Cape golden mole

GenBank: XM_006870413

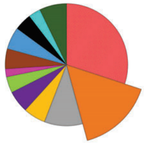
Chrysochloris asiatica

Afrosoricida 1/4
Chrysochloridae 1/1

1 species sharing the same primary sequence

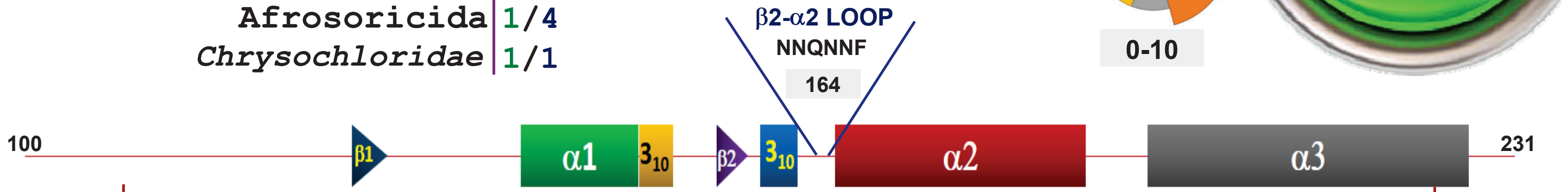
Hottentot golden mole
Amblysomus hottentotus

P36%



0-10

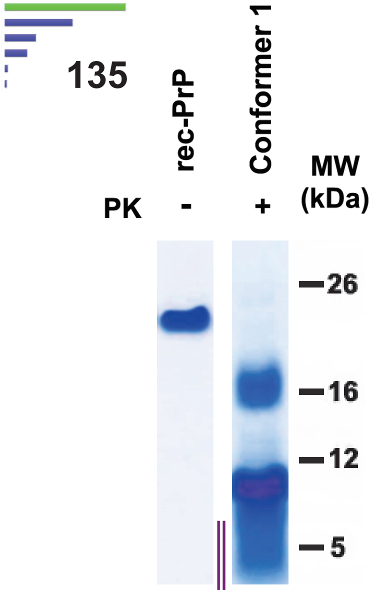
2.9



```
WNKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPPMHFGNDYEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCINITVKQHTTTTTKGENFTETDIKIMERVVEQMCITQYEKASLEYHRGSS-
     S     I  V                          MI     W                                   V   I    V                  V M         V   Q E QA YE R S
```

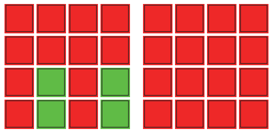
PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



204 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

Cape golden mole Not tested

In vivo studies

TgVole (1x) Not tested

Cape golden mole Not tested

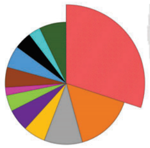
pLDDT
[89.33]

Protein code: 1128

Lesser hedgehog tenrec

GenBank: BK064944

P29%



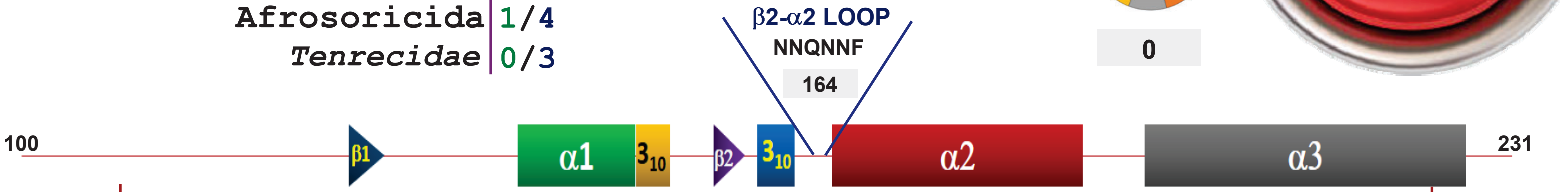
0

0

Echinops telfairi

Afrosoricida 1/4
Tenrecidae 0/3

Distinct primary sequence across species



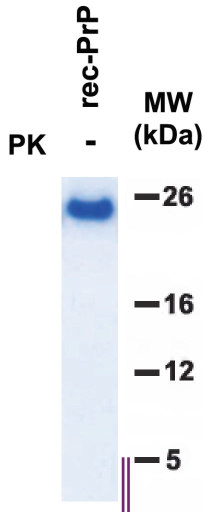
```
WNKPSKPKTNAKQMLGAAAAGAVVGGLGGYVVGSAMSRPLMHFGNDYEDRYYRENMHRYPNQVYYYRPVQEYNNQNNFVHDCVNITVKHHTTTTTTKGENFTETDVKIMERVVEQMCVTQYQQASLDYQRGLR-
          I HVA               ML       MI     W         N           DQ               I  Q  V               M              KE QA YE RSS
```

PrP sequence differs by 20 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

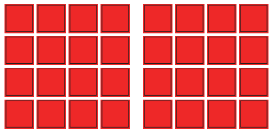
ΔΔG: ND



233 AA

NO MISFOLDING

0
Conformers



In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

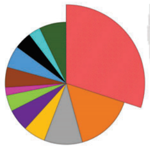
pLDDT
[92.61]

Protein code: 1082

Talazac's shrew tenrec

GenBank: BK063959

P29%



0

0

Microgale talazaci

Afrosoricida 1/4
Tenrecidae 0/3

β2-α2 LOOP
SNQNNF
273

```
WNKPNKPKTNTKHMLGAAAAGAVVGGLGGYMVGSAMSRPLMHFGNDYEDRYYRENMHRYPNQVFYRPVQEYSNQNNFVHDCVNFTVKEHTTTTTTKGENFTQTDIKIMERVVEQMCITQYQQASLEYQEYQR-
      S     I  VA                   L        MI     W         N      Y    DQ N             I I Q  V           E  V M         V     KE QA Y GRSS
```

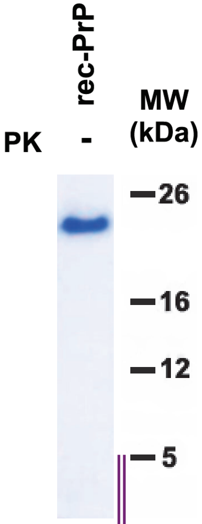
PrP sequence differs by 24 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

ΔΔG: ND



214 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[96.16]

Protein code: 3087

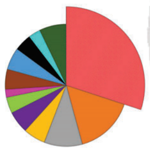
Tailless tenrec

GenBank: AY133060

Tenrec ecaudatus

Afrosoricida 1/4
Tenrecidae 0/3

P29%



0

0

β2-α2 LOOP
NNQNNF
164

```
WNKPNKPKTNTKQVLGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNDYEDRYYRENMHRYPNQVYYRPVQEYNNQNNFVHDCVNITVKQHTTTTTTKGENFTETDVKIMERVVEQMCITQYQQASLDYQRGLH-
    S    I H A                                MI     W          N          DQ                        I    V                M          V     KE QA YE RSS
```

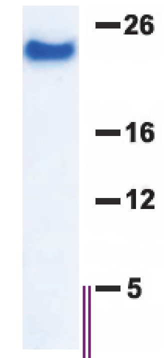
PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND

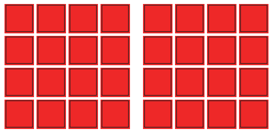
PK
rec-PrP
-
MW (kDa)



224 AA

NO MISFOLDING

0
Conformers



In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[93.05]

Distinct primary sequence across species

Protein code: 1347

Mongolian gazelle

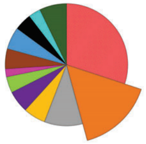
GenBank: AB473615

Distinct primary sequence across species

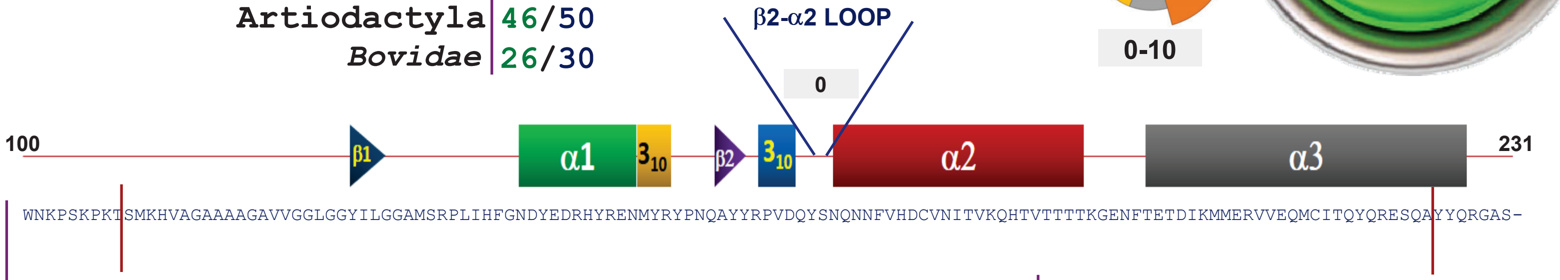
Procapra gutturosa

Artiodactyla	46/50
Bovidae	26/30

P39%



0-10



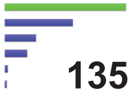
WNKPSKPKTSMKHVAGAAAAGAVVGGLGGYILGGAMSRPLIHFGNDYEDRHYRENMYRYPNQAYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-

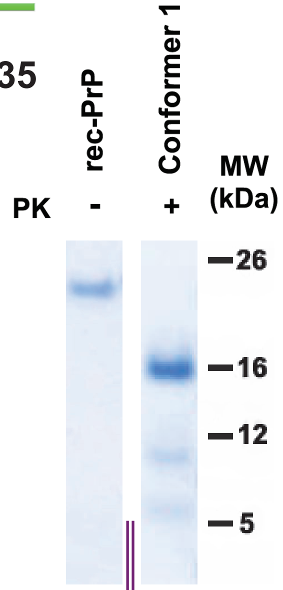
PrP sequence differs by 0 amino acids from the bank vole PrP (see in red)

No deletions

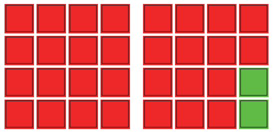
No insertions

It shows polymorphic variants





220 AA



1

Conformers

Tm^{Exp}: ND

ΔΔG: -9.58

In vitro studies

Not tested
TgVole (1x)

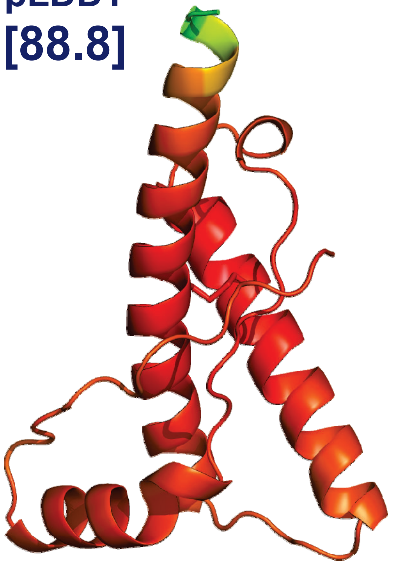
Not tested
Mongolian gazelle

In vivo studies

Not tested
TgVole (1x)

Not tested
Mongolian gazelle

pLDDT
[88.8]



Protein code: 1143

Impala

GenBank: BK063929

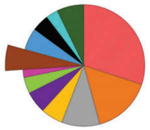
Aepyceros melampus

Artiodactyla 46/50
Bovidae 26/30

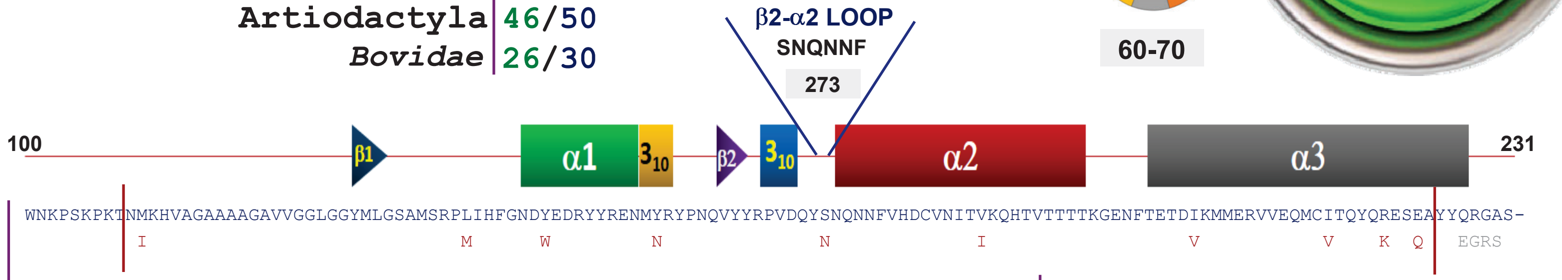
Distinct primary sequence across species

P77%

67.5



60-70



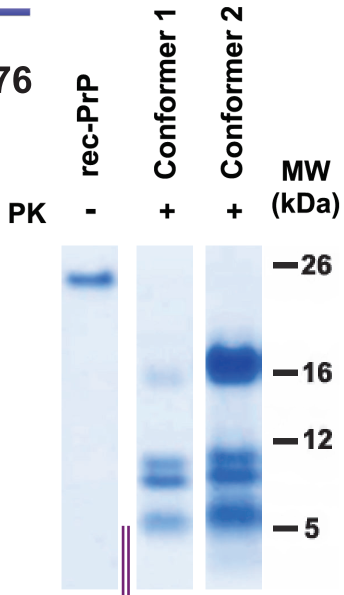
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-

I M W N N I V V K Q EGRS

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

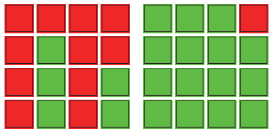
No deletions
No insertions
No polymorphic variants found

76



220 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -14.79

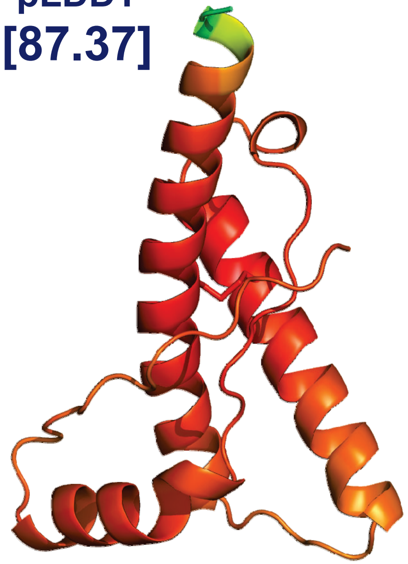
In vitro studies

TgVole (1x)	Not tested
Impala	Not tested

In vivo studies

TgVole (1x)	Not tested
Impala	Not tested

pLDDT
[87.37]



Protein code: 3047

Pronghorn

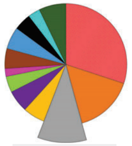
GenBank: AF156187

Antilocapra americana

Distinct primary sequence across species

`Artiodactyla` 46/50
`Antilocapridae` 1/1

P55%



10-20

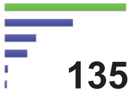
19.6

β2-α2 LOOP
SNQNTF
75

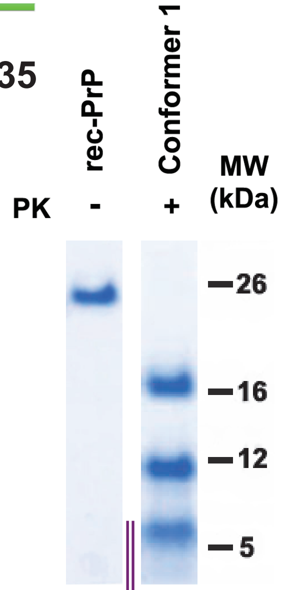
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNTFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-
           I                         M     W        N                N  N      I                V         V  K    EGRS
```

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

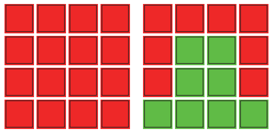


135



220 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -12.73

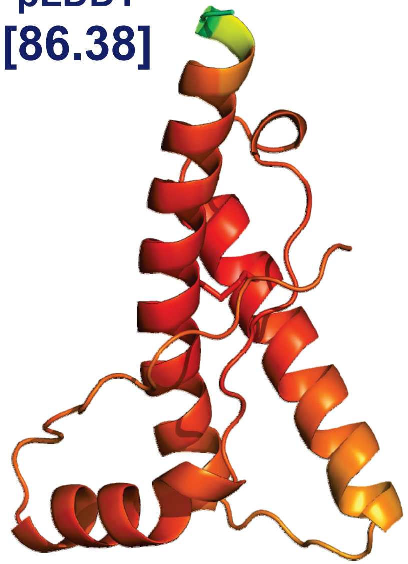
***In vitro* studies**

TgVole (1x)	**Not tested**
Pronghorn	**Not tested**

***In vivo* studies**

TgVole (1x)	**Not tested**
Pronghorn	**Not tested**

pLDDT
[86.38]



Protein code: 0945

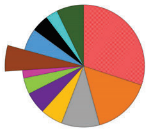
Blackbuck

GenBank: AY720706

Antilope cervicapra

Artiodactyla 46/50
Bovidae 26/30

P75%



60-70

62.5

7 species sharing the same primary sequence

Springbok
Antidorcas marsupialis

Thomson's gazelle
Eudorcas thomsonii

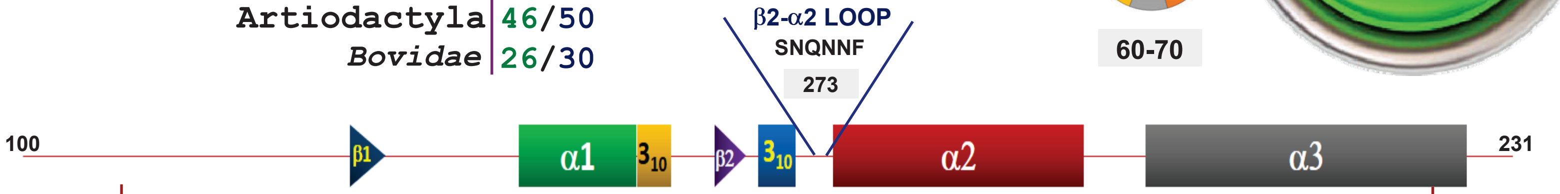
Dorcas gazelle
Gazella dorcas

Goitered gazelle
Gazella subgutturosa

Dama gazelle
Nanger dama

Grant's gazelle
Nanger granti

Przewalski's gazelle
Procapra przewalskii

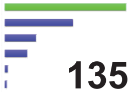


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-

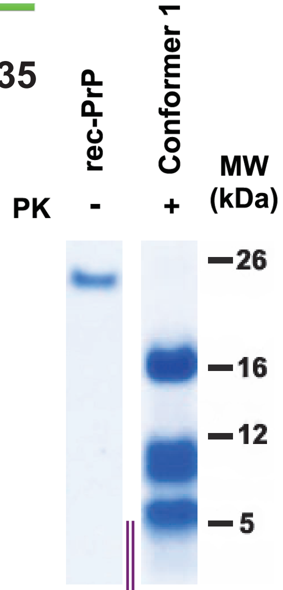
I M W N N I V V K EGRS

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

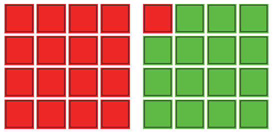


135



220 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -12.66

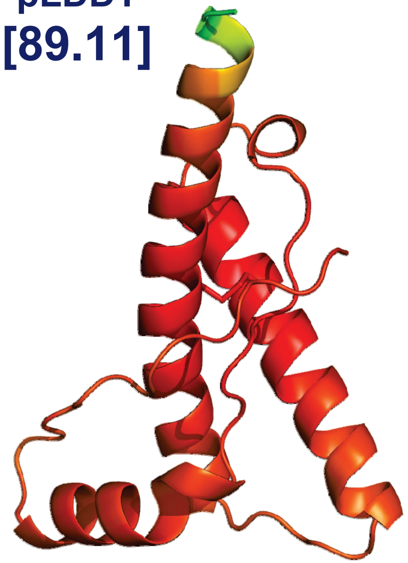
In vitro studies

TgVole (1x)	Not tested
Blackbuck	Not tested

In vivo studies

TgVole (1x)	Not tested
Blackbuck	Not tested

pLDDT
[89.11]



Protein code: 1350

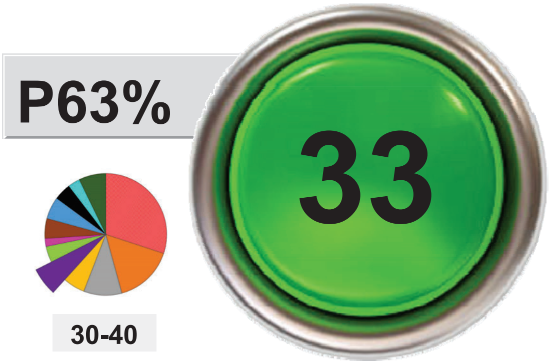
North Sulawesi babirusa

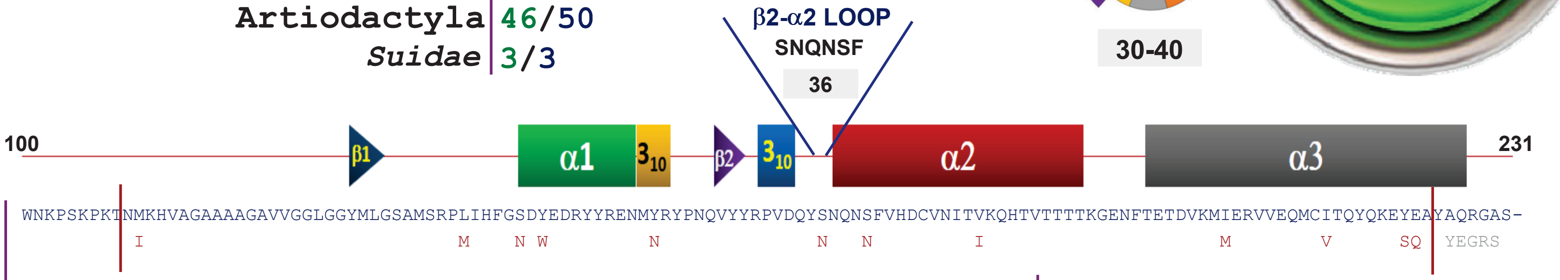
GenBank: BK064782

Babyrousa celebensis

Artiodactyla	46/50
Suidae	3/3

P63%





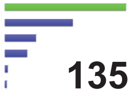
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDVKMIERVVEQMCITQYQKEYEAYAQRGAS-
           I                           M    N W         N                  N   N          I                     M        V      SQ  YEGRS
```

