2_alpha_2_HS_glycoprotein_Gallus_gallus:0.07368313,XP_003209234.1_alpha_2
```

[BLAST to find more sequences](#)



## View of sequences and phylogenetic analyses

Multiple sequence alignments and phylogenetic trees can be downloaded to a local computer or visualized on a web browser (powered by [msviewer](#)).



### 3. Phyletic patterns

Patterns of phyletic distribution of each protein in 39 species of vertebrates and invertebrates are available.



#### Phyletic patterns

[Species](#) | [Drops and diseases](#) | [Proteins](#) | [Domains&PPI](#) | [Proteins \(A-z\)](#)

[How to cite Phylobone](#)

- 01 - *Homo sapiens* 02 - *Pan troglodytes* 03 - *Pan paniscus* 04 - *Gorilla gorilla* 05 - *Pongo abelii* 06 - *Crotopus curvicaudus*
- 07 - *Mus musculus* 08 - *Rattus norvegicus* 09 - *Felis catus* 10 - *Canis lupus familiaris* 11 - *Cervus elaphus* 12 - *Cervus bairdii*
- 13 - *Cervus canadensis* 14 - *Odocoileus virginianus* 15 - *Muntiacus muntjak* 16 - *Martiacus reevesi* 17 - *Capra hircus* 18 - *Ovis aries*
- 19 - *Bos taurus* 20 - *Sus scrofa* 21 - *Alligator mississippiensis* 22 - *Alligator sinensis* 23 - *Columba livia* 24 - *Gallus gallus*
- 25 - *Hedymeles malloccus* 26 - *Scotus leucis* 27 - *Buteo hemerodromus* 28 - *Buteo swainsoni* 29 - *Bubo holohaelothus* 30 - *Chrysis latipes*
- 31 - *Spodopogon auratus* 32 - *Sphecia clayi* 33 - *Patonia minata* 34 - *Strongylocentrotus purpuratus* 35 - *Chasmodon melanocephalus*
- 36 - *Apis mellifera* 37 - *Caenorhabditis elegans* 38 - *Zeyia charanisi* 39 - *Actinia tenebrosa*

PBID	Phyletic pattern
PB0001	01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
PB0002	01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
PB0003	01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
PB0004	01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
PB0005	01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
PB0006	01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
PB0007	01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
PB0008	01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
PB0009	01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
PB0010	01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39



Species are color grouped taxonomically. More details of these patterns can be obtained by clicking on the Phylobone's identification code (e.g. [PB0001](#)).



PB0001


PHYLETIC PATTERNS

[Click here to access PB0001 functional information](#)

Taxonomic	Groups	Taxid	Species	Common Name	Proteins
Vertebrates	Primates	9606	Homo sapiens	Human	NP_001613.2
Vertebrates	Primates	9598	Pan troglodytes	Chimp	XP_002445201.2
Vertebrates	Primates	9597	Pan paniscus	Chimp	XP_008953275.2
Vertebrates	Primates	9593	Gorilla gorilla	Gorilla	XP_018879284.1
Vertebrates	Primates	1827	Pongo abelii	Orangutan	XP_024100753.1
Vertebrates	Rabbits & hares	9986	Oryctolagus cuniculus	Rabbit	XP_002716503.3
Vertebrates	Rodents	10090	Mus musculus	Mouse	NP_038493.1
Vertebrates	Rodents	10116	Rattus norvegicus	Rat	XP_038943961.1
Vertebrates	Carnivores	9685	Felis catus	Cat	XP_006936266.1
Vertebrates	Carnivores	9615	Canis lupus familiaris	Dog	XP_005639845.1
Vertebrates	Even-toed ungulates	9860	Canis lupus familiaris	Cervidae	CW505631.1
Vertebrates	Even-toed ungulates	2100816	Canis lupus familiaris	Cervidae	KAF4020912.1
Vertebrates	Even-toed ungulates	1574408	Canis lupus familiaris	Cervidae	XP_043329409.1
Vertebrates	Even-toed ungulates	9974	Odocoileus virginianus	Cervidae	XP_020734476.1