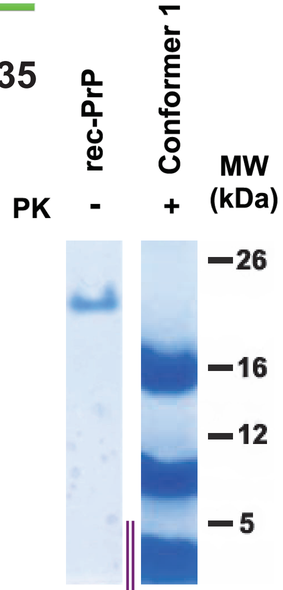
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

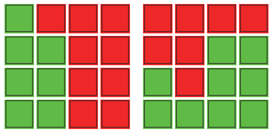
No polymorphic variants found





213 AA

1
Conformers



Tm^{Exp}: ND

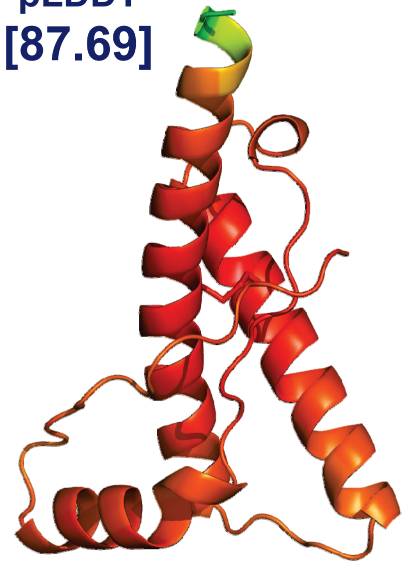
ΔΔG: -12.04

In vitro studies

TgVole (1x) Not tested

North Sulawesi babirusa Not tested

pLDDT
[87.69]



In vivo studies

TgVole (1x) Not tested

North Sulawesi babirusa Not tested

Distinct primary sequence across species

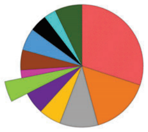
Protein code: 3940

Domestic yak

GenBank: KC137646

P69%

45.2



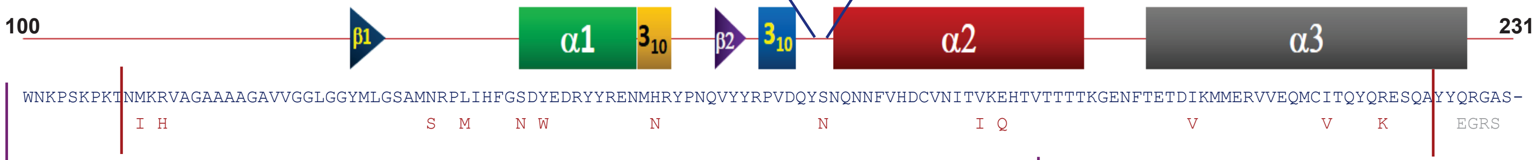
40-50

Bos grunniens

Artiodactyla 46/50

Bovidae 26/30

β2-α2 LOOP
SNQNNF
273

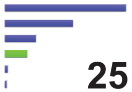


```
WNKPSKPKTNMKRVAGAAAAGAVVGGLGGYMLGSAMNRPLIHFGSDYEDRYYRENMHRYPNQVYYRPVDQYSNQNNFVHDCVNITVKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-
          I H                       S  M    N W         N              N             I Q                V           V    K      EGRS
```

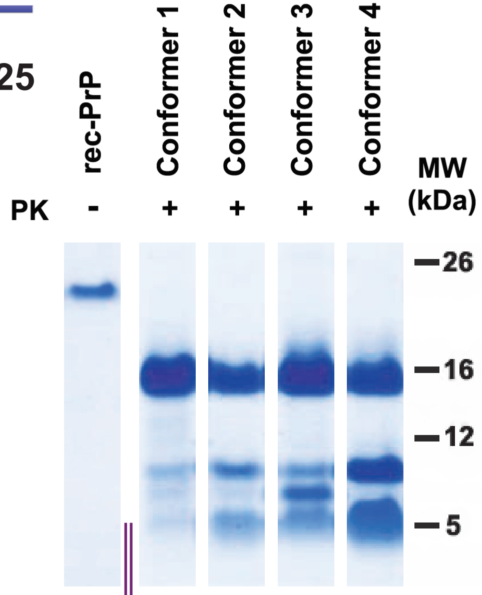
PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
It shows polymorphic variants

Distinct primary sequence across species

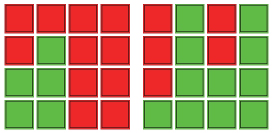


25



220 AA

4
Conformers



Tm^{Exp}: ND

ΔΔG: -4.17

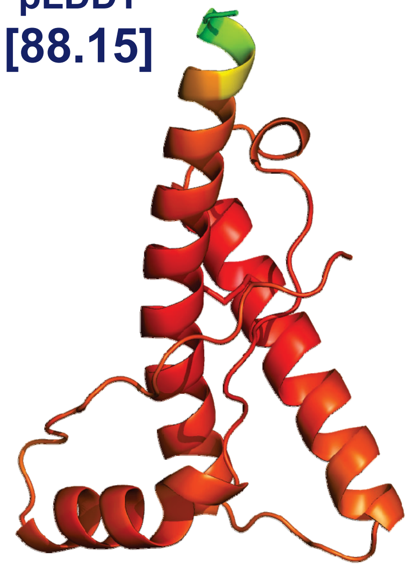
In vitro studies

TgVole (1x)	Not tested
Domestic yak	Not tested

In vivo studies

TgVole (1x)	Not tested
Domestic yak	Not tested

pLDDT
[88.15]



Cow

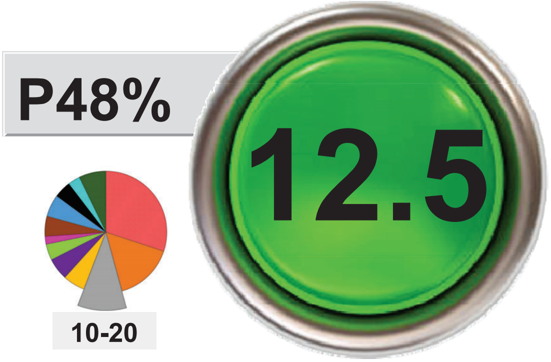
GenBank: NM_181015

Bos taurus

Artiodactyla	46/50
Bovidae	26/30

4 species sharing the same primary sequence

- **American bison** *Bison bison*
- **European bison** *Bison bonasus*
- **Gayal** *Bos frontalis*
- **Banteng** *Bos javanicus*



β2-α2 LOOP
SNQNNF
273

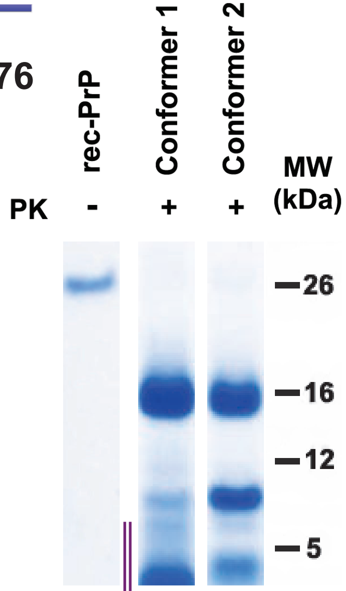
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMHRYPNQVYYRPVDQYSNQNNFVHDCVNITVKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-
           I                          M    N W         N                N                I Q                 V          V   K      EGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions

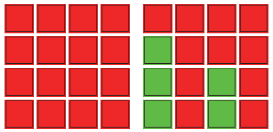
No insertions

It shows polymorphic variants



220 AA

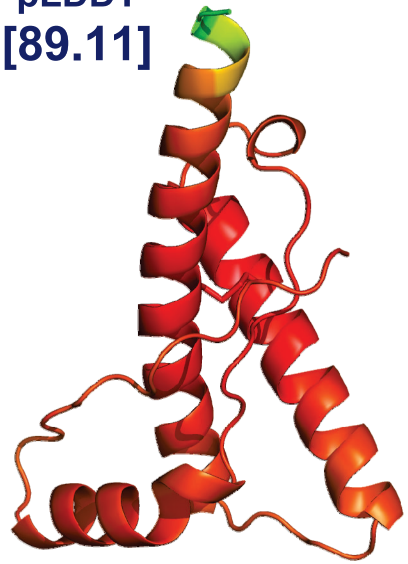
2
Conformers



Tm^{Exp}: ND

ΔΔG: -10.33

pLDDT
[89.11]



In vitro studies

TgVole (1x)	Propagate
Cow	Propagate

In vivo studies

TgVole (1x)	Infectious
TgCow	Not tested

Protein code: 0201

Distinct primary sequence across species

Nilgai

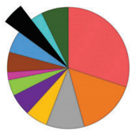
GenBank: AY720700

Boselaphus tragocamelus

Artiodactyla	46/50
Bovidae	26/30

P88%

85.7



80-90

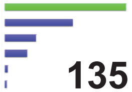
β2-α2 LOOP
SNQNNF
273

WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMNRPLIHFGNDYEDRYYRENMHRYPNQVYYRPVDQYSNQNNFVRDCVNITVKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYQTESQAYYQRGAS-

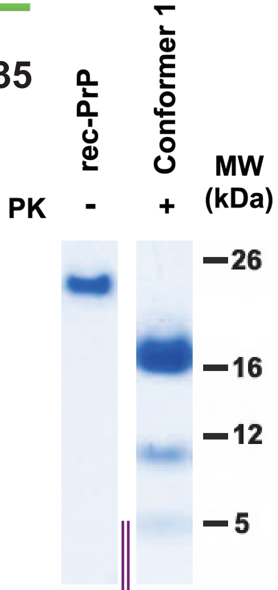
I S M W N N H I Q V V K EGRS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



135

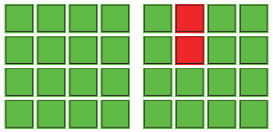


220 AA

Tm^{Exp}: ND

ΔΔG: -7.53

1
Conformers



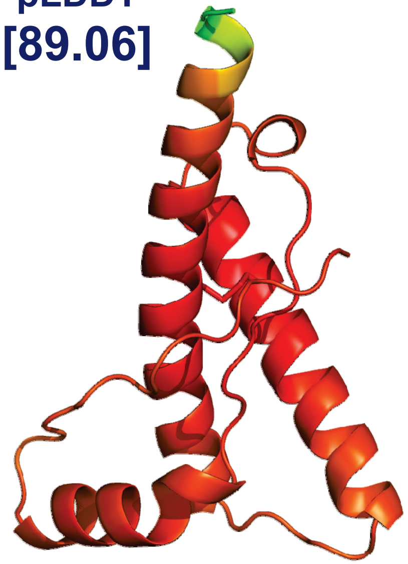
In vitro studies

TgVole (1x)	Not tested
Nilgai	Not tested

In vivo studies

TgVole (1x)	Not tested
Nilgai	Not tested

pLDDT
[89.06]



Protein code: 1357

Distinct primary sequence across species

Water buffalo

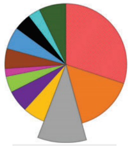
GenBank: MK342630

Bubalus bubalis

Artiodactyla 46/50
Bovidae 26/30

P51%

16.1



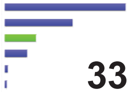
10-20

β2-α2 LOOP
SNQNNF
273

```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMHRYPNQVYYRPVDQYSNQNNFVHDCVNITVKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-
           I  V                          M      W         N              N             I Q                   V          V    K     EGRS
```

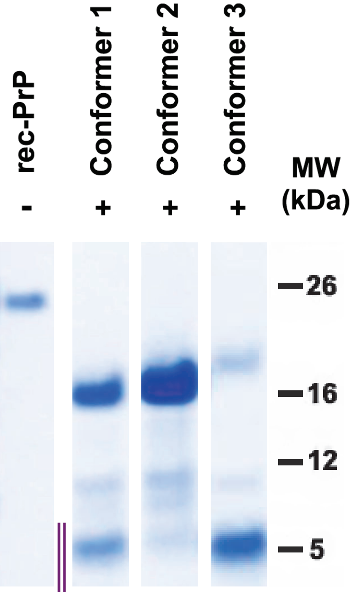
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
It shows polymorphic variants



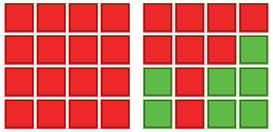
33

PK



220 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: -12.88

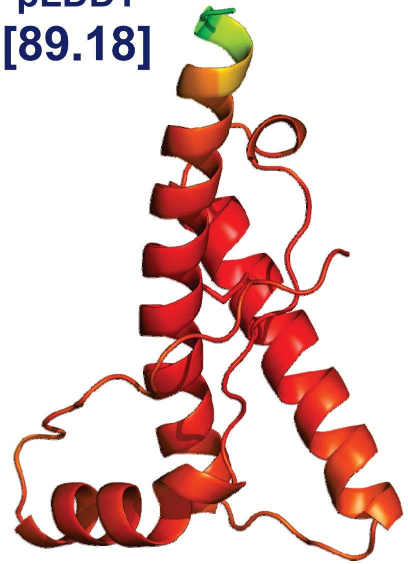
***In vitro* studies**

TgVole (1x)	**Not tested**
Water buffalo	**Not tested**

***In vivo* studies**

TgVole (1x)	**Not tested**
Water buffalo	**Not tested**

pLDDT
[89.18]



Protein code: 1198

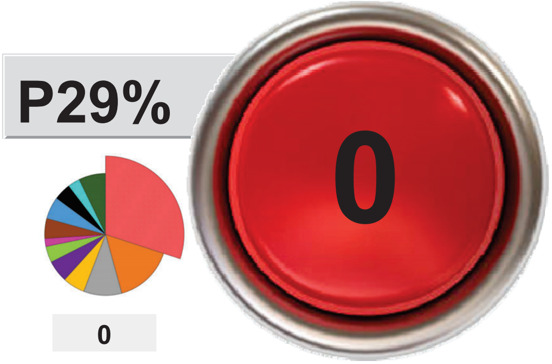
Distinct primary sequence across species

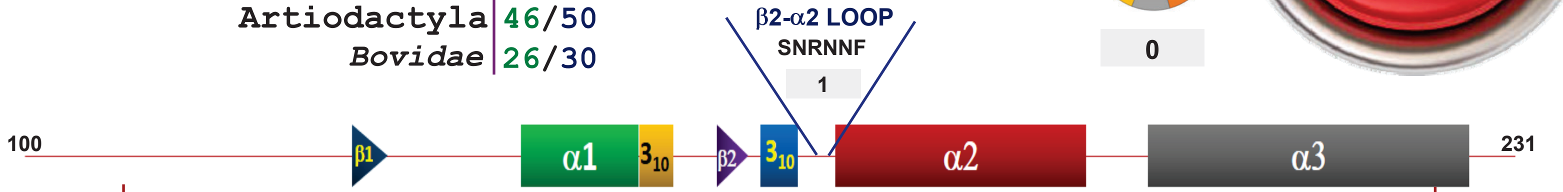
Anoa

GenBank: BK063916

Bubalus depressicornis

Artiodactyla	46/50
Bovidae	26/30





WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMHRYPNQVYYRPVDQYSNRNNFVHDCVNITVKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-

I V M W N N Q I Q V V K EGRS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

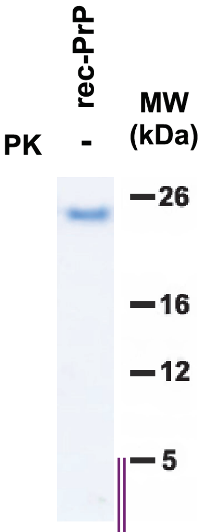
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -12.62

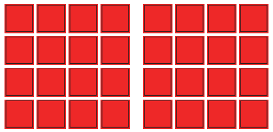


220 AA

NO MISFOLDING

0

Conformers



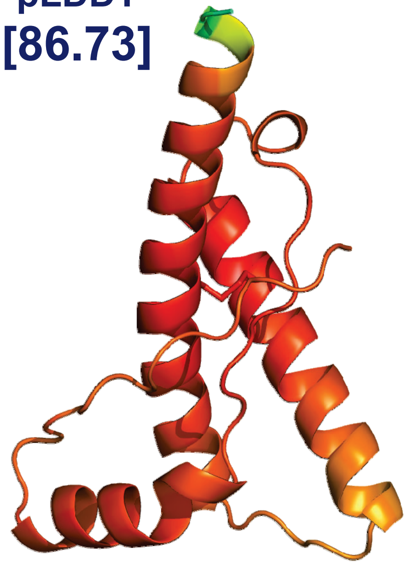
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [86.73]



Protein code: 1363

Distinct primary sequence across species

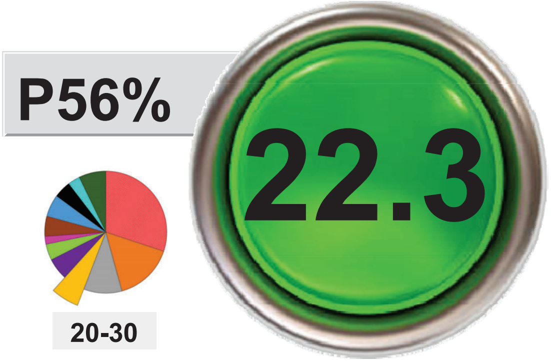
Takin

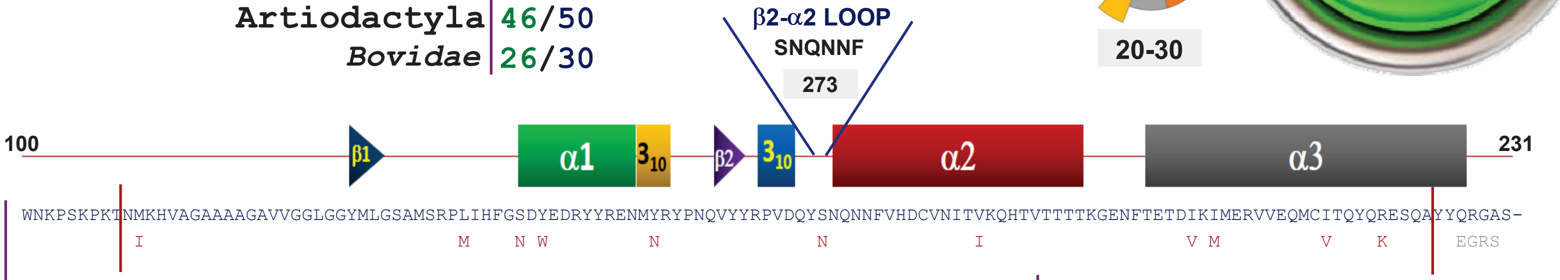
GenBank: AB060290

Budorcas taxicolor

Artiodactyla	46/50
Bovidae	26/30

P56%



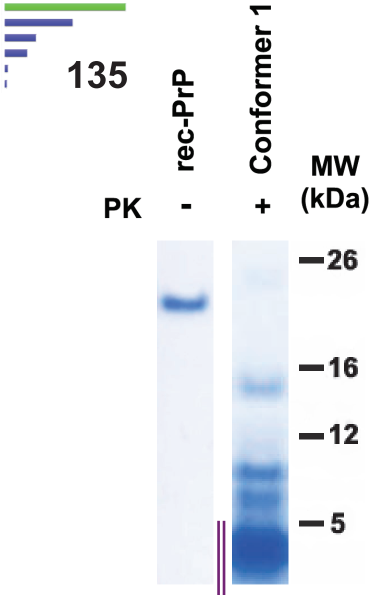


PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

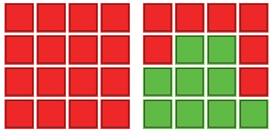
No deletions

No insertions

No polymorphic variants found



212 AA



1

Conformers

Tm^{Exp}: ND

ΔΔG: -12.4

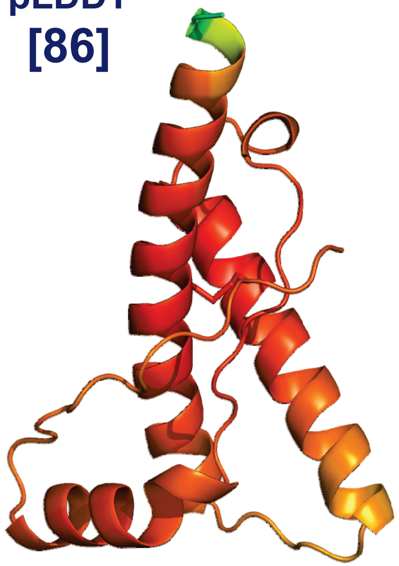
***In vitro* studies**

TgVole (1x)	**Not tested**
Takin	**Not tested**

***In vivo* studies**

TgVole (1x)	**Not tested**
Takin	**Not tested**

pLDDT
[86]



Protein code: 1348

Bactrian camel

GenBank: HQ204566

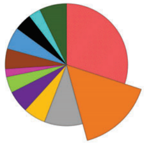
Camelus bactrianus ferus

Artiodactyla 46/50
Camelidae 2/2

1 species sharing the same primary sequence

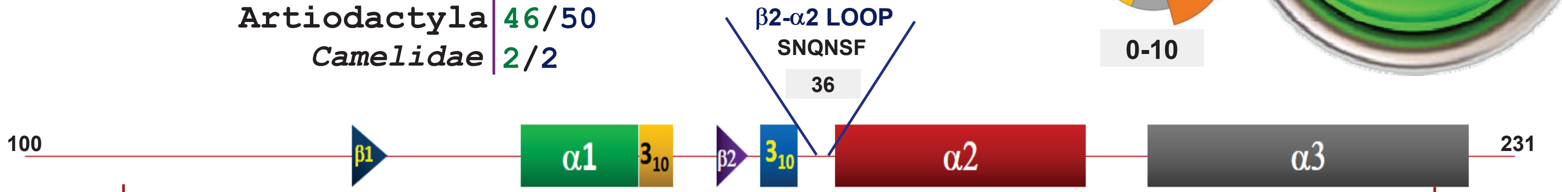
Camel
Camelus dromedarius

P45%



0-10

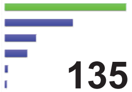
8.9



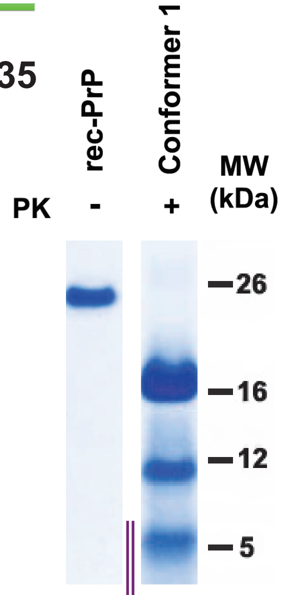
```
WNKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQREYQASYGRGAS-
         NI                            M      W         N        R     N   N         I                              V    K S  Y EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

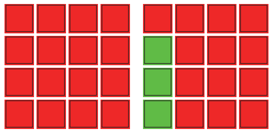


135



212 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -3.78

In vitro studies

TgVole (1x) Not tested

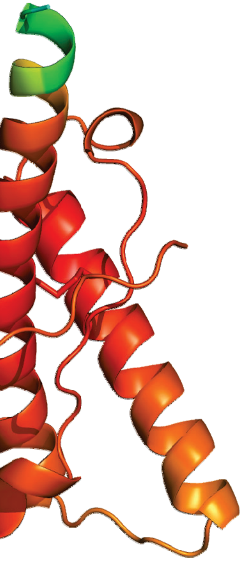
Bactrian camel Not tested

In vivo studies

TgVole (1x) Not tested

Bactrian camel Not tested

pLDDT
[85.87]



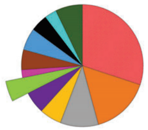
Protein code: 0544

Chacoan peccary

GenBank: BK063918

P67%

40



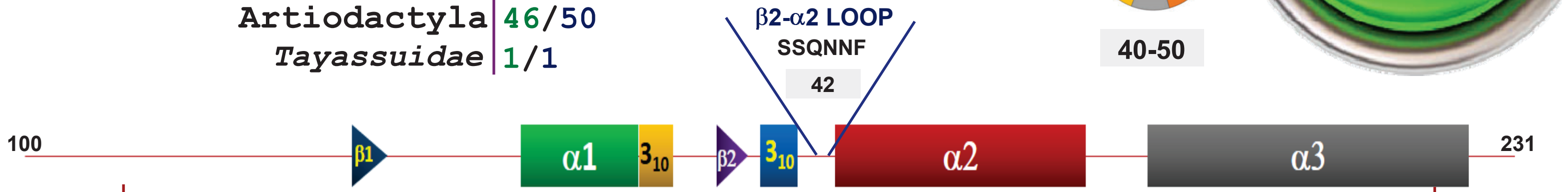
40-50

Collared peccary
Dicotyles tajacu

1 species sharing the same primary sequence

Catagonus wagneri

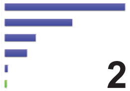
Artiodactyla	46/50
Tayassuidae	1/1



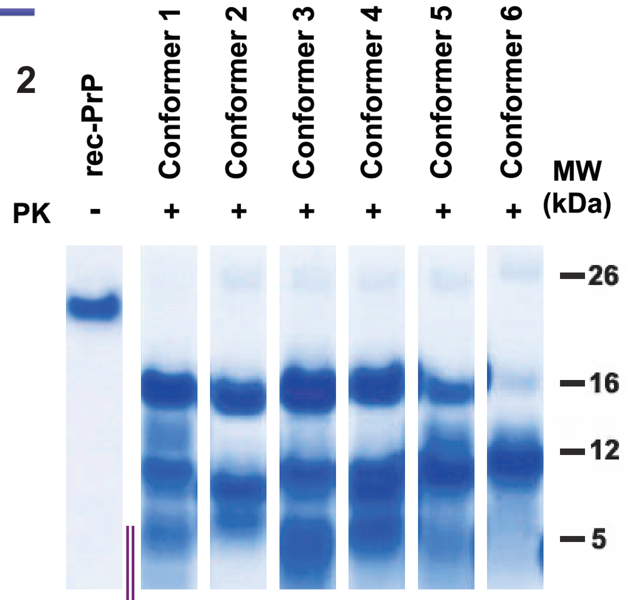
```
WNKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYSSQNNFVHDCVNITIKQHTVTTTTKGENFTETDIKMMERVVEQMCTTQYQREYEAYAQRGAS-
         NI                            M    N W         N              NN                               V           V    K SQ  YEGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

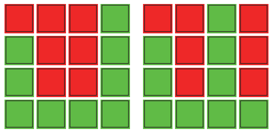


2



213 AA

6
Conformers



Tm^{Exp}: ND

ΔΔG: -17.92

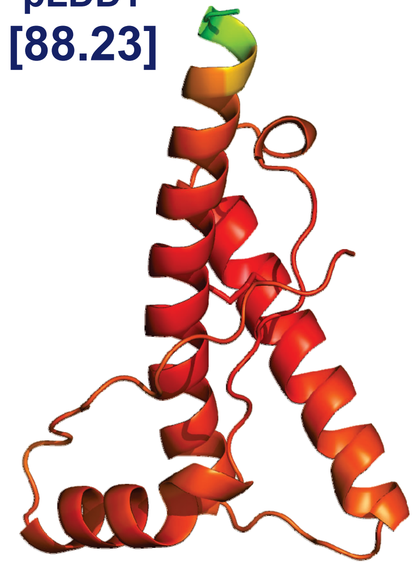
***In vitro* studies**

TgVole (1x)	**Not tested**
Chacoan peccary	**Not tested**

***In vivo* studies**

TgVole (1x)	**Not tested**
Chacoan peccary	**Not tested**

pLDDT
[88.23]



Protein code: 2022

Elk

GenBank: EU032294

Cervus elaphus canadensis

Artiodactyla 46/50

Cervidae 6/6

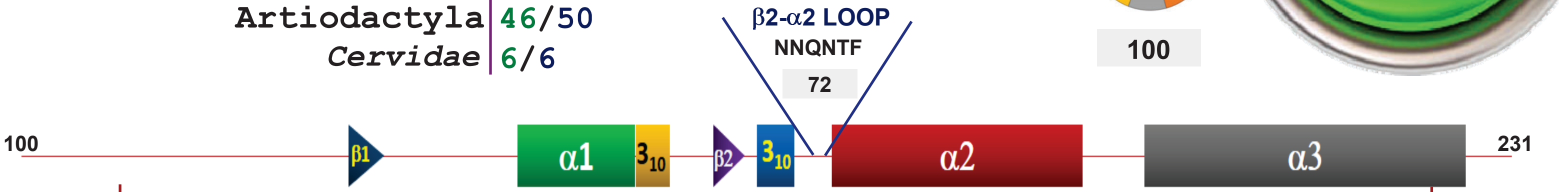
3 species sharing the same primary sequence

Indian hog deer
Axis porcinus

Sika deer
Cervus nippon

Thorold's deer
Przewalskium albirostris

P100%



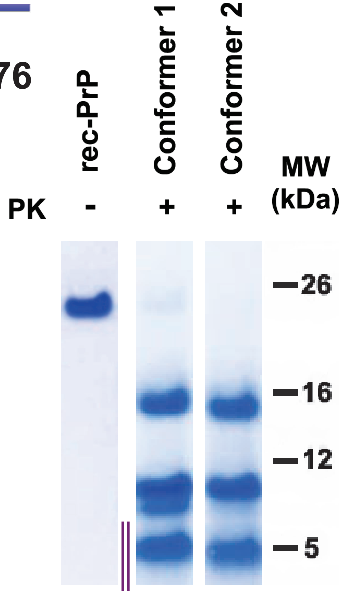
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNTFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-
          I                        M    W        N          N     I           V       V  K Q  EGRS
```

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

No deletions

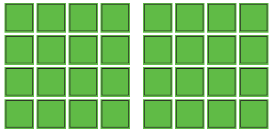
No insertions

It shows polymorphic variants



212 AA

2 Conformers



Tm^{Exp}: 69 ºC

ΔΔG: -11.73

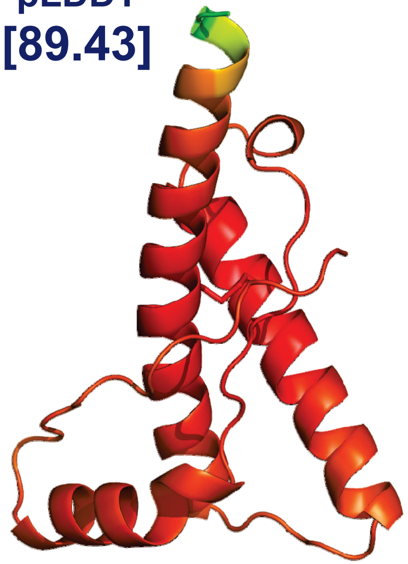
In vitro studies

TgVole (1x)	Propagate
Elk	Propagate

In vivo studies

TgVole (1x)	Infectious
TgElk	Ongoing

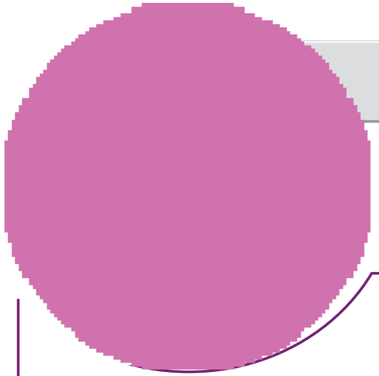
pLDDT [89.43]



Protein code: 1178

Blue wildebeest

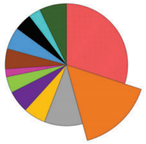
GenBank: EF165086



Connochaetes taurinus

Artiodactyla 46/50
Bovidae 26/30

P39%

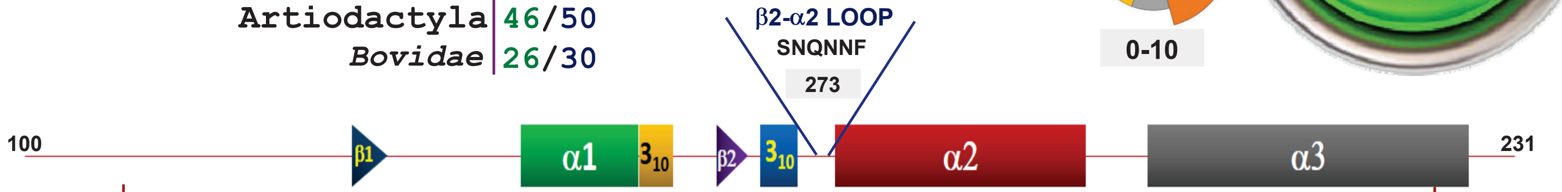


0-10

3.6

1 species sharing the same primary sequence

Black wildebeest
Connochaetes gnou

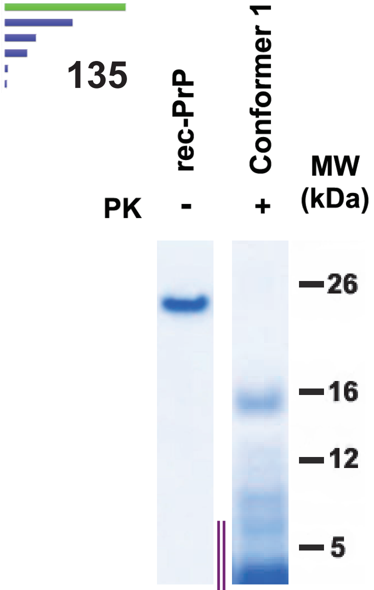


WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQRESQAYYQRGAS-

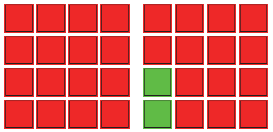
I V M W N N I V M V K EGRS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



212 AA



1
Conformers

Tm^{Exp}: ND

ΔΔG: -8.49

In vitro studies

TgVole (1x) Not tested

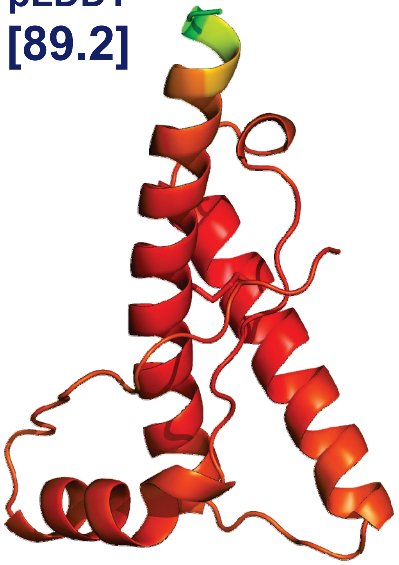
Blue wildebeest Not tested

In vivo studies

TgVole (1x) Not tested

Blue wildebeest Not tested

pLDDT
[89.2]



Protein code: 1414

Fallow deer

GenBank: EF139175

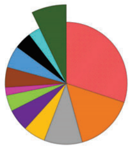
Dama dama

Artiodactyla 46/50
Cervidae 6/6

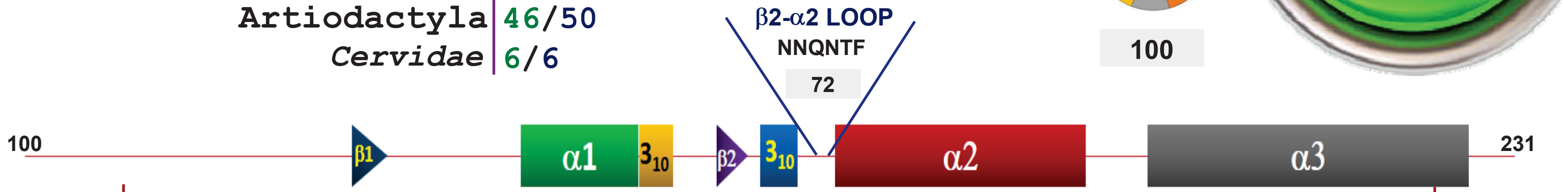
Distinct primary sequence across species

P100%

100



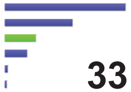
100



```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMNRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNTFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-
            I                            S  M      W         N                    N         I                   V          V    K  Q  EGRS
```

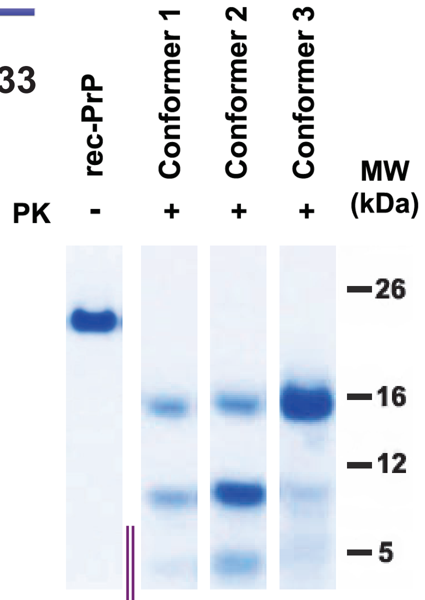
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



33

212 AA



3
Conformers

Tm^{Exp}: 66.8 ºC

ΔΔG: -10.8

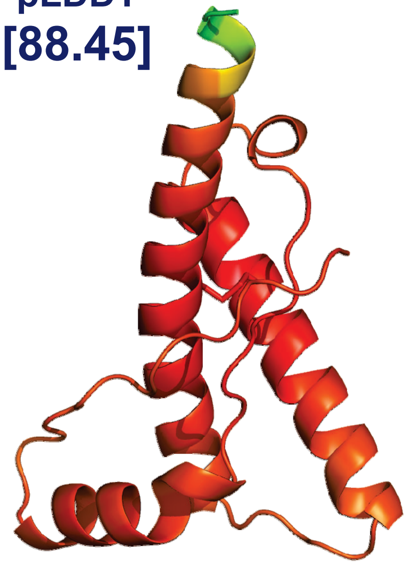
In vitro studies

TgVole (1x)	Not tested
Fallow deer	Not tested

In vivo studies

TgVole (1x)	Not tested
Fallow deer	Not tested

pLDDT
[88.45]



Protein code: 0980

Reticulata giraffe

GenBank: AF113942

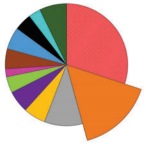
Giraffa camelopardalis reticulata

Artiodactyla	46/50
Giraffidae	2/2

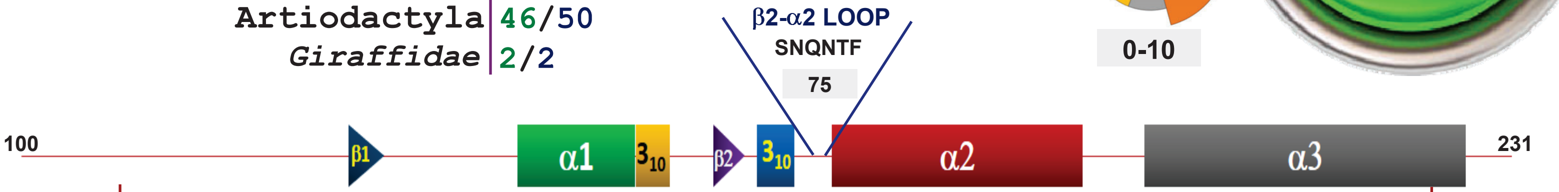
Distinct primary sequence across species

P35%

1.6



0-10



```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNTFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-
            I  V                                 M      W         N              N   N         I                  V           V    K  Q  EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

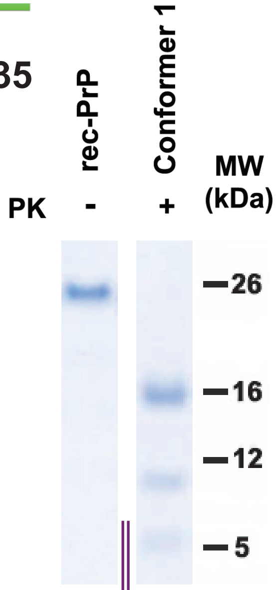
No deletions

No insertions

No polymorphic variants found

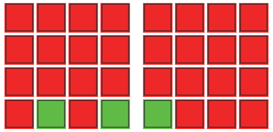
135

220 AA



1

Conformers



Tm^{Exp}: ND

ΔΔG: -14.52

***In vitro* studies**

TgVole (1x) Not tested

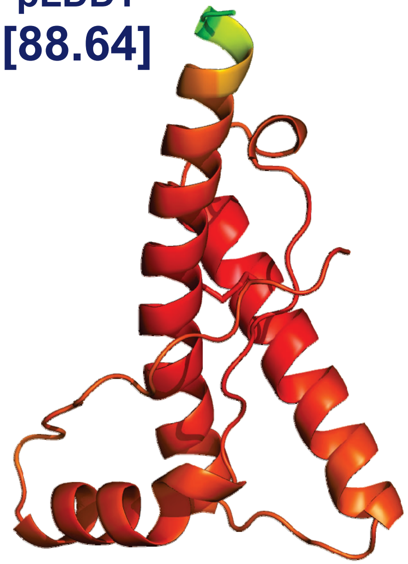
Reticulata giraffe Not tested

***In vivo* studies**

TgVole (1x) Not tested

Reticulata giraffe Not tested

pLDDT
[88.64]