Vertebrates	Even-toed ungulates	9888	Muntiacus muntjak	Cervidae	KAB0359885.1
Vertebrates	Even-toed ungulates	9886	Muntiacus reevesi	Cervidae	KAB0374113.1
Vertebrates	Even-toed ungulates	9925	Capra hircus	Goat	XP_005475218.1
Vertebrates	Even-toed ungulates	9940	Ovis aries	Sheep	NP_001009802.1
Vertebrates	Even-toed ungulates	9913	Bos taurus	Bull	NP_774409.1
Vertebrates	Even-toed ungulates	9943	Sus scrofa	Pig	XP_005652426.1
Vertebrates	Reptiles	8496	Alligator mississippiensis	Reptile	XP_006260830.2
Vertebrates	Reptiles	38654	Alligator sinensis	Reptile	XP_006017187.1
Vertebrates	Birds	8932	Columba livia	Pigeon	XP_005506453.1
Vertebrates	Birds	9031	Gallus gallus	Chicken	XP_422744.2
Vertebrates	Birds	9103	Meleagris gallopavo	Turkey	XP_003209234.1
Vertebrates	Frogs and toads	8355	Xenopus laevis	Frog	XP_018119102.1
Vertebrates	Frogs and toads	8407	Rana temporaria	Frog	XP_049005297.1
Vertebrates	Bony fishes	7955	Danio rerio	Zebrafish	AS5555
Vertebrates	Bony fishes	105023	Nothobranchius furzeri	African killifish	XP_015832120.1
Vertebrates	Bony fishes	8090	Oryzias latipes	Japanese rice fish	XP_004078952.1
Vertebrates	Bony fishes	8175	Sparus aurata	Orata	XP_030257367.1
Chordata	Tunicata	7725	Styela clava	Asian tunicate	
Invertebrates	Echinoderm	46514	Patina miniata	Starfish	
Invertebrates	Echinoderm	7668	Strongylocentrotus purpuratus	Sea urchin	
Invertebrates	Insects	7227	Drosophila melanogaster	Fruit fly	
Invertebrates	Insects	7460	Apis mellifera	Honey bee	
Invertebrates	Nematoda	6239	Caenorhabditis elegans	Worm	
Invertebrates	Cephalopoda	158019	Sepia pharaonis	Cuttlefish	
Invertebrates	Cnidaria	4105	Actinia tenebrosa	Anemone	

## 4. [Drugs and diseases](#)

Information gathered from KEGG and DrugBank databases on diseases, drugs and metabolic pathways.



Database

[Phyletic patterns](#) | [Proteins](#) | [Selected species](#) | [Domains&PPI](#) | [Proteins \(A-Z\)](#)

[How to cite Phylobone](#)


PBID	Uniprot	KEGG	Drugbank	Disease	Pathway
FS0001	P02765	hsa.197	DB09130 DB01593 DB14487 DB14533 DB14548	H00303	
FS0002	P61769	hsa.567	DB02740 DB09130 DB04646 DB11130	H00845 H01303 H02434	hsa04512 hsa05163 hsa05166 hsa05168 hsa05169 hsa05170
			DB02711 DB07734 DB07016 DB07521 DB04850 DB07091 DB04845 DB07088 DB07131 DB07095 DB07115 DB07097 DB04819 DB04910 DB04824 DB04849 DB04729 DB07600 DB04721 DB04722 DB02207 DB07277 DB07350 DB02549 DB02548 DB07105 DB04970 DB07366 DB04824 DB07125 DB04842 DB07499 DB07461 DB07120 DB07190 DB07241 DB07353 DB07558 DB07089 DB04844 DB04841 DB07718 DB03136 DB02223 DB07460 DB07376 DB04841 DB04846 DB04845 DB04845 DB04841 DB07934 DB04842 DB07459 DB07460 DB07458 DB13151 DB00025 DB11146 DB06228 DB01756 DB07083 DB00006 DB00100 DB13152 DB09204 DB09130 DB01159 DB04811 DB04976 DB04819 DB07027 DB07133 DB07143 DB07005 DB04945 DB00005 DB01225 DB05214 DB07381 DB03841 DB07278 DB01747 DB04604 DB09332 DB00001 DB13978 DB04126 DB00170 DB08828 DB13979 DB04604 DB04945 DB04928 DB07145 DB07522 DB07522 DB07645 DB07976 DB04859 DB04853 DB04945 DB07229 DB08181 DB04951 DB07444 DB01248 DB12598 DB01123 DB04786 DB05777 DB04677 DB09107 DB14738 DB04898 DB15173 DB14487 DB04810		
FS0004	P01893	hsa.4256	DB01323	H00000	
FS0005	P21810	hsa.633		H02187	
FS0006	P02946	hsa.6678	DB11093 DB11348 DB14481	H00506	
FS0007	O15335	hsa.1101			hsa04151 hsa05100 hsa05152 hsa05185
FS0008	P02743	hsa.325	DB02710 DB07580 DB09130 DB01651 DB01593 DB14487		

PBID: PB0077  
 Uniprot: P04114  
 Uniprot URL: <https://rest.uniprot.org/uniprotkb/P04114.txt>  
 Drugbank: DB11886; Infigratinib.  
 Drugbank: DB00877; Sirolimus.  
 Drugbank: DB14533; Zinc chloride.  
 Drugbank: DB14548; Zinc sulfate, unspecified form.  
 KEGG: hsa1338  
 +drug: D08946 | Mipomersen sodium (USAN); Kynamro (TN)  
 +disease: H00155 | Familial hypercholesterolemia; Autosomal dominant hypercholesterolaemia  
 +disease: H01270 | Familial hypobetalipoproteinemia  
 +disease: H02505 | Atherosclerosis  
 +pathway: hsa04975 | Fat digestion and absorption - Homo sapiens (human)  
 +pathway: hsa04977 | Vitamin digestion and absorption - Homo sapiens (human)  
 +pathway: hsa04979 | Cholesterol metabolism - Homo sapiens (human)  
 +pathway: hsa05417 | Lipid and atherosclerosis - Homo sapiens (human)  
 //



### 5. Selected species

List of species included in the Phylobone database and link to protein sequences of each species. This page contains taxids and links to NCBI's taxonomy and Wikipedia web pages.



**Selected species**  
Phylectic patterns | Drugs and diseases | Proteins | Domains&PPI | Proteins (A-Z)  
How to cite Phylobone

Species	Common Name	Taxonomic	Groups	N. Proteins
00 - Homo sapiens	Human	Vertebrates	Primates (taxid:9606)	489 (in 255 groups)
01 - Pan troglodytes	Chimp	Vertebrates	Primates (taxid:9598)	256 (in 255 groups)
02 - Pan paniscus	Chimp	Vertebrates	Primates (taxid:9597)	257 (in 255 groups)
03 - Gorilla gorilla	Gorilla	Vertebrates	Primates (taxid:9593)	247 (in 247 groups)
04 - Pongo abelii	Orangutan	Vertebrates	Primates (taxid:9587)	255 (in 255 groups)
05 - Oryctolagus cuniculus	Rabbit	Vertebrates	Rabbits & hares (taxid:10086)	244 (in 244 groups)
06 - Mus musculus	Mouse	Vertebrates	Rodents (taxid:10090)	253 (in 253 groups)
07 - Rattus norvegicus	Rat	Vertebrates	Rodents (taxid:10116)	253 (in 253 groups)
08 - Felis catus	Cat	Vertebrates	Carnivores (taxid:9485)	250 (in 250 groups)
09 - Canis lupus familiaris	Dog	Vertebrates	Carnivores (taxid:9615)	249 (in 249 groups)
10 - Canis lupus	Cervidae	Vertebrates	Even-toed ungulates (taxid:9860)	167 (in 167 groups)
11 - Canis lupus	Cervidae	Vertebrates	Even-toed ungulates (taxid:1200816)	172 (in 172 groups)
12 - Canis canadensis	Cervidae	Vertebrates	Even-toed ungulates (taxid:150408)	249 (in 249 groups)
13 - Odocoileus virginianus	Cervidae	Vertebrates	Even-toed ungulates (taxid:9913)	243 (in 243 groups)
14 - Muntiacus muntjak	Cervidae	Vertebrates	Even-toed ungulates (taxid:9988)	202 (in 202 groups)
15 - Muntiacus reevesi	Cervidae	Vertebrates	Even-toed ungulates (taxid:9986)	186 (in 186 groups)
16 - Capra hircus	Goat	Vertebrates	Even-toed ungulates (taxid:9920)	251 (in 251 groups)
17 - Ovis aries	Sheep	Vertebrates	Even-toed ungulates (taxid:9940)	251 (in 251 groups)
18 - Bos taurus	Bull	Vertebrates	Even-toed ungulates (taxid:9913)	252 (in 252 groups)