Pygmy hippopotamus

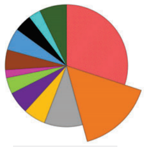
GenBank: AB919084

Hexaprotodon liberiensis

Artiodactyla 46/50
Hippopotamidae 2/2

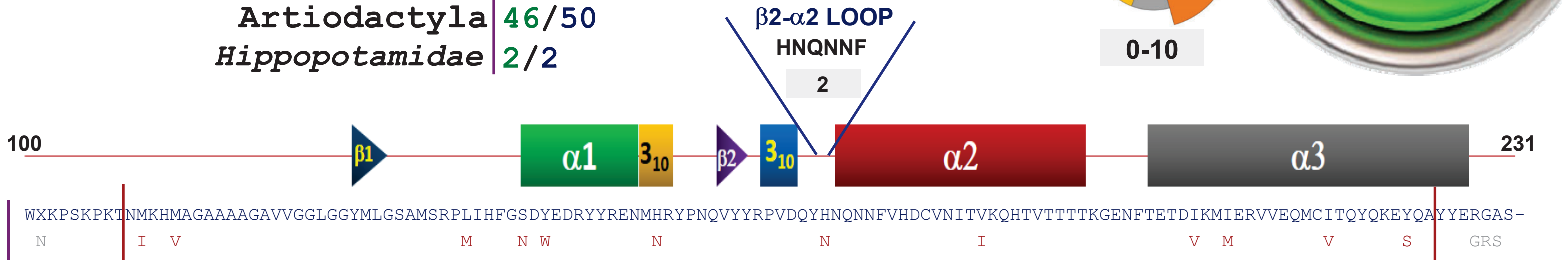
Distinct primary sequence across species

P45%



0-10

8.9



WXKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMHRYPNQVYYRPVDQYHNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMIERVVEQMCITQYQKEYQAYYERGAS-

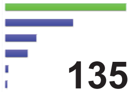
N I V M N W N N I V M V S GRS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

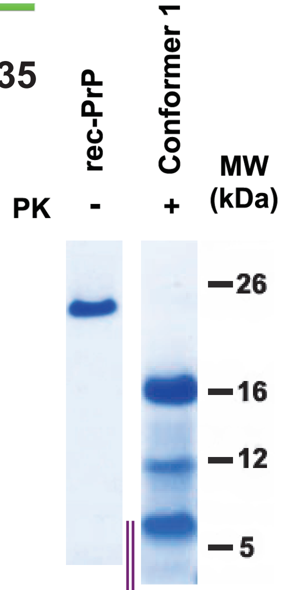
No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



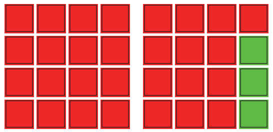
135



212 AA

1

Conformers



In vitro studies

Not tested
TgVole (1x)

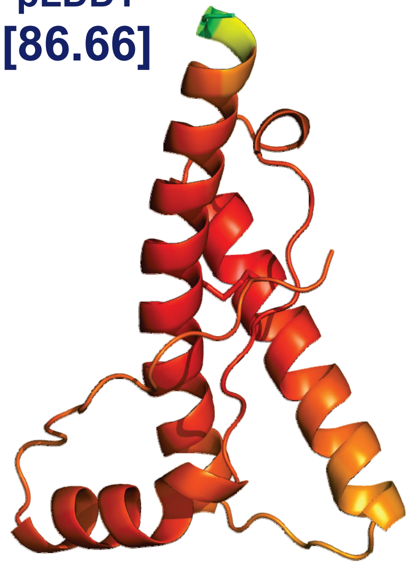
Not tested
Pygmy hippopotamus

In vivo studies

Not tested
TgVole (1x)

Not tested
Pygmy hippopotamus

pLDDT
[86.66]



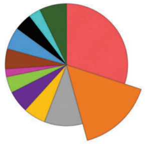
Protein code: 0946

Hippopotamus

GenBank: AB919083

P34%

0.9



0-10

Hippopotamus amphibius

Artiodactyla 46/50

Hippopotamidae 2/2

β2-α2 LOOP
HNQNNF
2

WXKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMHRYPNQVYYRPVDQYHNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMIERVVEQMCITQYQKEYQAYYERGAS-

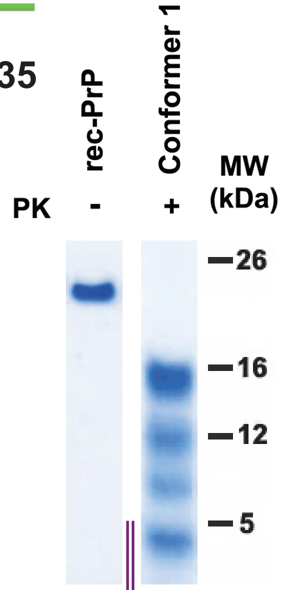
N I V M N W N N I V M V S GRS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

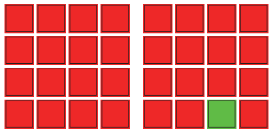
Distinct primary sequence across species

135



212 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

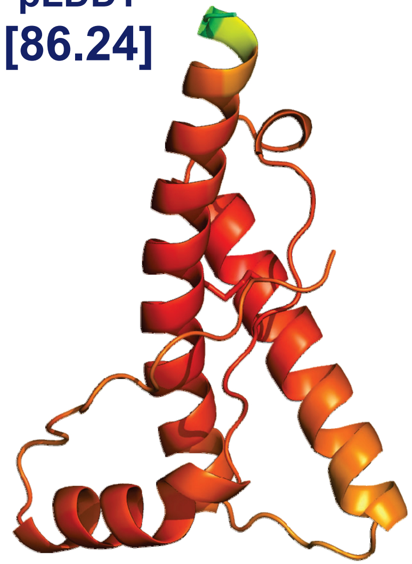
Hippopotamus Not tested

In vivo studies

TgVole (1x) Not tested

Hippopotamus Not tested

pLDDT
[86.24]



Protein code: 1359

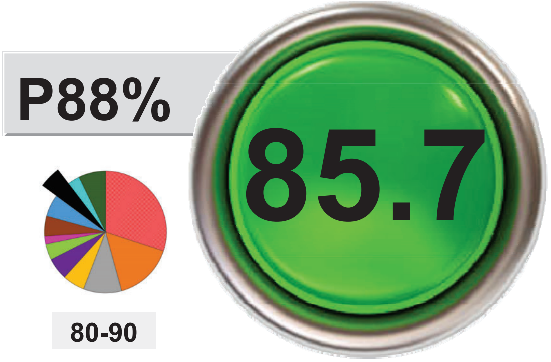
Sable antelope

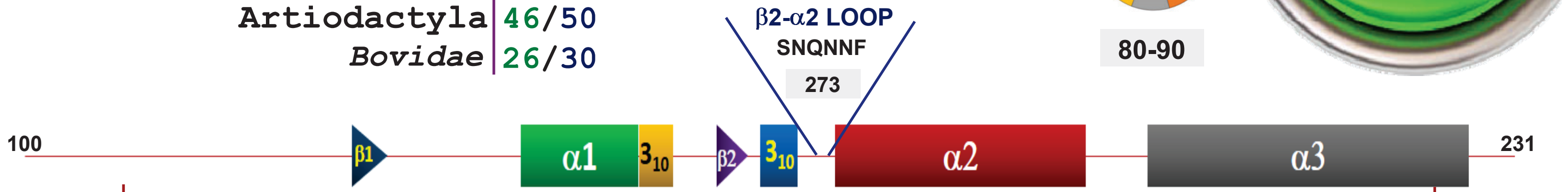
GenBank: BK064056

Hippotragus niger niger

Artiodactyla	46/50
Bovidae	26/30

P88%





WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQRESQAYYQRGAS-

I M W N N I V M V K EGRS

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

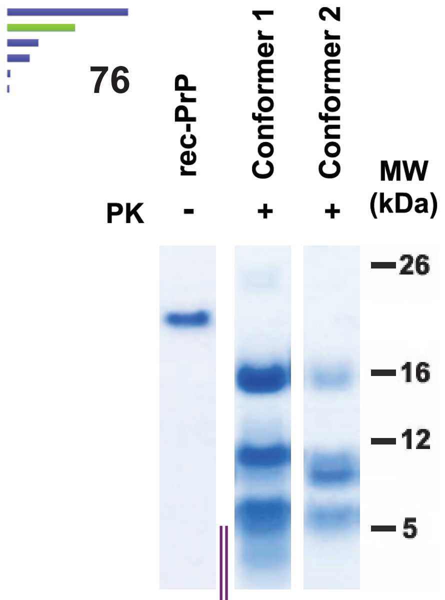
No deletions

No insertions

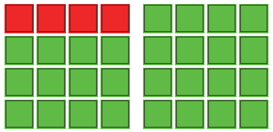
It shows polymorphic variants

5 species sharing the same primary sequence

- **Addax** *Addax nasomaculatus*
- **Hirola** *Beatragus hunteri*
- **Common tsessebe** *Damaliscus lunatus*
- **Roan antelope** *Hippotragus equinus*
- **Scimitar oryx** *Oryx dammah*



212 AA



2

Conformers

Tm^{Exp}: ND

ΔΔG: -11.98

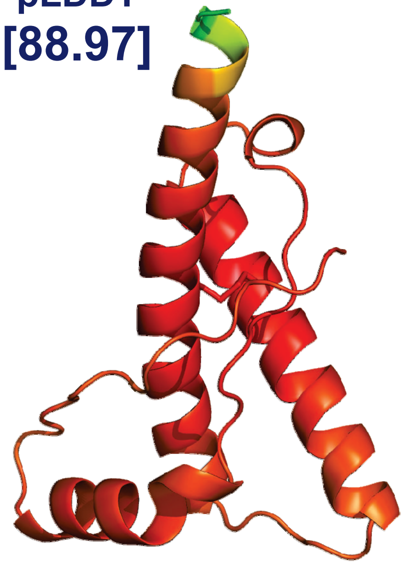
***In vitro* studies**

TgVole (1x)	Not tested
Sable antelope	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Sable antelope	Not tested

pLDDT [88.97]



Protein code: 3225

Distinct primary sequence across species

Waterbuck

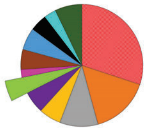
GenBank: EF165087

Kobus ellipsiprymnus

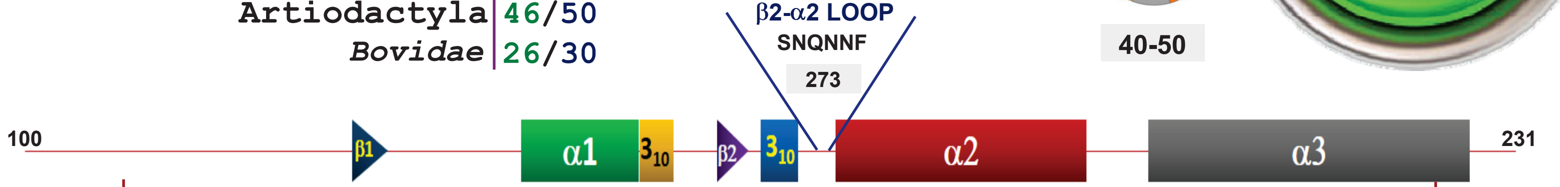
Artiodactyla	46/50
Bovidae	26/30

P69%

44.6



40-50

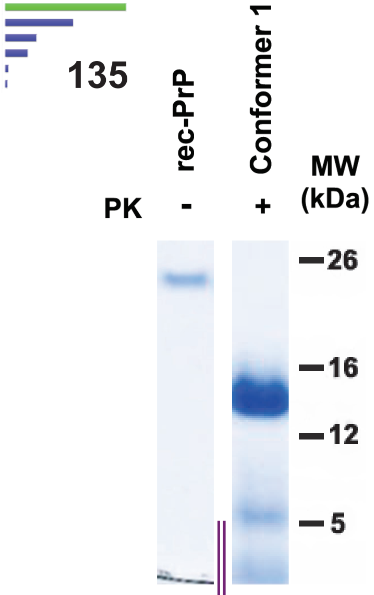


WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-

I V M W N N I V V K Q EGRS

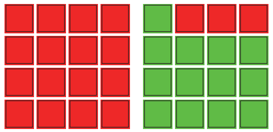
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



220 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -12.69

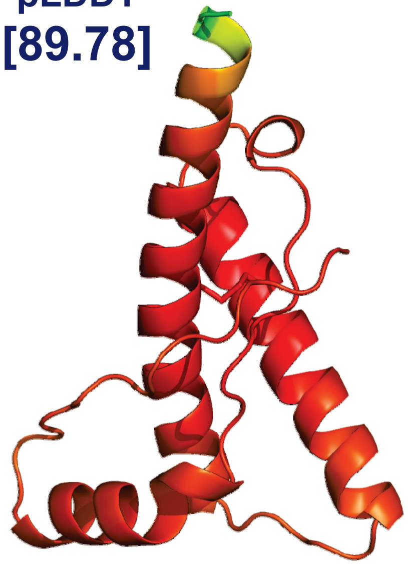
In vitro studies

TgVole (1x)	Not tested
Waterbuck	Not tested

In vivo studies

TgVole (1x)	Not tested
Waterbuck	Not tested

pLDDT
[89.78]



Protein code: 1351

Nile lechwe

GenBank: EF165088

Kobus megaceros

Artiodactyla 46/50

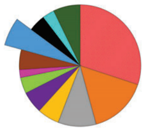
Bovidae 26/30

1 species sharing the same primary sequence

Lechwe
Kobus leche leche

P82%

71.8



70-80

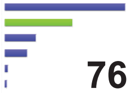
β2-α2 LOOP
SNQNNF
273

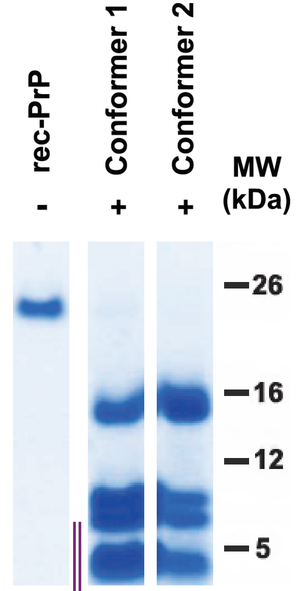
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQRESEAYYQRGAS-

I M W N N I V M V K Q EGRS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

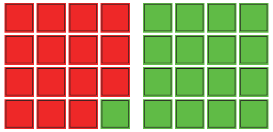
No deletions
No insertions
No polymorphic variants found





212 AA

2
Conformers



Tm^{Exp}: 69.6 ºC

ΔΔG: -13.74

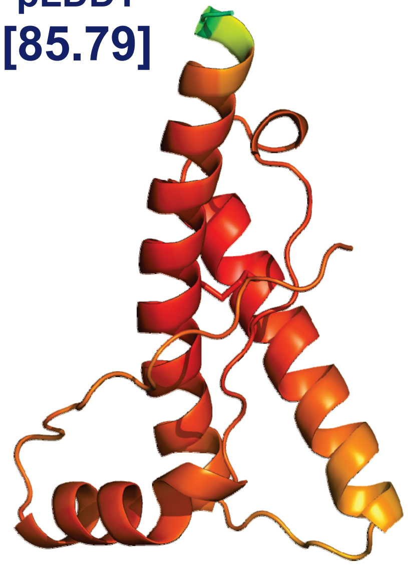
In vitro studies

TgVole (1x)	Not tested
Nile lechwe	Not tested

In vivo studies

TgVole (1x)	Not tested
Nile lechwe	Not tested

pLDDT
[85.79]



Protein code: 1448

Gerenuk

GenBank: BK064079

Litocranius walleri

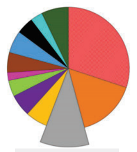
Artiodactyla 46/50
Bovidae 26/30

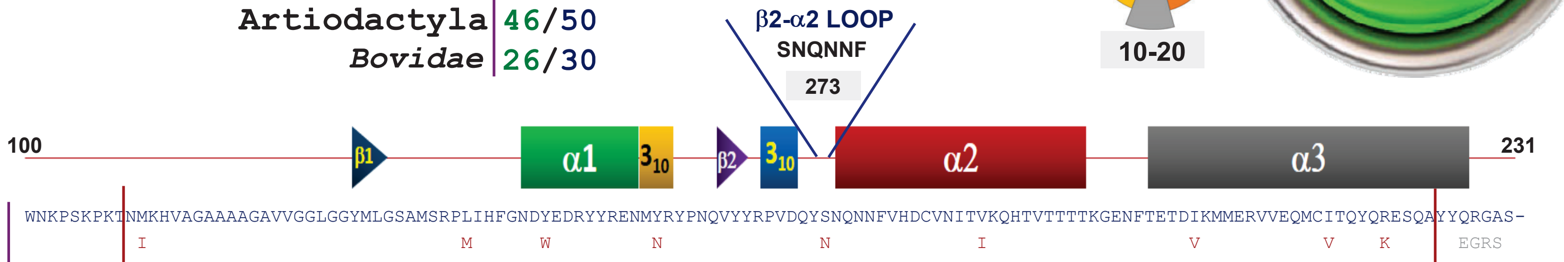
5 species sharing the same primary sequence

- ● **Harvey's red duiker** *Cephalophus natalensis harveyi*
- ● **Kirk's dik-dik** *Madoqua kirkii*
- ● **Suni** *Neotragus moschatus*
- ● **Klipspringer** *Oreotragus oreotragus*
- ● **Oribi** *Ourebia ourebi*

P48%

12.5


10-20



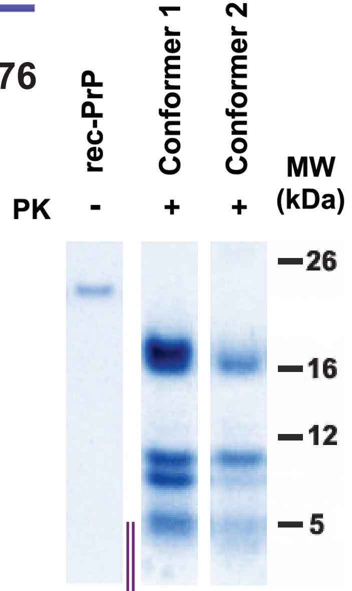
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-

I M W N N I V V K EGRS

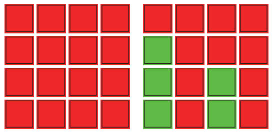
PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found


76



220 AA


2 Conformers

Tm^{Exp}: ND

ΔΔG: -13.08

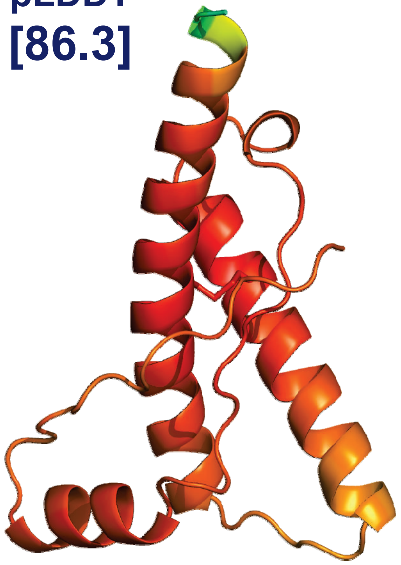
***In vitro* studies**

TgVole (1x)	Not tested
Gerenuk	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Gerenuk	Not tested

pLDDT [86.3]