19 - Sus scrofa	Pig	Vertebrates	Even-toed ungulates (taxid:9932)	251 (in 251 groups)
20 - Alligator mississippiensis	Reptile	Vertebrates	Reptiles (taxid:8486)	243 (in 243 groups)
21 - Alligator sinensis	Reptile	Vertebrates	Reptiles (taxid:38665)	238 (in 238 groups)
22 - Colaptes auratus	Pigeon	Vertebrates	Birds (taxid:8123)	224 (in 224 groups)
23 - Gallus gallus	Chicken	Vertebrates	Birds (taxid:9913)	244 (in 244 groups)
24 - Meleagris gallopavo	Turkey	Vertebrates	Birds (taxid:9133)	214 (in 214 groups)
25 - Xenopus laevis	Frog	Vertebrates	Frogs and toads (taxid:8332)	245 (in 245 groups)
26 - Rana temporaria	Frog	Vertebrates	Frogs and toads (taxid:8607)	245 (in 245 groups)
27 - Danio rerio	Zebrafish	Vertebrates	Bony fishes (taxid:7955)	282 (in 251 groups)
28 - Nothobranchius furcatus	African killifish	Vertebrates	Bony fishes (taxid:10603)	246 (in 246 groups)
29 - Oryzias latipes	Japanese rice fish	Vertebrates	Bony fishes (taxid:8005)	247 (in 247 groups)
30 - Sparus aurata	Quete	Vertebrates	Bony fishes (taxid:8173)	250 (in 250 groups)
31 - Styela clava	Asian bivalve	Chordata	Tunicata (taxid:7723)	188 (in 188 groups)
32 - Patina minata	Starfish	Invertebrates	Echinoderm (taxid:46115)	179 (in 179 groups)
33 - Strongylocentrotus purpuratus	Sea urchin	Invertebrates	Echinoderm (taxid:3568)	183 (in 183 groups)
34 - Drosophila melanogaster	Fruit fly	Invertebrates	Insects (taxid:7227)	134 (in 134 groups)
35 - Apis mellifera	Honey bee	Invertebrates	Insects (taxid:7880)	181 (in 151 groups)
36 - Caenorhabditis elegans	Worm	Invertebrates	Nematoda (taxid:6233)	115 (in 115 groups)
37 - Saccharomyces cerevisiae	Cultured yeast	Invertebrates	Cephalopoda (taxid:138019)	119 (in 119 groups)
38 - Actinia tenebrosa	Anemone	Invertebrates	Cnidaria (taxid:8120)	158 (in 158 groups)

```

← → ↻ phylobone.com/DATABASE/SPECIES/9606.txt
>NP_001613.2 alpha-2-HS-glycoprotein isoform 2 preproprotein [Homo sapiens | PB0001
MKSLLVLLQLAQLGCHSAFHGGLIYRQPCNDPTEEAALVAIDYINQLFNGYKHTLQIDBVKVMP
QOQSFELFEITDITLLETCHVLDPTTPVAVCSQVQLKHAIVGDCDFQLLIDGKFSVYVAKCDSGDSAE
DVRVFCQDCLLAFIANDVTVHAKALAAFNQNGSFLSEIIEAQLVPLFPIYVTSQVCA
KEATAEKNLAEKQYGFKATLSEKLGAEAVTCVMTQGVPSQSPQFEGANAVFTVPDPAFSS
PFLGAPGLPAGSPFDSHVLAAAPGGLHRAHYDRLRFTMGVLSVSGEVSHPKRTKTVQVPSVGA
AGPVVPCGRIHFFK
>NP_004039.1 beta-2-microglobulin precursor [Homo sapiens | PB0002
MRSVALAVLALLSLGLEAIQRTPKIQVYSRHPAENGKSNFLNCSVGFHPSDIPVDLLKNGRIEKVE
HSDLFSFSDNSFLLLYTTFTEKDEYACRNVHVLSPKIVKRWDM
>NP_000497.1 prothrombin preproprotein [Homo sapiens | PB0003
MAHVRGLQPCCLAAALCSLVHSQHVFLAPQARSLLRVRRAMTFLEVRKRNLERECVEETCSYEEA
FEALLESFADVDFWAKTACTATPRKLAALGNGAEGLVTVRGRVMTSSEICQLWRFRPHF
EINSTFPGADLQMFQNFNDSSTGWCYITDPTVVRQECISFVCGQDQVAVMTFPRSGSVNLSPEL
EQCVPRDQGGYQGLAVTTBGLFLAWASAQAALSKHQDFNSAVQLVFCRNPDPGDEEGVVCYVAGK
GDFQYCDLNYCEAVVEETGDLGDSRAIGRRTATSEYQTFNFRPTFGSGRACDGLPLFKKSLK
TERELLESYIDGRIVEGSDAEIOMSPWVPLFKSKQELLGCGSLISDNWVLTAKCLLFPWDNFTEN
DLLVRIGKHSRTRVERNIERISMLEKIIHYHRYNRENLDLADLAKLKKVAFSDIYHVPCLDRPTAA
SLLQAGYKGRVTCWGNLKTWTANVKGQPSVLQVNLPIVERVPCQDSTRITIDNMFCAQYDQDGR
GDACEGSGGPFVMSFPNRRWYMGIVSWGEGCDRDRGKYGFYTHFRKLLKQVVDQFGE
>NP_000891.2 matrix Gla protein isoform 2 preproprotein [Homo sapiens | PB0004
MKSLLVLLAALAVLTVLCEHSEHSEYELNFFINRRNMTFISQQRWAKVQRIRERSKPVHELNR
EACDDYRLCERYMVGTYNAYRYFRKRRGTR
>NP_001702.1 biglycan preproprotein [Homo sapiens | PB0005
MPLNRLVLLALQALPFQGRGFDPTLDDGPFMNDDEASGADTSGVLDPSVTPYTSAMCFQGCCH
LRVVCQSLGKSVFPEISFDPTLLDQNDISELRDQDFGLQLHALVQVNRKSRHEKAFSPFLK
QVLYISKHNLVEIPFNLSVSEVLRHHRKIRVYKQVPSGLKNNCTIEMGCHLENGFEGADPLK
NVLISEAKLGTIPDLPTLNEHLNHNKIQALELLELLRYLKLVLGLGHGQIRMIENGLSFLPLTR
ELHLNDKLARVPSGLDQLKLLQVYVLSNNTIRVGVNDFCPMGFQVRAVYNGISLNFNPFVVEVQFA
TFRVCYDRLAIQFGNYK
>NP_003109.1 SPARC isoform 1 precursor [Homo sapiens | PB0006
MRWIFFLLAGRALAQQEALPOETVEVETVAEVEVSVGANPVQVGVGDFDGAETEEVEVVAEN
FCQNHKSRKVKCELDENWPMCVQDFPSCFPIGFEKVCSDNKTIPSCHFFATCTLEKTKGKH
LHLDYIGPCPKYIPPCDSELEFPLMRDMLKNVLYLVEEDNNLLEKQKLRVKKIHEKRLKLEAG
HPVELLARDFKNYMYIPVHNPQGLDQHPIDGYSHTLAPLAPLIMECHTRFETCDLNDKY
IALDEWAGFCGRKQDIDKDLVI
>NP_001258.2 chondroaderin precursor [Homo sapiens | PB0007
MVRPMLLSLGLLGLLPAALACPNCRHSDLDQHVICDKVGLQIKPKVSEKTKLLNQRNPFVLAANS
FRAMPNLVSLGHCQIREVAAAGAFGLKQLIYLHSHNDVRLVRAAGAFDDELTYLVDHNKVTLEPR
GLSLVNLVLTQLNNTIRELRAGAFPCADKQVLRVLSNLSALSIOPALDVENLAKFVYDQGLSSY
PSAALSKLRVBEELKSNPLKSIDNAFQSGRYLETMLDNLNLEKSPDAGLGVTLKRVHLENLRL

```

### 6. Domains and protein-protein Interactions

PBID	Domains Hit	Domains Features	Prot-Prot Interactions	EggnoG Mapper
PB0001	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0002	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0003	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0004	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0005	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0006	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0007	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0008	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0009	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0010	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0011	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0012	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>
PB0013	<a href="#">Hit Data</a>	<a href="#">Feat Data</a>	<a href="#">PPI</a>	<a href="#">EggnoG</a>

This page contains internal links to domain (hits and features), protein-protein interactions and results from the eggno mapper. Phylobone codes give access to general information about proteins (e.g. [PB0001](#)).



## Domain hits (example)

Information of protein domains have been pre-computed with the NCBI's Batch [CD-Search tool](#).