Protein code: 3257

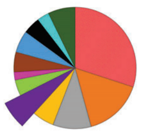
Alpine musk deer

GenBank: AY723286

Moschus chrysogaster

Artiodactyla 46/50
Moschidae 2/2

P66%



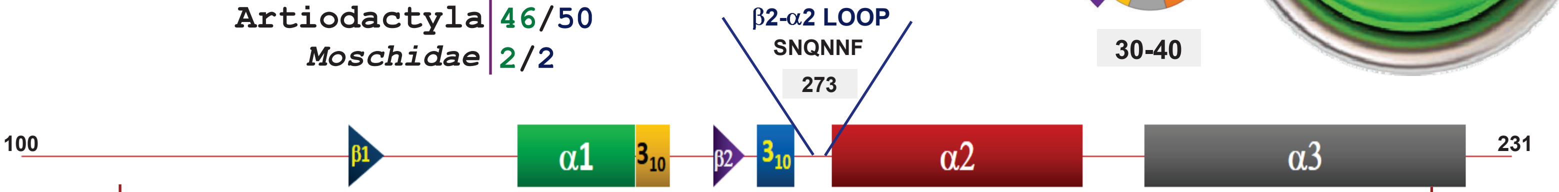
39.3

30-40

2 species sharing the same primary sequence

Dwarf musk deer
Moschus berezovskii

Saiga antelope
Saiga tatarica



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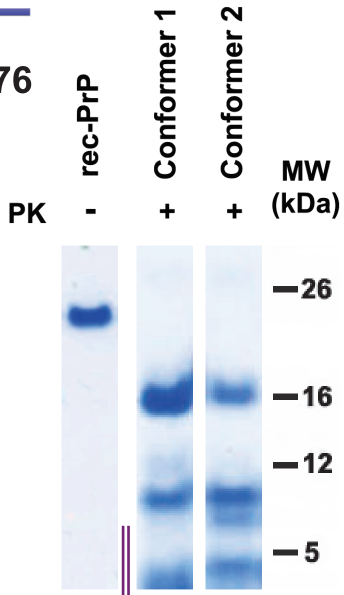
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQRESQAYYQRGAS-
          I                             M    W       N          N         I                    V M      V   K      EGRS
```

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

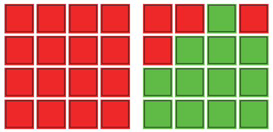
No deletions
No insertions
No polymorphic variants found

76



212 AA

2
Conformers



Tm^Exp: ND

ΔΔG: -12.34

In vitro studies

TgVole (1x) Not tested

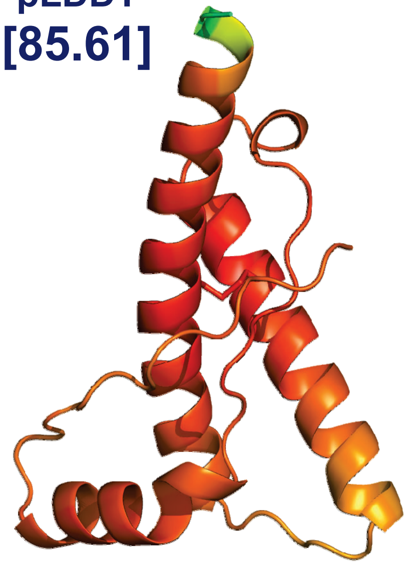
Alpine musk deer Not tested

In vivo studies

TgVole (1x) Not tested

Alpine musk deer Not tested

pLDDT
[85.61]



Protein code: 0920

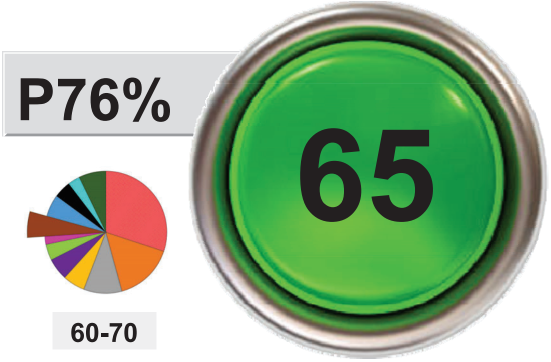
Siberian musk deer

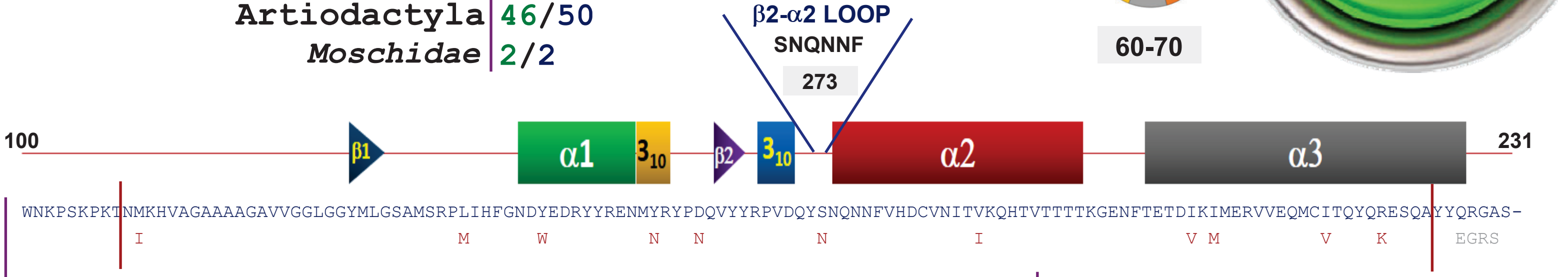
GenBank: BK063923

Moschus moschiferus

Artiodactyla 46/50
Moschidae 2/2

P76%





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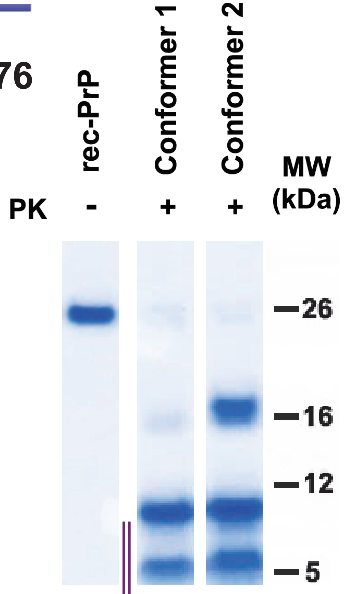
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPDQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQRESQAYYQRGAS-
          I                                M       W            N   N            N              I                     V M          V    K       EGRS
```

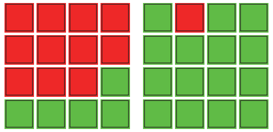
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species



212 AA



2
Conformers

Tm^{Exp}: ND

ΔΔG: -11.59

***In vitro* studies**

TgVole (1x) — Not tested

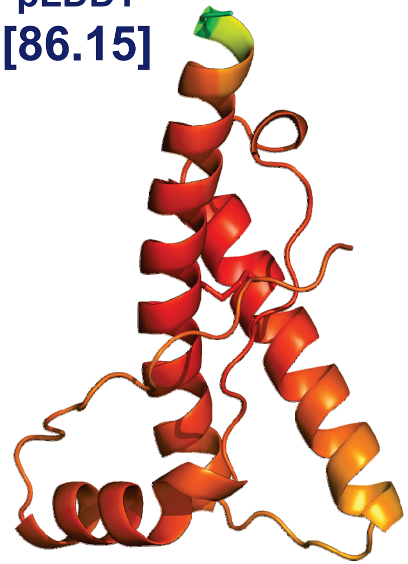
Siberian musk deer — Not tested

***In vivo* studies**

TgVole (1x) — Not tested

Siberian musk deer — Not tested

pLDDT
[86.15]



Protein code: 2032

Indian muntjac

GenBank: BK064098

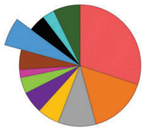
Muntiacus muntjak

Artiodactyla 46/50
Cervidae 6/6

Distinct primary sequence across species

P82%

71.8



70-80

β2-α2 LOOP
NNQNTF
72

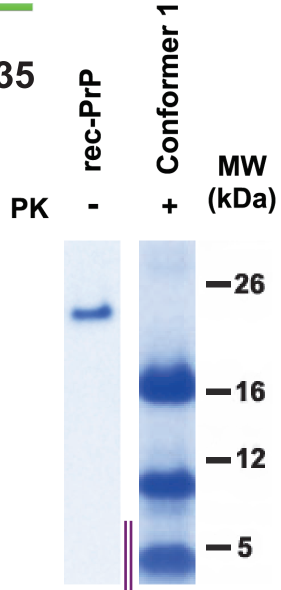
`WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNTFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-`

`I M W N N I V V K Q EGRS`

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

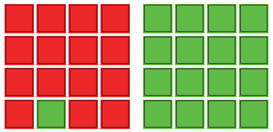
No deletions
No insertions
No polymorphic variants found

135



212 AA

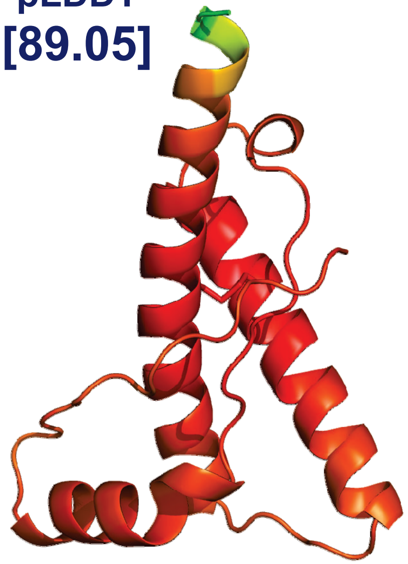
1
Conformers



Tm^{Exp}: ND

ΔΔG: -14.89

pLDDT
[89.05]



In vitro studies

TgVole (1x) — Not tested

Indian muntjac — Not tested

In vivo studies

TgVole (1x) — Not tested

Indian muntjac — Not tested

Protein code: 3277

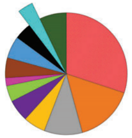
Reeves's muntjac

GenBank: KC788406

Muntiacus reevesi

Artiodactyla 46/50
Cervidae 6/6

P92% **96.4**

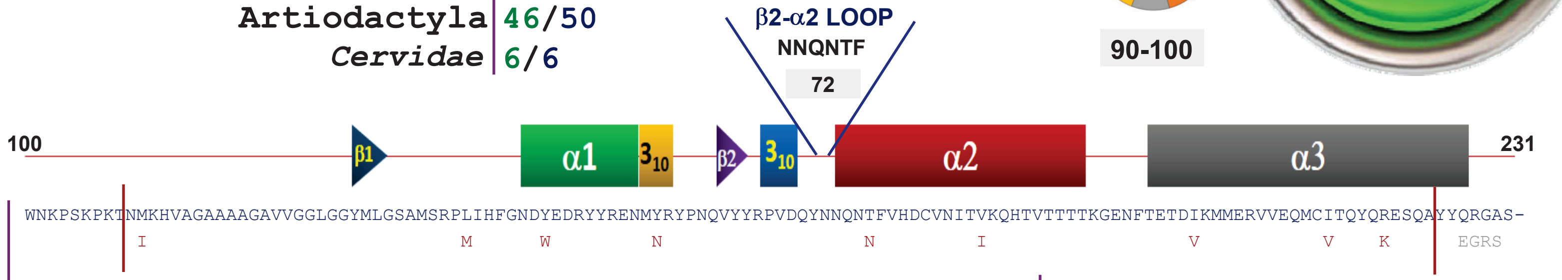


90-100

2 species sharing the same primary sequence

Hairy-fronted muntjac
Muntiacus crinifrons

Gongshan muntjac
Muntiacus gongshanensis

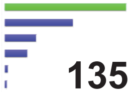


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNTFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-

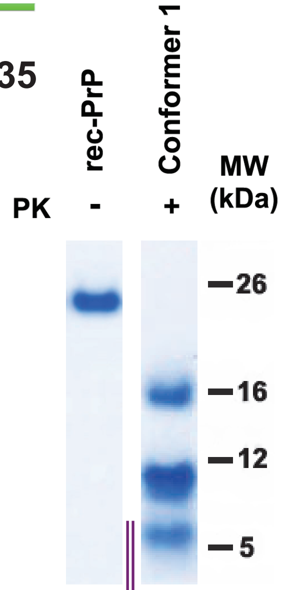
I M W N N I V V K EGRS

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



135



212 AA

Tm^{Exp}: 68.1 ºC

ΔΔG: -13.83

In vitro studies

TgVole (1x) Not tested

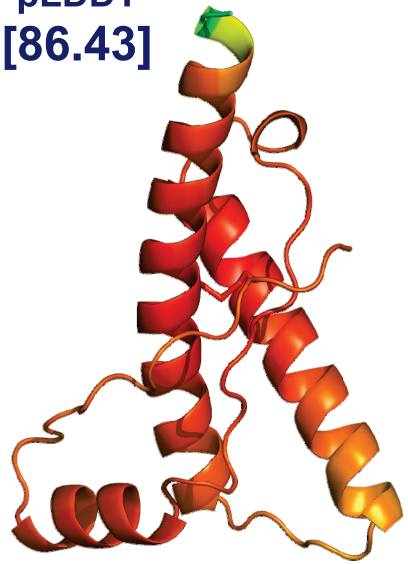
Reeves's muntjac Not tested

In vivo studies

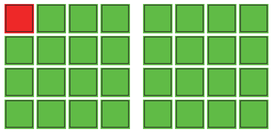
TgVole (1x) Not tested

Reeves's muntjac Not tested

pLDDT [86.43]



1
Conformers



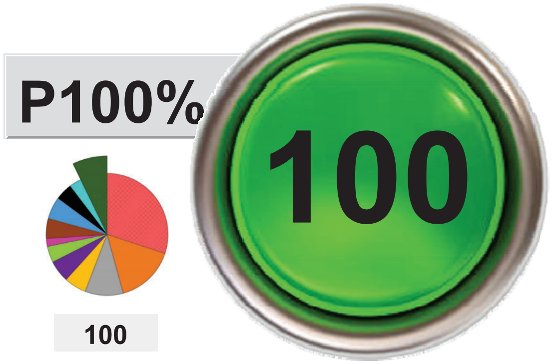
Protein code: 0950

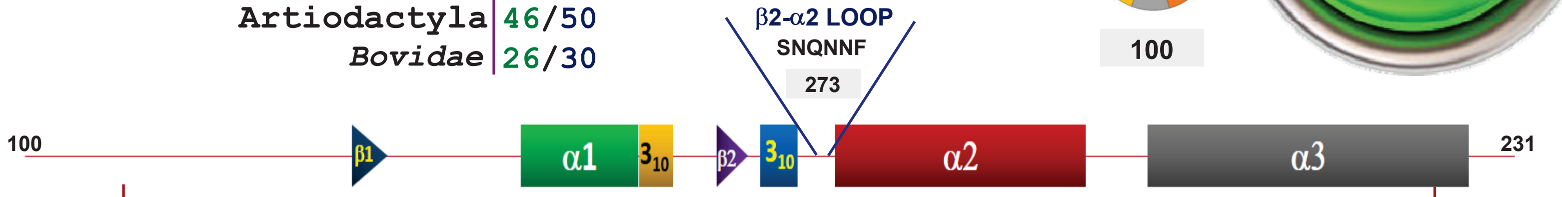
Royal antelope

GenBank: BK064112

Neotragus pygmaeus

Artiodactyla 46/50
Bovidae 26/30



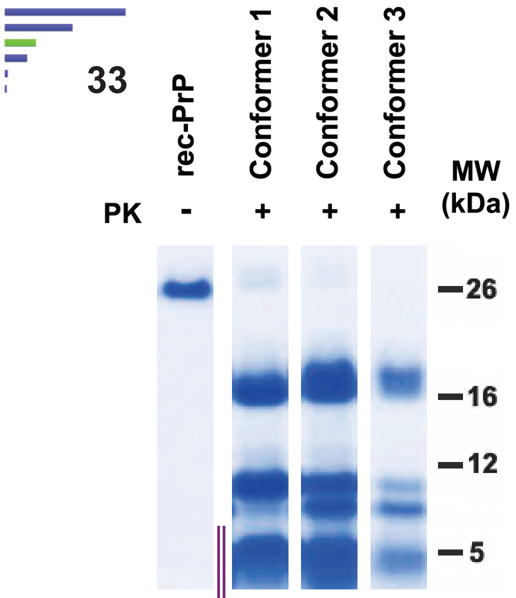


WNKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-
NI M W N N I V V K EGRS

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species



212 AA

3
Conformers

Tm^{Exp}: ND

ΔΔG: -11.29

In vitro studies

TgVole (1x) Not tested

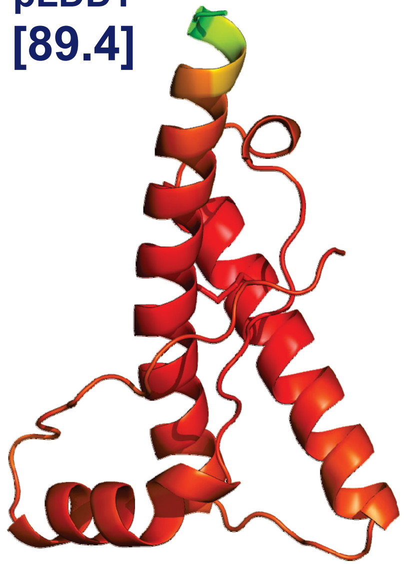
Royal antelope Not tested

In vivo studies

TgVole (1x) Not tested

Royal antelope Not tested

pLDDT
[89.4]



Protein code: 3292

Mule deer

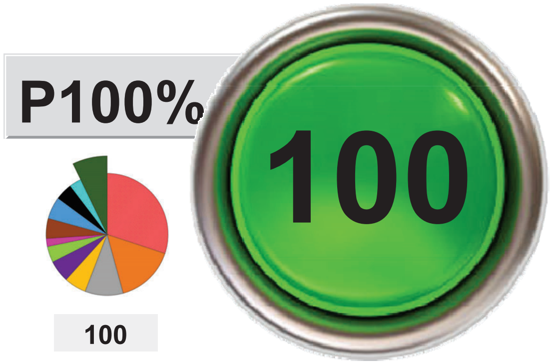
GenBank: MT709729

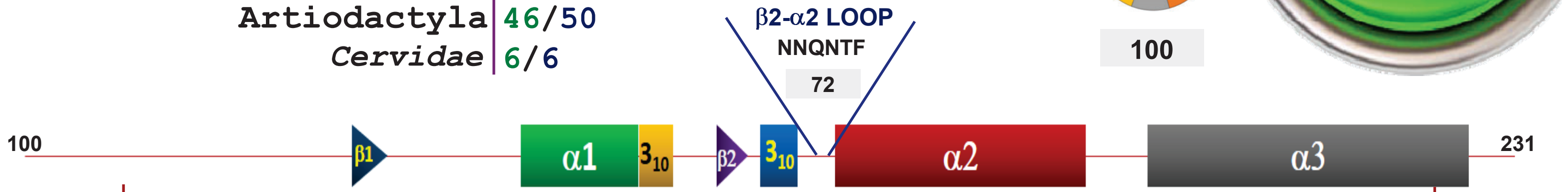
Odocoileus hemionus

Artiodactyla 46/50
Cervidae 6/6

7 species sharing the same primary sequence

- **Moose** *Alces alces*
- **Roe deer** *Capreolus capreolus*
- **Siberian roe deer** *Capreolus pygargus*
- **Water deer** *Hydropotes inermis*
- **White-tailed deer** *Odocoileus virginianus*
- **Reindeer** *Rangifer tarandus*
- **Eld's deer** *Rucervus eldii thamin*





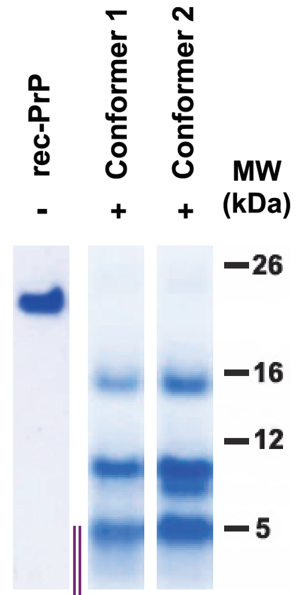
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNTFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-

I M W N N I V V K EGRS

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
It shows polymorphic variants

76



212 AA

2 Conformers

Tm^{Exp}: 67.7 ºC

ΔΔG: -21.62

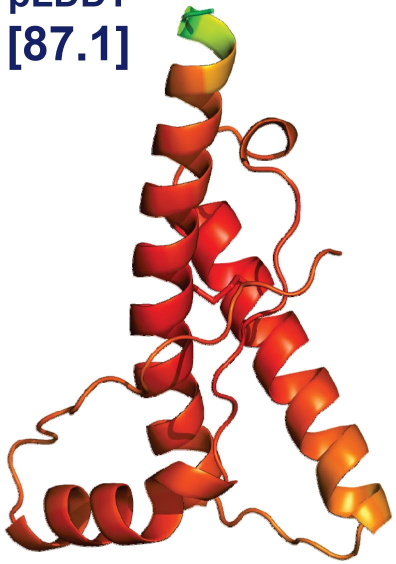
In vitro studies

TgVole (1x)	Propagate
Mule deer	Propagate

In vivo studies

TgVole (1x)	Infectious
TgMule deer	Ongoing

pLDDT [87.1]



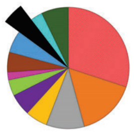
Protein code: 0174

Okapi

GenBank: BK064032

P88%

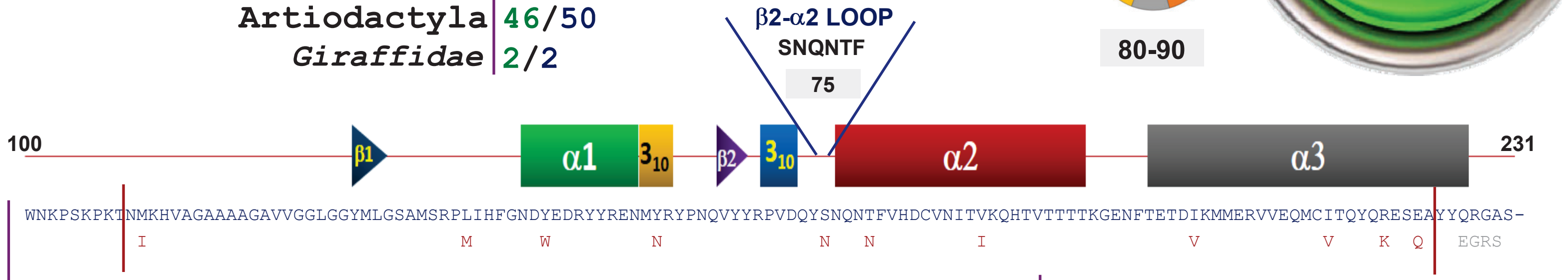
87.1



80-90

Okapia johnstoni

Artiodactyla	46/50
Giraffidae	2/2



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNTFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-