### DOMAINS

Query	Hit type	PSSM-ID	From	To	E-Value	Bitscore	Accession	Short name	Incomplete	Superfamily
Q#1 ->NP_001613.2 alpha-2-HS-glycoprotein isoform 2 prepr oprotein [Homo sapiens]	specific	214484	31	133	8.56776e-11	58.2085	<a href="#">smart00043</a>	CY	-	<a href="#">cl09238</a>
Q#1 ->NP_001613.2 alpha-2-HS-glycoprotein isoform 2 prepr oprotein [Homo sapiens]	superfamily	447698	149	233	3.73868e-09	53.1071	<a href="#">cl09238</a>	CY superfamily	-	=
Q#2 ->XP_030257367.1 alpha-2 -HS-glycoprotein-like [Sparus aurata]	superfamily	447698	27	128	3.78768e-09	53.5861	<a href="#">cl09238</a>	CY superfamily	-	=
Q#2 ->XP_030257367.1 alpha-2 -HS-glycoprotein-like [Sparus aurata]	superfamily	447698	139	221	2.78317e-05	42.3216	<a href="#">cl09238</a>	CY superfamily	-	=
Q#3 ->XP_004078952.1 alpha-2 -HS-glycoprotein [Oryzias lat ipes]	specific	214484	27	128	2.81256e-10	57.0529	<a href="#">smart00043</a>	CY	-	<a href="#">cl09238</a>
Q#3 ->XP_004078952.1 alpha-2 -HS-glycoprotein [Oryzias lat ipes]	superfamily	447698	139	202	2.17809e-05	42.7068	<a href="#">cl09238</a>	CY superfamily	C	=

## Domain features (example)

### DOMAINS

Query	Type	Title	coordinates	complete size	mapped size	source domain
Q#1 ->NP_001613.2 alpha-2-HS-glycoprotein isoform 2 prepr oprotein [Homo sapiens]	specific	putative proteinase inhibition site	Q71,Q72,P73,G75	5	4	238002
Q#1 ->NP_001613.2 alpha-2-HS-glycoprotein isoform 2 prepr oprotein [Homo sapiens]	specific	putative proteinase inhibition site	D148,Q189,L190,V191,S196	5	5	238002
Q#2 ->XP_030257367.1 alpha-2 -HS-glycoprotein-like [Sparus aurata]	specific	putative proteinase inhibition site	Y64,T65,T66,G70	5	4	238002
Q#2 ->XP_030257367.1 alpha-2 -HS-glycoprotein-like [Sparus aurata]	specific	putative proteinase inhibition site	G139,Q182,I183,V184,G187	5	5	238002
Q#3 ->XP_004078952.1 alpha-2 -HS-glycoprotein [Oryzias lat ipes]	specific	putative proteinase inhibition site	G139,Q182,V183,V184,G186	5	5	238002

## Protein-protein interactions (Example)

Predictions of protein-protein interactions gathered from [IntAct](#) repository of domains.





PPI

ID(s) Interactor A	ID(s) Interactor B	Alt. ID(s) Interactor A	Alt. ID(s) Interactor B	Alias(es) Interactor A	Alias(es) Interactor B	Interaction detection method(s)	Publication 1st author(s)	Publication Identifier(s)	Taxid(s)
uniprotkb:O75259   uniprotkb:O6AT5   uniprotkb:CRUP6   ensemble:ENSP0000221801   ensemble:ENSP0000487390   uniprotkb:BSIU58   intact:EBI-358318   uniprotkb:P22087	uniprotkb:P02765		uniprotkb:O14961   uniprotkb:O14962   uniprotkb:CRP152   uniprotkb:ABK9N6   uniprotkb:Q20731   ensemble:ENSP0000393887   intact:EBI-1223374   uniprotkb:P02765	psi-mi:fbtl_human(display_short)   psi-mi:RNA 2'-O-methyltransferase fibrillarin(display_long)   uniprotkb:FB1(gene name)   uniprotkb:US sRNA 2'-O-methyltransferase fibrillarin(gene name synonym)   uniprotkb:34 kDa nucleolar sclerodermis antigen(gene name synonym)   uniprotkb:Histone-glutamine methyltransferase(gene name synonym)   uniprotkb:FB1(gene name synonym)   uniprotkb:FLRN(gene name synonym)   IntAct:FBRL(author assigned name)	psi-mi:fetua_human(display_short)   psi-mi:Alpha-2-HS-glycoprotein(display_long)   uniprotkb:AHSG(gene name)   uniprotkb:Fetuin-Alginate name synonym   uniprotkb:Fetuin(gene name synonym)   uniprotkb:FR02743(orf name)   uniprotkb:Ba-alpha-2-glycoprotein(gene name synonym)   uniprotkb:Alpha-2-Z-globulin(gene name synonym)   IntAct:AHSG(author assigned name)	psi-mi:"MI:1314" (proximity-dependent biotin identification)	Li X. et al (2018)	intact:EBI-16744398   pubmed:29568061   medrxiv:26301	taxid:961   taxid:961   sapiens
uniprotkb:P35219	uniprotkb:P02765	uniprotkb:Q32MY2   uniprotkb:ABKDA5   uniprotkb:BSKQZ7   ensemble:ENSP0000314407   intact:EBI-718700   uniprotkb:P35219	uniprotkb:O14961   uniprotkb:O14962   uniprotkb:CRP152   uniprotkb:ABK9N6   uniprotkb:Q20731   ensemble:ENSP0000393887   intact:EBI-1223374   uniprotkb:P02765	psi-mi:cahb_human(display_short)   psi-mi:Carbonic anhydrase-related protein(display_long)   uniprotkb:Carbonic anhydrase VIII(gene name synonym)   uniprotkb:CALS(gene name synonym)   uniprotkb:CA8(gene name)   IntAct:CA8(author assigned name)	psi-mi:fetua_human(display_short)   psi-mi:Alpha-2-HS-glycoprotein(display_long)   uniprotkb:AHSG(gene name)   uniprotkb:Fetuin-Alginate name synonym   uniprotkb:Fetuin(gene name synonym)   uniprotkb:FR02743(orf name)   uniprotkb:Ba-alpha-2-glycoprotein(gene name synonym)   uniprotkb:Alpha-2-Z-globulin(gene name synonym)   IntAct:AHSG(author assigned name)	psi-mi:"MI:0007"(anti tag coimmunoprecipitation)	Huttlin EL et al (2017)	intact:EBI-15481134   doi:10.1038/nature22366   pubmed:28514442   medrxiv:25778	taxid:961   taxid:961   sapiens
uniprotkb:ASA3E0	uniprotkb:P02765	uniprotkb:AANC34   ensemble:ENSP0000386786   intact:EBI-6150673   uniprotkb:ASA3E0	uniprotkb:O14961   uniprotkb:O14962   uniprotkb:CRP152   uniprotkb:ABK9N6   uniprotkb:Q20731   ensemble:ENSP0000393887   intact:EBI-1223374   uniprotkb:P02765	psi-mi:potef_human(display_short)   psi-mi:POTE ankyrin domain family member Fc(display_long)   uniprotkb:A26C1(gene name synonym)   uniprotkb:ANKRD26-like family C member 18(gene name synonym)   uniprotkb:Chimeric POTE-actin protein(gene name synonym)   uniprotkb:POTE(gene name)   IntAct:POTE(author assigned name)	psi-mi:fetua_human(display_short)   psi-mi:Alpha-2-HS-glycoprotein(display_long)   uniprotkb:AHSG(gene name)   uniprotkb:Fetuin-Alginate name synonym   uniprotkb:Fetuin(gene name synonym)   uniprotkb:FR02743(orf name)   uniprotkb:Ba-alpha-2-glycoprotein(gene name synonym)   uniprotkb:Alpha-2-Z-globulin(gene name synonym)   IntAct:AHSG(author assigned name)	psi-mi:"MI:0007"(anti tag coimmunoprecipitation)	Huttlin EL et al (2017)	intact:EBI-15481134   doi:10.1038/nature22366   pubmed:28514442   medrxiv:25778	taxid:961   taxid:961   sapiens
uniprotkb:O09064   uniprotkb:O09144   uniprotkb:O14510   uniprotkb:O32273   uniprotkb:QB8K64		uniprotkb:O14961   uniprotkb:O14962   uniprotkb:CRP152   uniprotkb:ABK9N6   uniprotkb:Q20731   ensemble:ENSP0000393887   intact:EBI-1223374   uniprotkb:P02765	uniprotkb:O14961   uniprotkb:O14962   uniprotkb:CRP152   uniprotkb:ABK9N6   uniprotkb:Q20731   ensemble:ENSP0000393887   intact:EBI-1223374   uniprotkb:P02765	psi-mi:snad3_mouse(display_short)   psi-mi:Mothers against decapentaplegic homolog 3(display_long)   uniprotkb:SMAD3(gene name)	psi-mi:fetua_human(display_short)   psi-mi:Alpha-2-HS-glycoprotein(display_long)   uniprotkb:AHSG(gene name)   uniprotkb:Fetuin-Alginate name synonym   uniprotkb:Fetuin(gene name synonym)   uniprotkb:FR02743(orf name)   uniprotkb:Ba-alpha-2-glycoprotein(gene name synonym)   uniprotkb:Alpha-2-Z-globulin(gene name synonym)   IntAct:AHSG(author assigned name)	psi-mi:"MI:0676"	Hutchins	intact:EBI-2550900	taxid:10

## Eggno mapper (Example)

Annotations from the [eggno mapper](#) have been included in a text box that can be directly copied and pasted into a spreadsheet for optimal visualization.