I M W N N N I V V K Q EGRS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

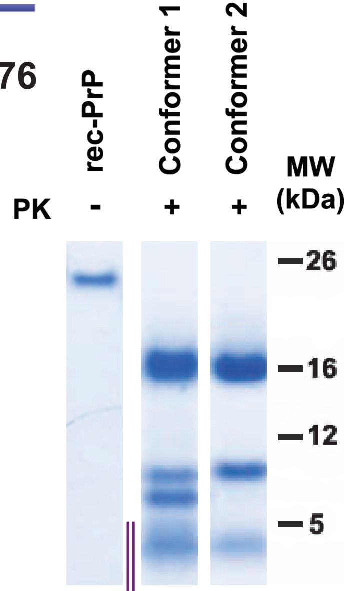
No deletions

No insertions

No polymorphic variants found

Distinct primary sequence across species

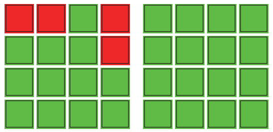
76



220 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: -12.63

In vitro studies

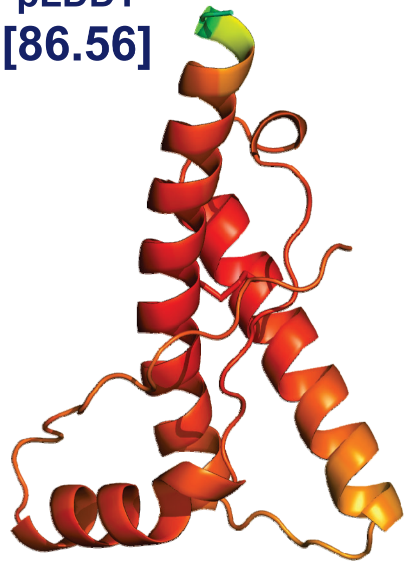
TgVole (1x)	Not tested
Okapi	Not tested

In vivo studies

TgVole (1x)	Not tested
Okapi	Not tested

pLDDT

[86.56]



Protein code: 3197

Gemsbok

GenBank: BK064117

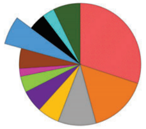
Oryx gazella

Artiodactyla 46/50
Bovidae 26/30

Distinct primary sequence across species

P83%

76.1



70-80

β2-α2 LOOP
SNQNNF
273

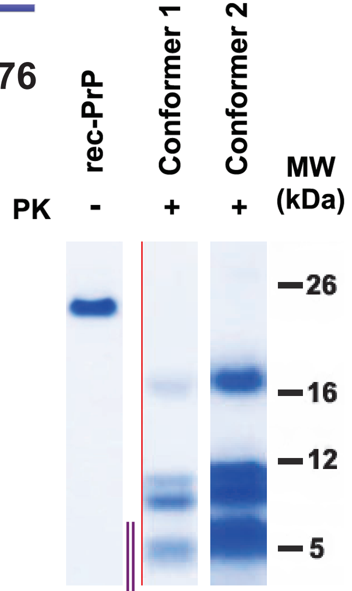
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQKESQAYYQRGAS-

I M W N N I V M V EGRS

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

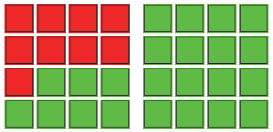
No deletions
No insertions
No polymorphic variants found

76



212 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -11.01

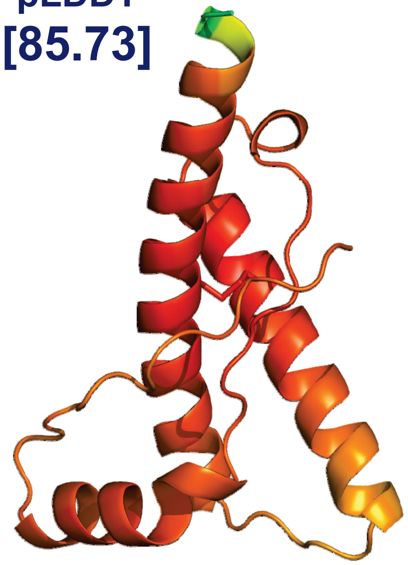
***In vitro* studies**

TgVole (1x)	Not tested
Gemsbok	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Gemsbok	Not tested

pLDDT
[85.73]



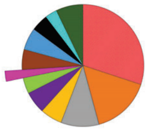
Protein code: 3297

Sheep

GenBank: NM_001009481

P73%

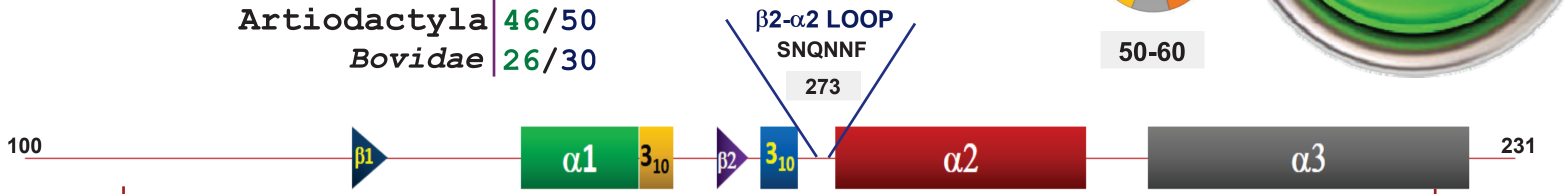
54.3



50-60

Ovis aries

Artiodactyla	46/50
Bovidae	26/30



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQRESQAYYQRGAS-

I M W N N I V M V K EGRS

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

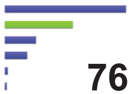
No deletions

No insertions

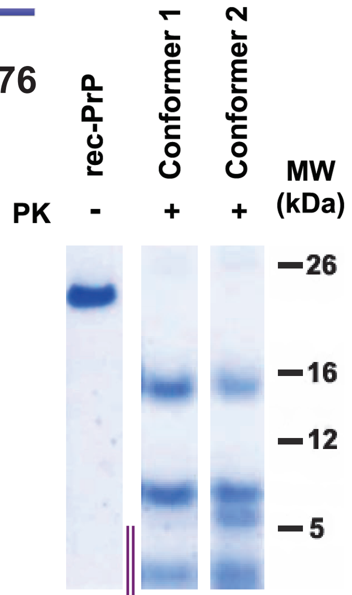
It shows polymorphic variants

18 species sharing the same primary sequence

Goat	*Capra hircus*
Dall sheep	*Ovis dalli*
Muskox	*Ovibos moschatus*
Alpine ibex	*Capra ibex*
Markhor	*Capra falconeri*
Iberian ibex	*Capra pyrenaica*
Barbary sheep	*Ammotragus lervia*
Pyrenean chamois	*Rupicapra pyrenaica*
Arabian tahr	*Hemitragus jayakari*
Japanese serow	*Capricornis crispus*
Mountain goat	*Oreamnos americanus*
Chinese goral	*Naemorhedus griseus*
Siberian ibex	*Capra sibirica*
Tibetan antelope	*Pantholops hodgsonii*
Nilgiri tahr	*Hemitragus hylocrius*
Argali	*Ovis ammon*
Snow sheep	*Ovis nivicola lydekkeri*
Bharal	*Pseudois nayaur*



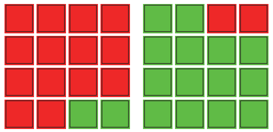
76



212 AA

2

Conformers

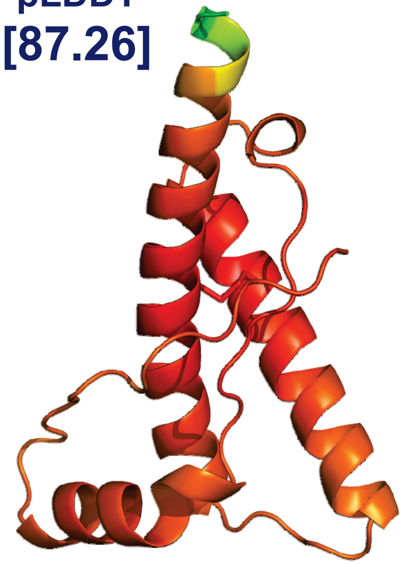


Tm^{Exp}: 71.7 ºC

ΔΔG: -11.89

pLDDT

[87.26]



In vitro studies

TgVole (1x)	Propagate
TgSheep	Propagate

In vivo studies

TgVole (1x)	Infectious
TgSheep	Infectious

Protein code: 0195

Bighorn sheep

GenBank: DQ648476

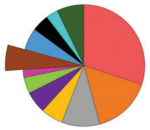
Ovis canadensis

Artiodactyla 46/50

Bovidae 26/30

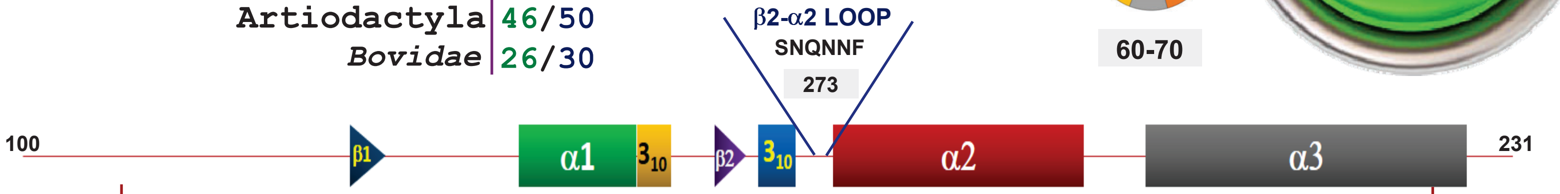
Distinct primary sequence across species

P75%



60-70

62.5



```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMGRVVEQMCITQYQRESQAYYQRGAS-
           I                        M      W         N              N            I                     V M E     V    K      EGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

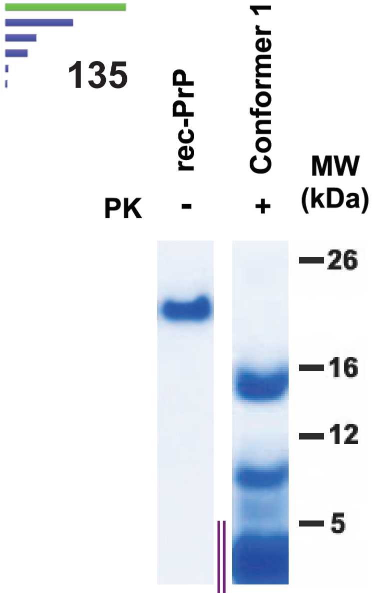
No deletions

No insertions

It shows polymorphic variants

Tm^{Exp}: ND

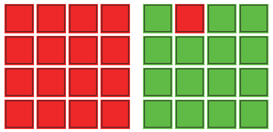
ΔΔG: -9.13



212 AA

1

Conformers



In vitro studies

TgVole (1x) Not tested

Bighorn sheep Not tested

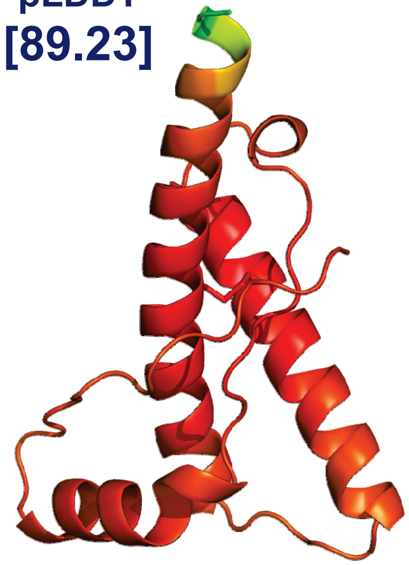
In vivo studies

TgVole (1x) Not tested

Bighorn sheep Not tested

pLDDT

[89.23]



Protein code: 1478

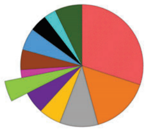
Common warthog

GenBank: BK063968

Phacochoerus africanus

Artiodactyla 46/50
Suidae 3/3

P71%



40-50

48.6

1 species sharing the same primary sequence

Red river hog
Potamochoerus porcus

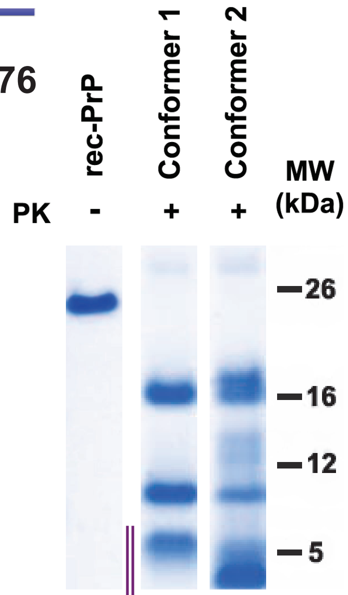
β2-α2 LOOP
SNQNSF
36

```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMNRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDVKMIERVVEQMCITQYQKEYEAYAQRGAS-
          I                            S  M    N W        N                N  N      I                 M     V     SQ  YEGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

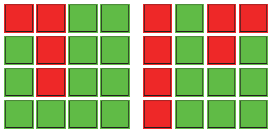
No deletions
No insertions
No polymorphic variants found

76



213 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -13.67

In vitro studies

TgVole (1x) — Not tested

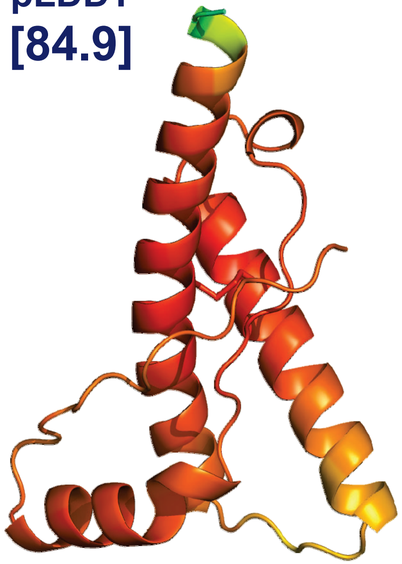
Common warthog — Not tested

In vivo studies

TgVole (1x) — Not tested

Common warthog — Not tested

pLDDT
[84.9]



Protein code: 3101

Maxwell's duiker

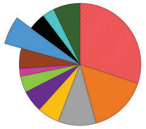
GenBank: BK064126

Philantomba maxwellii

Artiodactyla 46/50
Bovidae 26/30

Distinct primary sequence across species

P81% **71.4**



70-80

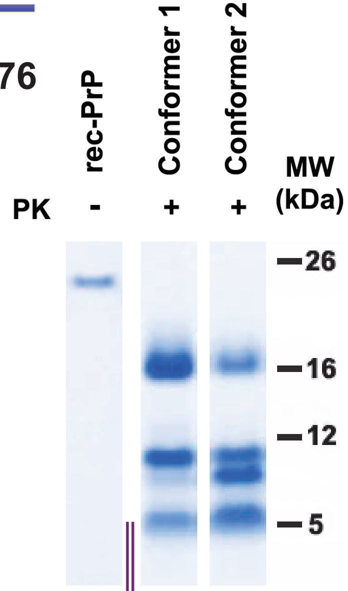
β2-α2 LOOP
SNQNNF
273

```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-
          I                         M     W        N            N          I               V         V   K     EGRS
```

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

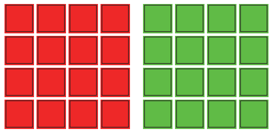
No deletions
No insertions
No polymorphic variants found

76



220 AA

2 Conformers



Tm^{Exp}: ND

ΔΔG: -11.79

***In vitro* studies**

TgVole (1x) Not tested

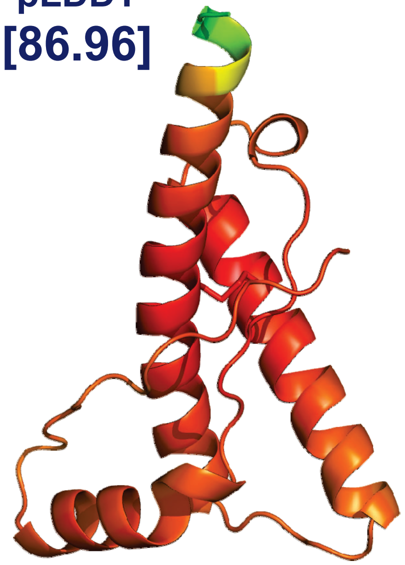
Maxwell's duiker Not tested

***In vivo* studies**

TgVole (1x) Not tested

Maxwell's duiker Not tested

pLDDT [86.96]



Protein code: 3307

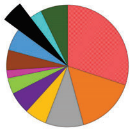
Reindeer

GenBank: MW804583

Rangifer tarandus

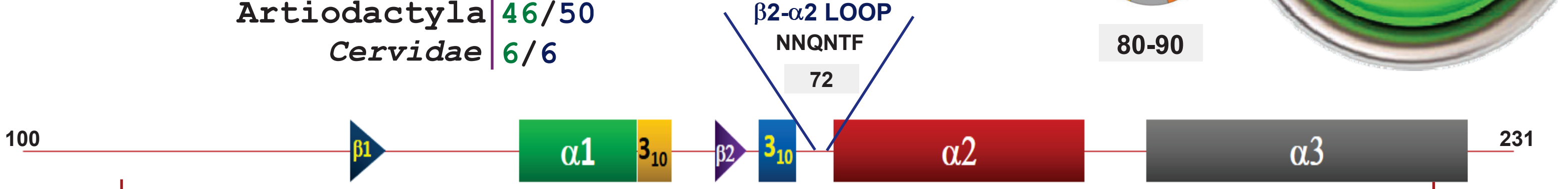
Artiodactyla	46/50
Cervidae	6/6

P89%



80-90

89.3



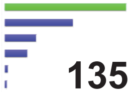
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMNRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNTFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-

I S M W N N I V V K EGRS

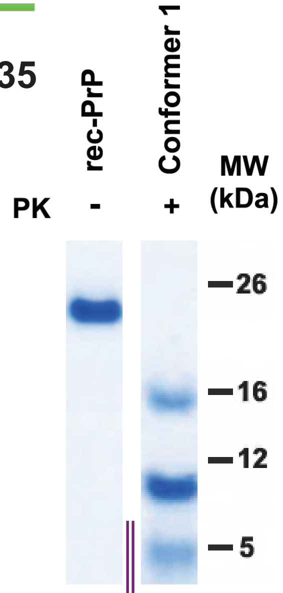
PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
It shows polymorphic variants

Distinct primary sequence across species

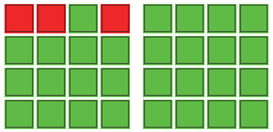


135



212 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -9.46

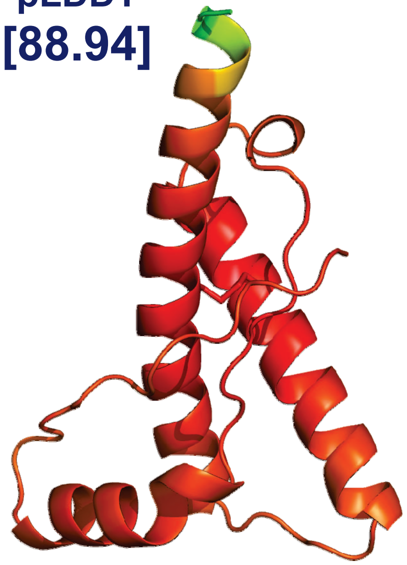
In vitro studies

TgVole (1x)	Not tested
Père David's deer	Not tested

In vivo studies

TgVole (1x)	Not tested
Père David's deer	Not tested

pLDDT
[88.94]



Protein code: 1450

Steenbok

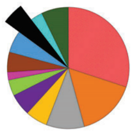
GenBank: BK064134

Raphicerus campestris

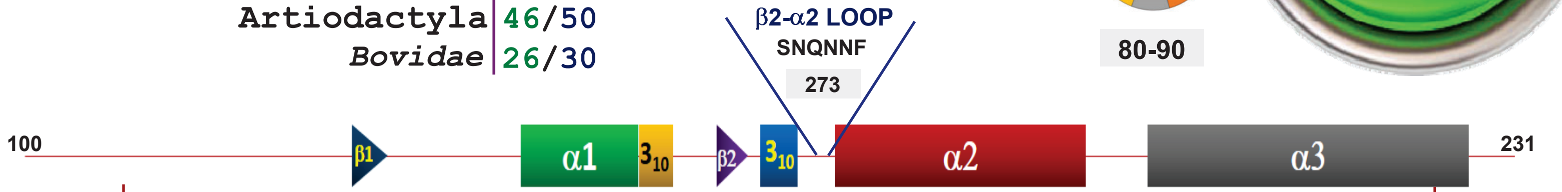
Artiodactyla 46/50
Bovidae 26/30

P89%

89.3



80-90



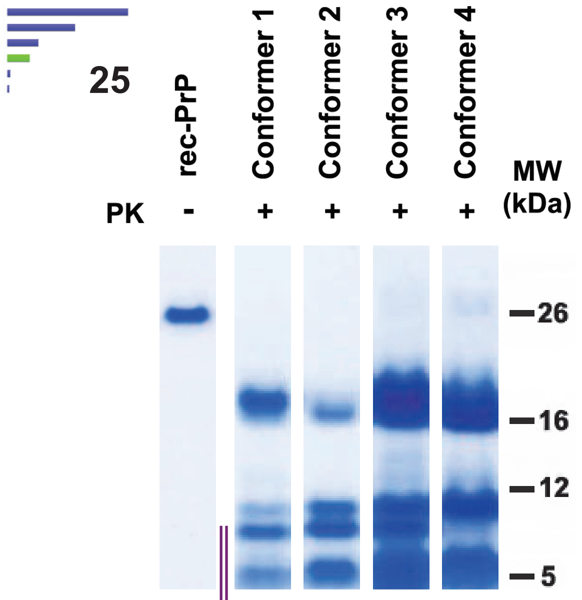
WNKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-

NI M W N N I V V K EGRS

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

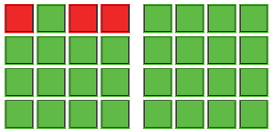
No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species



212 AA

4
Conformers



Tm^{Exp}**: ND**

ΔΔG: -11.02

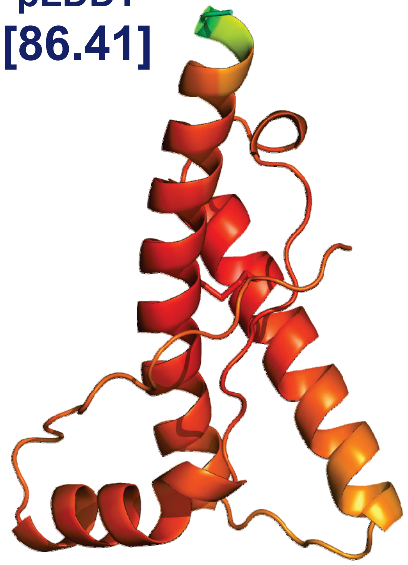
***In vitro* studies**

TgVole (1x)	Not tested
Steenbok	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Steenbok	Not tested

pLDDT
[86.41]



Protein code: 3318

Distinct primary sequence across species

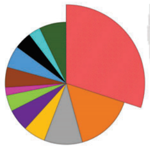
Bohor reedbuck

GenBank: BK064135

Redunca redunca

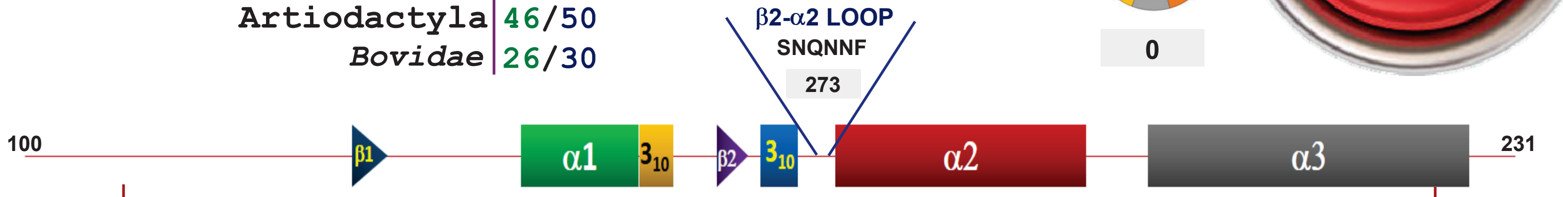
Artiodactyla	46/50
Bovidae	26/30

P29%



0

0



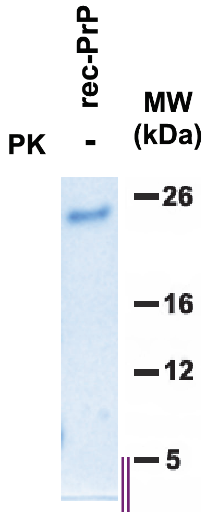
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-
           I                     M      W        N             N           I              V          V     K   Q  EGRS
```

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -14.8



220 AA

NO MISFOLDING

0
Conformers

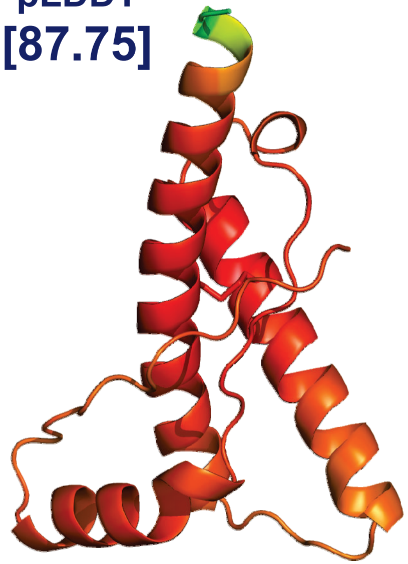
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[87.75]



Protein code: 3319

Distinct primary sequence across species

Pig

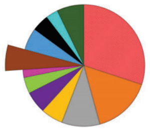
GenBank: L07623

Sus scrofa

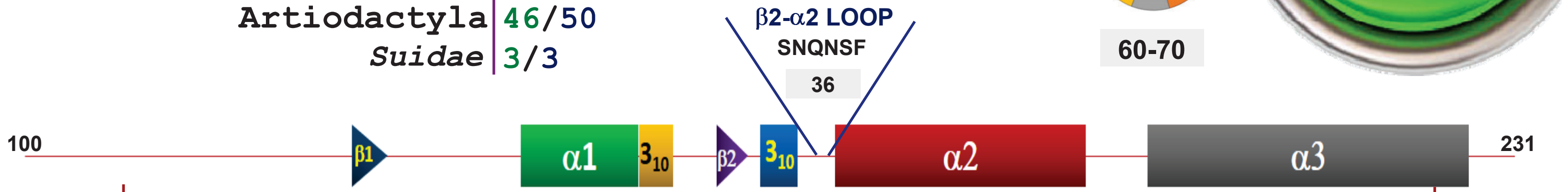
Artiodactyla 46/50
Suidae 3/3

P78%

67.9



60-70

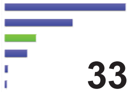


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDVKMIERVVEQMCITQYQKEYEAYAQRGAS-

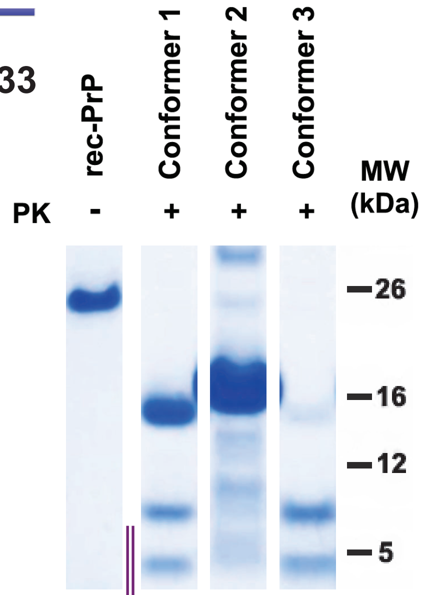
I M N W N N N I M V SQ YEGRS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

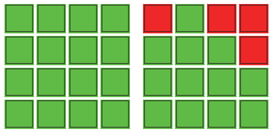


33



213 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: -15.44

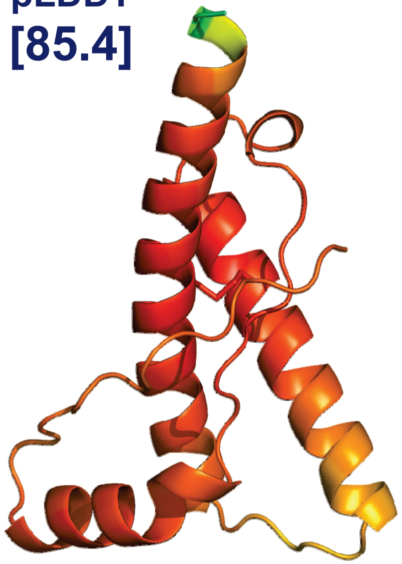
In vitro studies

TgVole (1x)	Propagate
Pig	Ongoing

In vivo studies

TgVole (1x)	Infectious
TgPig	Not tested

pLDDT
[85.4]



Protein code: 0243

Common duiker

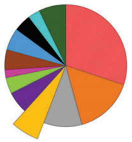
GenBank: BK064038

Sylvicapra grimmia

Artiodactyla 46/50
Bovidae 26/30

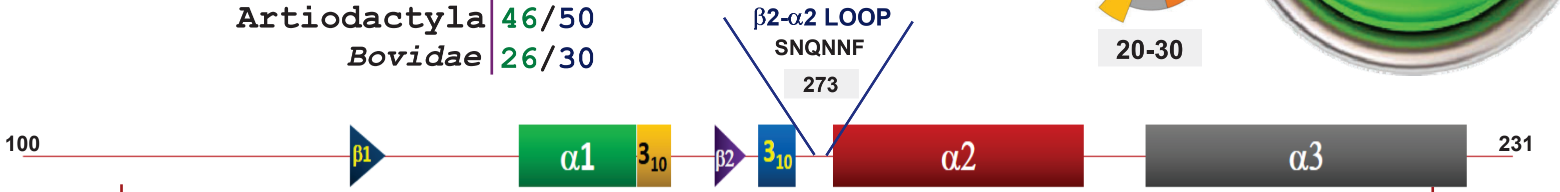
P58%

25



20-30

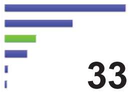
Distinct primary sequence across species

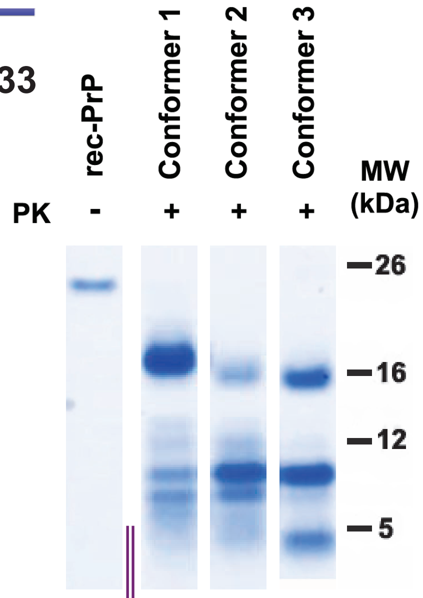


```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQRGAS-
           I  V                             M      W          N              N             I                  V           V    K         EGRS
```

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

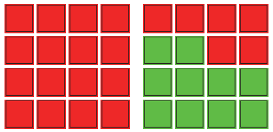
No deletions
No insertions
No polymorphic variants found





220 AA

3 Conformers



Tm^{Exp}: ND

ΔΔG: -12.74

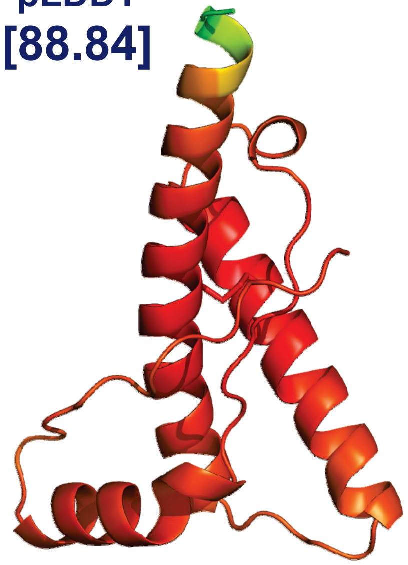
In vitro studies

TgVole (1x)	Not tested
Common duiker	Not tested

In vivo studies

TgVole (1x)	Not tested
Common duiker	Not tested

pLDDT [88.84]



Protein code: 3204

Distinct primary sequence across species

African buffalo

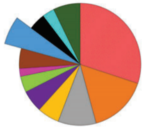
GenBank: AY720686

Syncerus caffer

Artiodactyla	46/50
Bovidae	26/30

P83%

75



70-80

β2-α2 LOOP
SNQNNF
273

WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMHRYPNQVYYRPVDQYSNQNNFVHDCVNITVKEHTVTTTTKGENFTETDVKMMERVVEQMCITQYQRESEAYYQRGAS-

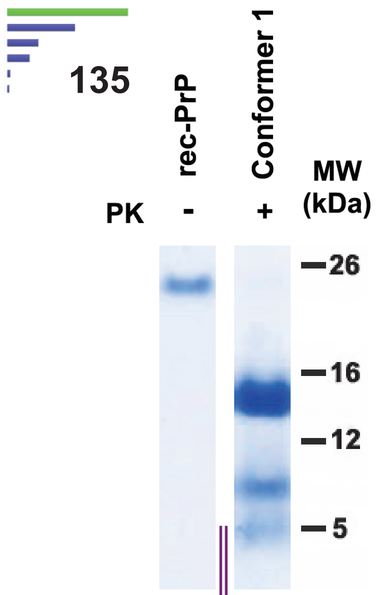
I M W N N I Q V K Q EGRS

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

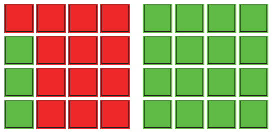
Tm^{Exp}: ND

ΔΔG: -10.06



220 AA

1
Conformers



In vitro studies

TgVole (1x) Not tested

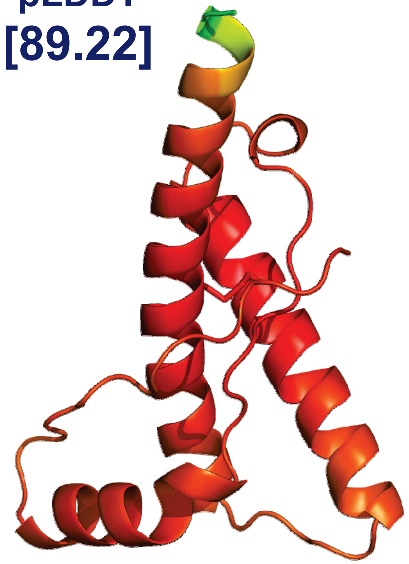
African buffalo Not tested

In vivo studies

TgVole (1x) Not tested

African buffalo Not tested

pLDDT
[89.22]

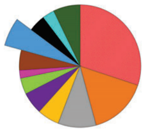


Protein code: 1434

Common eland

GenBank: EF165082

P81% **71.4**

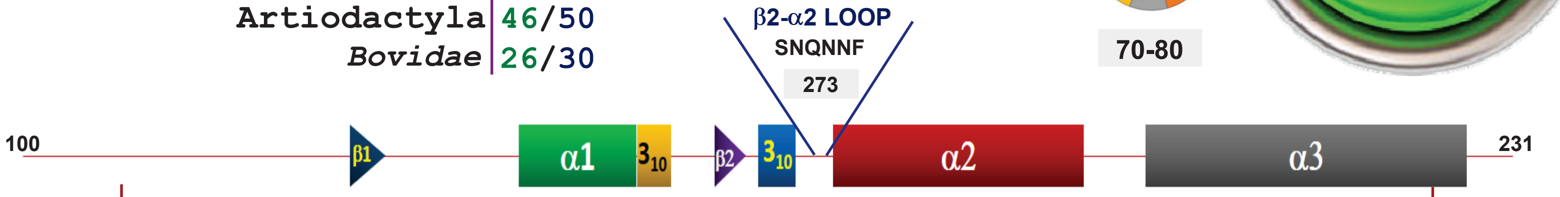


70-80

Taurotragus oryx

Artiodactyla 46/50
Bovidae 26/30

Distinct primary sequence across species

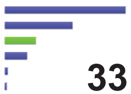


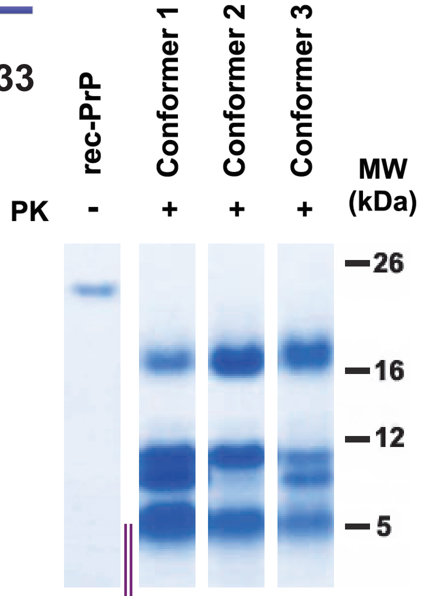
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-

I M N W N N I V V K Q EGRS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

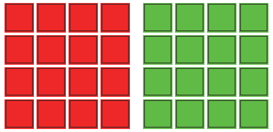
No deletions
No insertions
No polymorphic variants found





220 AA

3 Conformers



Tm^{Exp}: ND

ΔΔG: -24.41

***In vitro* studies**

TgVole (1x) Not tested

Common eland Not tested

***In vivo* studies**

TgVole (1x) Not tested

Common eland Not tested

pLDDT [92.23]

Protein code: 1379

Lowland nyala

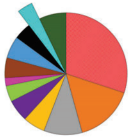
GenBank: EU032296

Tragelaphus angasii

Artiodactyla 46/50
Bovidae 26/30

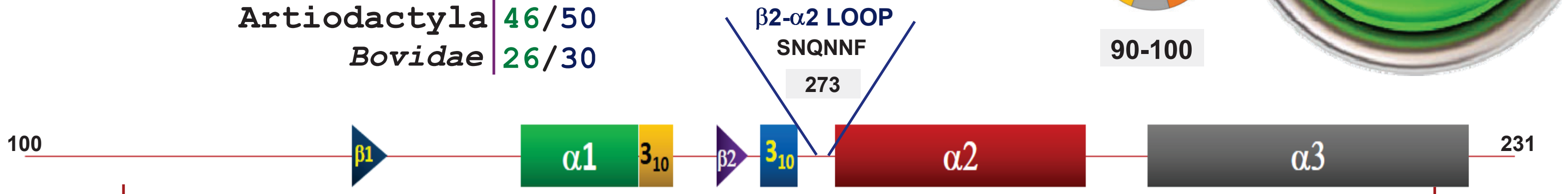
P90%

90.7



90-100

Distinct primary sequence across species

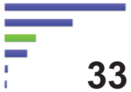


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-

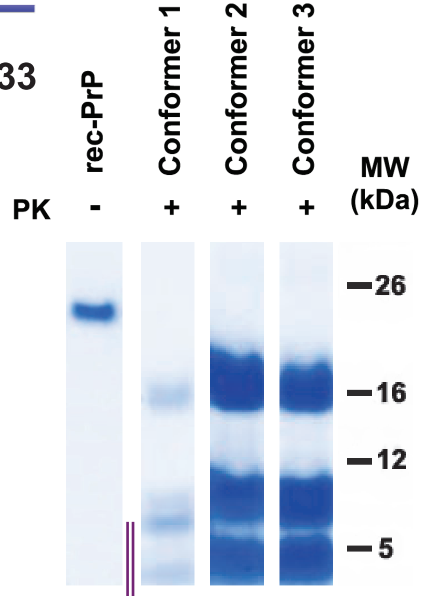
I M N W N N I V V K Q EGRS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

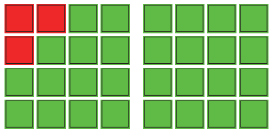


33



212 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: -10.1

In vitro studies

TgVole (1x) Not tested

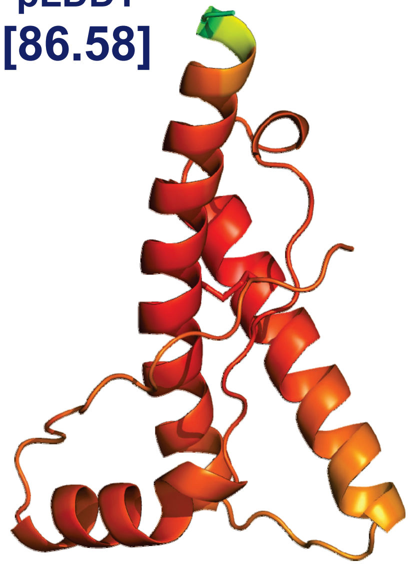
Lowland nyala Not tested

In vivo studies

TgVole (1x) Not tested

Lowland nyala Not tested

pLDDT
[86.58]



Protein code: 1327

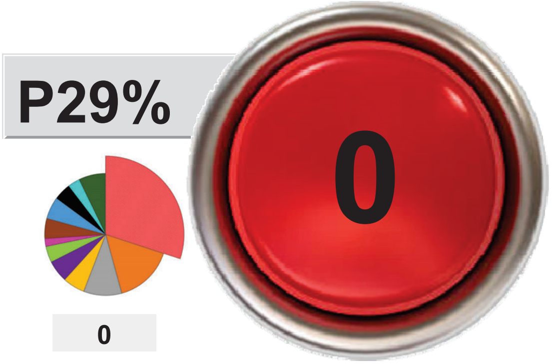
Mountain nyala

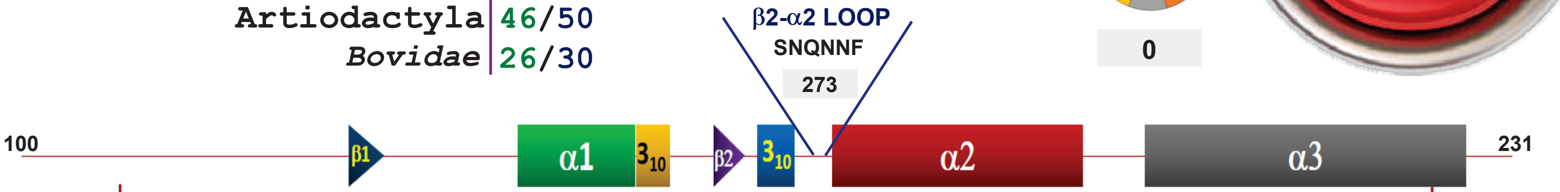
GenBank: BK064065

Tragelaphus buxtoni

Artiodactyla	46/50
Bovidae	26/30

Distinct primary sequence across species





WNKPNKPKTNMKHVAGAAAAGAVVGGPGGYLLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYGPVDQFSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQRESEAYYQRGAS-

S I L M M W N R YN I V M V K Q EGRS

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

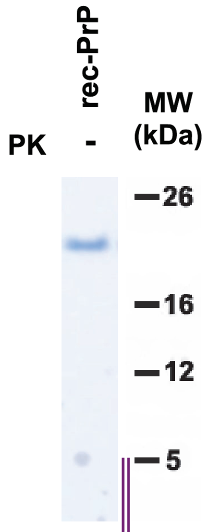
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

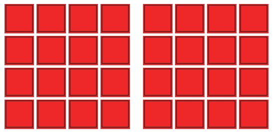
ΔΔG: -13.61



212 AA

NO MISFOLDING

0
Conformers



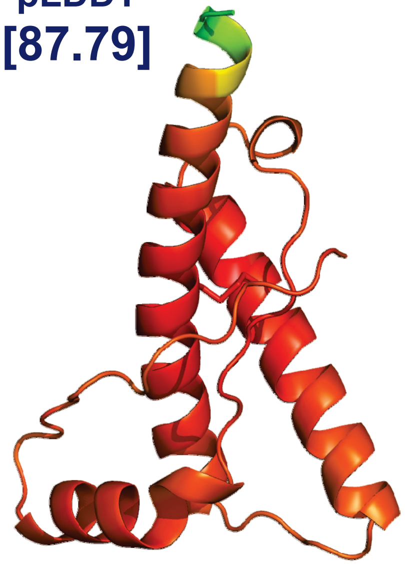
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[87.79]



Protein code: 3241

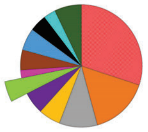
Lesser kudu

GenBank: AY720704

Tragelaphus imberbis

Artiodactyla 46/50
Bovidae 26/30

P69% **44.6**



40-50

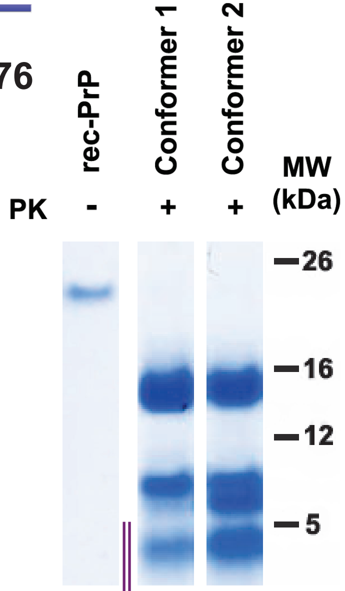
β2-α2 LOOP
SNQNNF
273