### Eggno Mapper

PB ID	query	seed_ortholog	evaluate	score	eggNOG_OGS	max_annot_lvl	COG_category									
Description	Preferred_name	Gos	EC	KEGG_ko	KEGG_Pathway	KEGG_Module	KEGG_Reaction									
KEGG_rclass	BRITE	KEGG_TC	CAZY	BiGG_Reaction	PFAMs											
PB0001	NP_001613.2	9606.ENSPO0000393887		6.29e-274	748.0											
2BVGM@1	root,2RYRI@2759	Eukaryota,38K34@33154	Opisthokonta,3BIHG@33208	Metazoa,3CYUW@33213	Bilateria,48C9N@7711	Chordata,4943T@7742	Vertebrata,3JB46@40674	Mammalia,35CEN@31416	Euarchoontoglires,4MC8B@9443	Primate s,4N6H3@9604	Hominidae	33208	Metazoa	T	Promotes endocytosis, possesses opsonic properties and influences the mineral phase of bone. Shows affinity for calcium and barium ions	AHSG
GO:0000003,GO:0001501,GO:0001503,GO:0001558,GO:0001775,GO:0001932,GO:0001933,GO:0002252,GO:0002263,GO:0002274,GO:0002275,GO:0002283,GO:0002366,GO:0002376,GO:0002443,GO:0002444,GO:0002446,GO:0002526,GO:0002576,GO:0003006,GO:0003674,GO:0004857,GO:0004860,GO:0004866,GO:0005575,GO:0005576,GO:0005615,GO:0005622,GO:0005623,GO:0005737,GO:0005783,GO:0005788,GO:0005794,GO:0005886,GO:0006464,GO:0006469,GO:0006807,GO:0006810,GO:0006887,GO:0006897,GO:0006907,GO:0006950,GO:0006952,GO:0006953,GO:0006954,GO:0006955,GO:0007275,GO:0007399,GO:0007417,GO:0007420,GO:0007548,GO:0008150,GO:0008152,GO:0008406,GO:0008584,GO:0009719,GO:0009725,GO:0009899,GO:0009966,GO:0009968,GO:0009987,GO:0010033,GO:0010243,GO:0010466,GO:0010563,GO:0010605,GO:0010646,GO:0010648,GO:0010951,GO:0012505,GO:0016020,GO:0016043,GO:0016192,GO:0019207,GO:0019210,GO:0019220,GO:0019222,GO:0019538,GO:0019887,GO:0021537,GO:0021543,GO:0021987,GO:0022414,GO:0022607,GO:0023051,GO:0023057,GO:0030100,GO:0030141,GO:0030162,GO:0030234,GO:0030278,GO:0030279,GO:0030292,GO:0030294,GO:0030308,GO:0030414,GO:0030500,GO:0030502,GO:0030900,GO:0031012,GO:0031091,GO:0031093,GO:0031099,GO:0031100,GO:0031323,GO:0031324,GO:0031347,GO:0031399,GO:0031400,GO:0031410,GO:0031974,GO:0031982,GO:0031983,GO:0032101,GO:0032268,GO:0032269,GO:0032501,GO:0032502,GO:0032868,GO:0032869,GO:0032870,GO:0032879,GO:0032940,GO:0032991,GO:0033673,GO:0034103,GO:0034105,GO:0034774,GO:0036211,GO:0036230,GO:0040008,GO:0042119,GO:0042221,GO:0042325,GO:0042326,GO:0043086,GO:0043170,GO:0043226,GO:0043227,GO:0043229,GO:0043230,GO:0043231,GO:0043233,GO:0043299,GO:0043312,GO:0043412,GO:0043434,GO:0043549,GO:0043687,GO:0043933,GO:0044085,GO:0044092,GO:0044237,GO:0044238,GO:0044260,GO:0044267,GO:0044421,GO:0044422,GO:0044424,GO:0044432,GO:0044433,GO:0044444,GO:0044446,GO:0044466,GO:0044467,GO:0044505,GO:0045124,GO:0045137,GO:0045321,GO:0045780,GO:0045807,GO:0045859,GO:0045861,GO:0045926,GO:0045936,GO:0046546,GO:0046626,GO:0046627,GO:0046661,GO:0046850,GO:0046852,GO:0046903,GO:0048513,GO:0048518,GO:0048519,GO:0048522,GO:0048523,GO:0048583,GO:0048585,GO:0048608,GO:0048731,GO:0048856,GO:0050727,GO:0050730,GO:0050732,GO:0050764,GO:0050766,GO:0050789,GO:0050790,GO:0050793,GO:0050794,GO:0050896,GO:0051049,GO:0051050,GO:0051093,GO:0051128,GO:0051130,GO:0051171,GO:0051172,GO:0051174,GO:0051179,GO:0051234,GO:0051239																