```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-
          I                           M      W         N             N           I            V          V    K  Q  EGRS
```

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

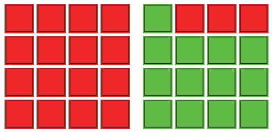
No deletions
No insertions
No polymorphic variants found

76



220 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -12.32

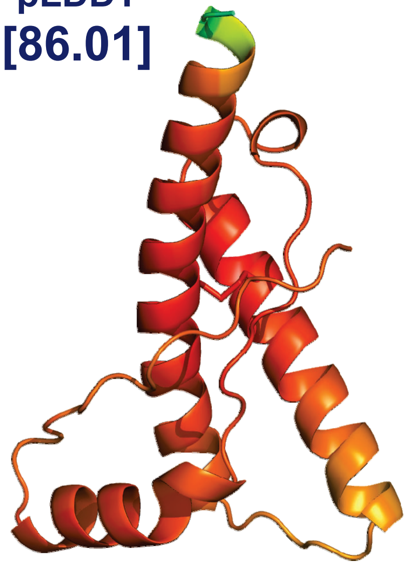
***In vitro* studies**

TgVole (1x)	Not tested
Lesser kudu	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Lesser kudu	Not tested

pLDDT
[86.01]



Distinct primary sequence across species

Harnessed bushbuck

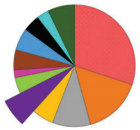
GenBank: BK063937

Tragelaphus scriptus

Artiodactyla 46/50

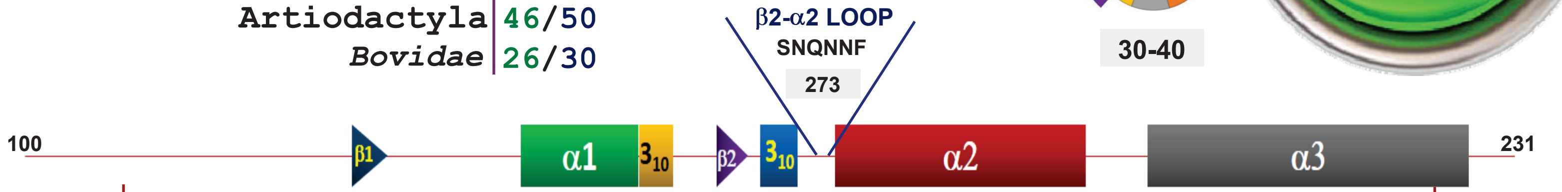
Bovidae 26/30

P66%



30-40

36.8



WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQRESEAYYQRGAS-

S I M W N N I V M V K Q EGRS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

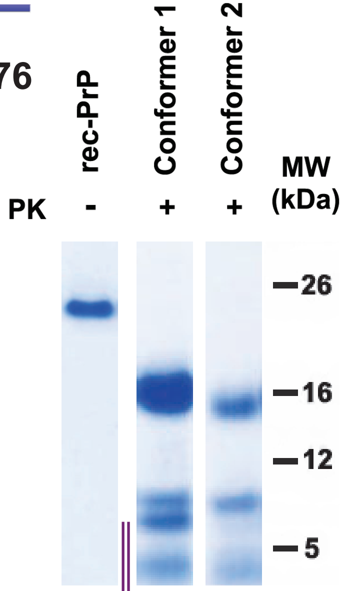
No deletions

No insertions

No polymorphic variants found

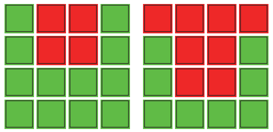
Distinct primary sequence across species

76



212 AA

2 Conformers



Tm^{Exp}: ND

ΔΔG: -15.56

***In vitro* studies**

TgVole (1x) Not tested

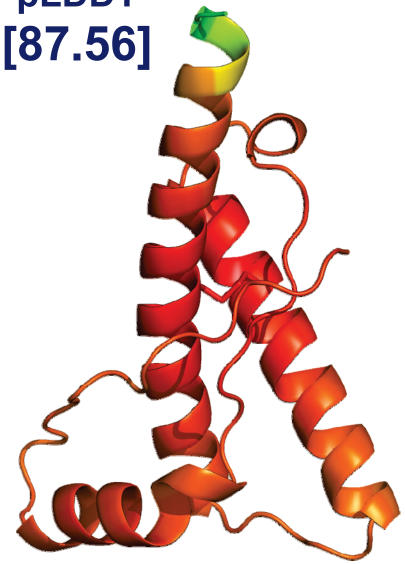
Harnessed bushbuck Not tested

***In vivo* studies**

TgVole (1x) Not tested

Harnessed bushbuck Not tested

pLDDT [87.56]



Protein code: 3060

Sitatunga

GenBank: EF165083

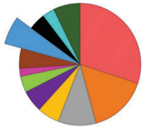
Tragelaphus spekii

Artiodactyla 46/50
Bovidae 26/30

1 species sharing the same primary sequence

Bongo
Tragelaphus eurycerus

P83%



70-80

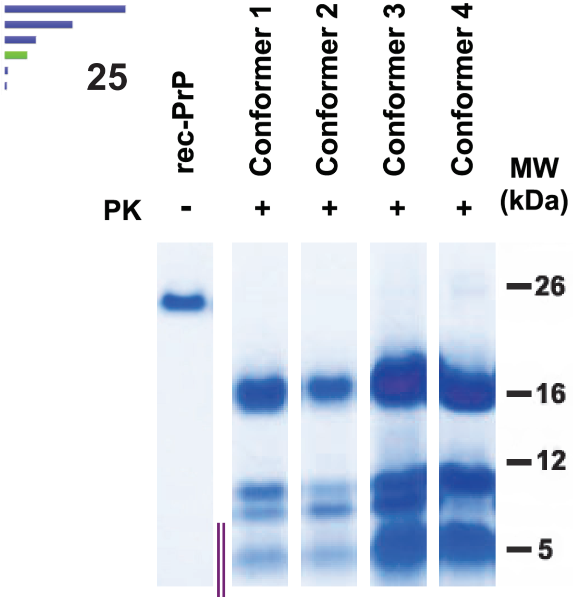
76.8

β2-α2 LOOP
SNQNNF
273

```
WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEAYYQRGAS-
     S    I                              M   N W         N               N          I                   V                V    K  Q    EGRS
```

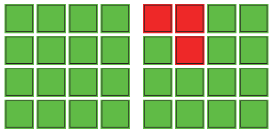
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



212 AA

4
Conformers



Tm^{Exp}: ND

ΔΔG: -10.2

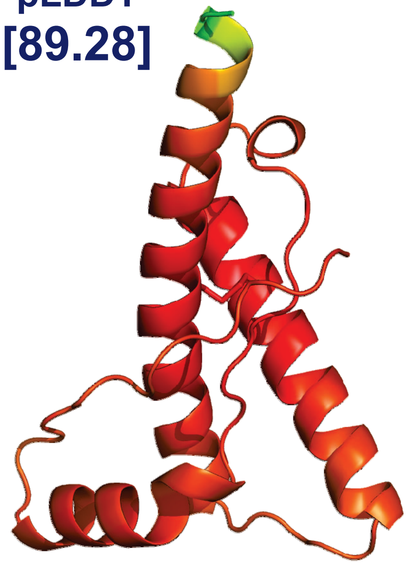
In vitro studies

TgVole (1x)	Not tested
Sitatunga	Not tested

In vivo studies

TgVole (1x)	Not tested
Sitatunga	Not tested

pLDDT
[89.28]



Distinct primary sequence across species

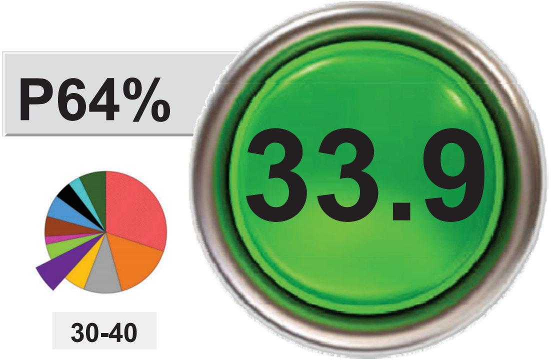
Greater kudu

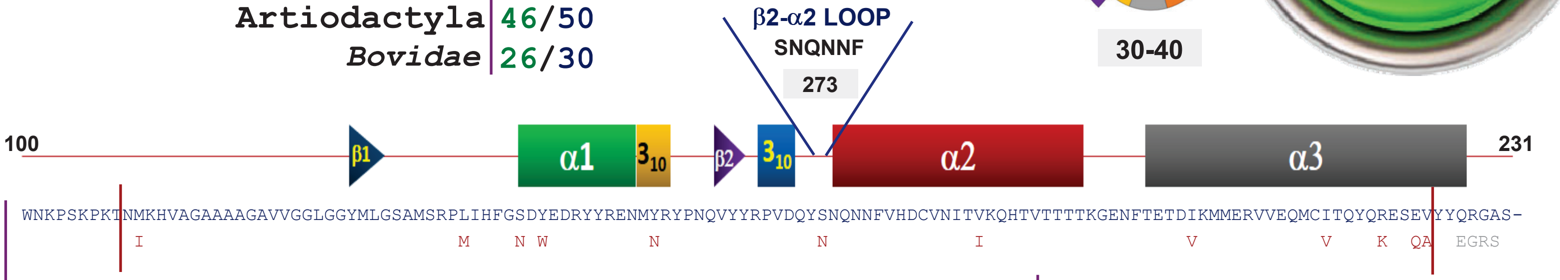
GenBank: EF165081

Tragelaphus strepsiceros

Artiodactyla 46/50
Bovidae 26/30

P64%



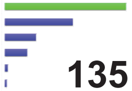


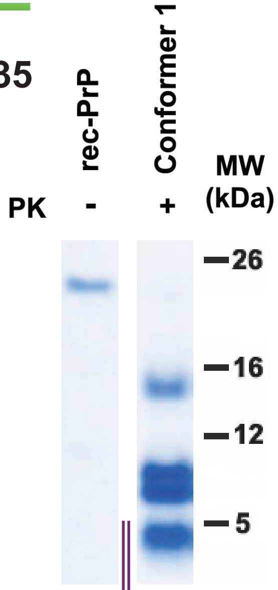
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESEVYYQRGAS-

I M N W N N I V V K QA EGRS

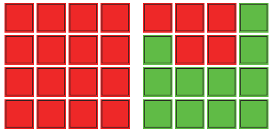
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
It shows polymorphic variants





220 AA



1 Conformers

Tm^{Exp}: ND

ΔΔG: -14.67

In vitro studies

TgVole (1x) Not tested

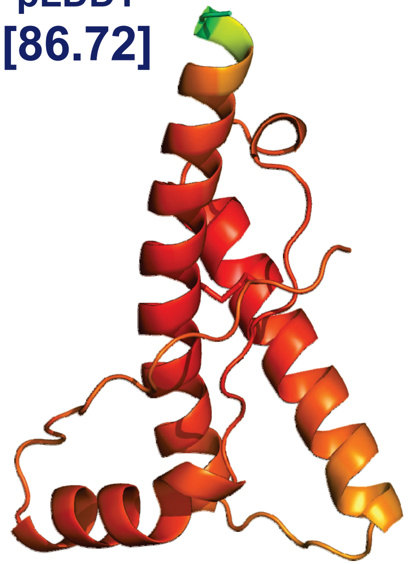
Greater kudu Not tested

In vivo studies

TgVole (1x) Not tested

Greater kudu Not tested

pLDDT [86.72]



Protein code: 1482

Java mouse-deer

GenBank: BK064004

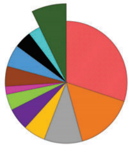
Tragulus javanicus

Artiodactyla	46/50
Tragulidae	1/1

1 species sharing the same primary sequence

Lesser mouse-deer
Tragulus kanchil

P100%



100

β2-α2 LOOP
SNQNNF
273

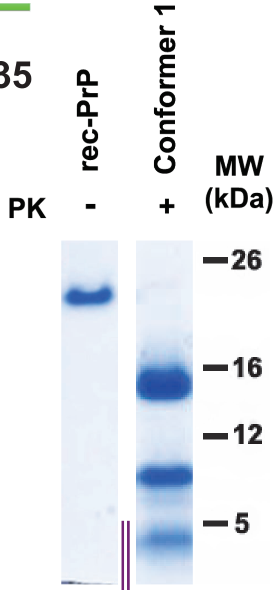
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQQESQAYYQRGAS-
           I                         M      W         N            N                                   V       V   K         EGRS
```

PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

135

211 AA



1
Conformers

Tm^{Exp}: ND

ΔΔG: -12.57

In vitro studies

TgVole (1x) Not tested

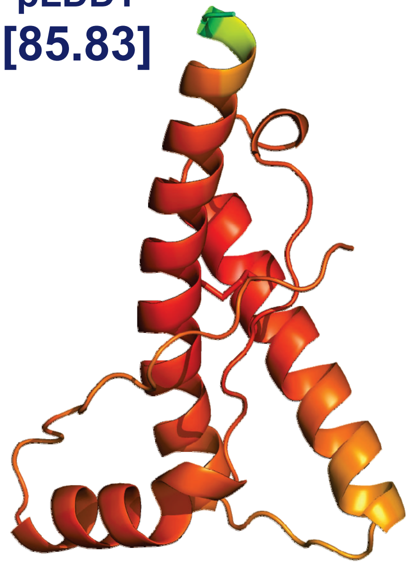
Java mouse-deer Not tested

In vivo studies

TgVole (1x) Not tested

Java mouse-deer Not tested

pLDDT
[85.83]



Protein code: 3165

Vicuna

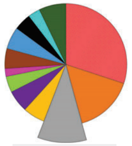
GenBank: BK063925

Vicugna vicugna

Artiodactyla 46/50
Camelidae 2/2

P47%

12



2 species sharing the same primary sequence

Guanaco
Lama glama cacsilensis

Alpaca
Vicugna pacos

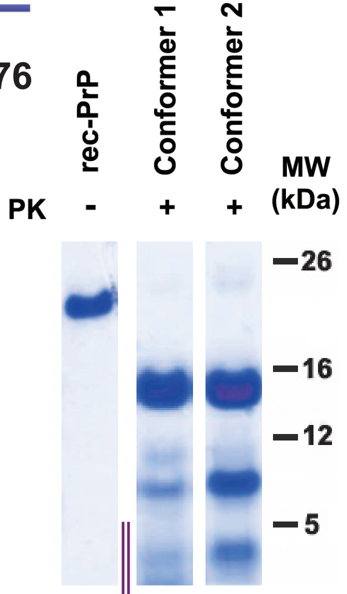
β2-α2 LOOP
SNQNSF
36

```
WNKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQREYQASYGRGAS-
          NI                              M      W          N         R      N   N         I                        V    K S  Y EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

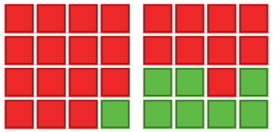
No deletions
No insertions
No polymorphic variants found

76



212 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -7.28

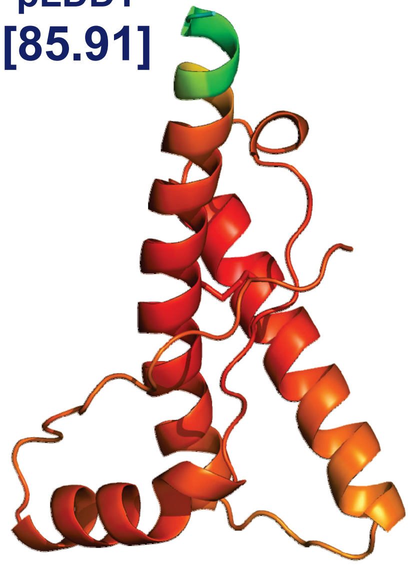
In vitro studies

TgVole (1x)	Not tested
Vicuna	Not tested

In vivo studies

TgVole (1x)	Not tested
Vicuna	Not tested

pLDDT
[85.91]



Protein code: 2088

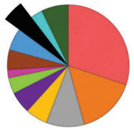
Dog

GenBank: KY649563

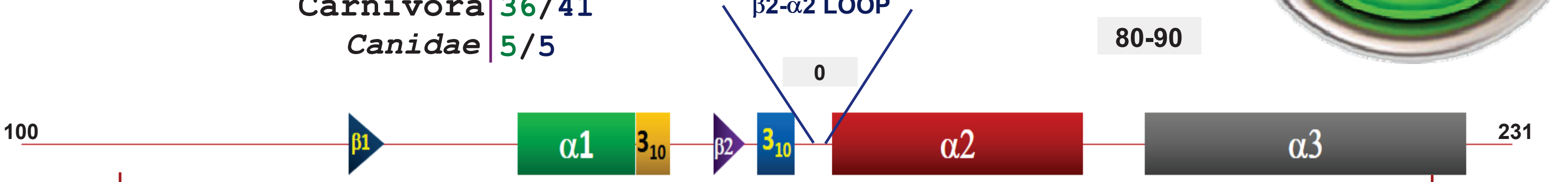
Canis lupus familiaris

Carnivora	36/41
Canidae	5/5

P87% **83.6**



80-90



WGKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPEQVYYYRPVDQYSNQNNFVRDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-

PrP sequence differs by 0 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

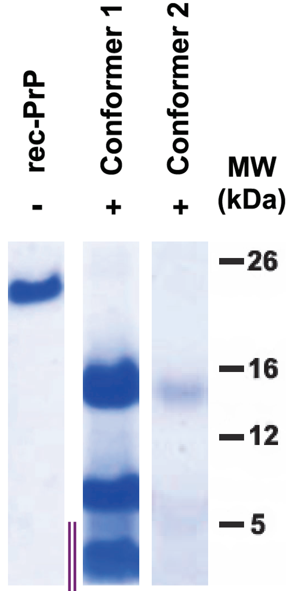
It shows polymorphic variants

Tm^{Exp}: ND

$\Delta\Delta G$: -2.04

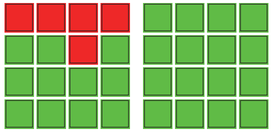
76

PK



213 AA

2
Conformers



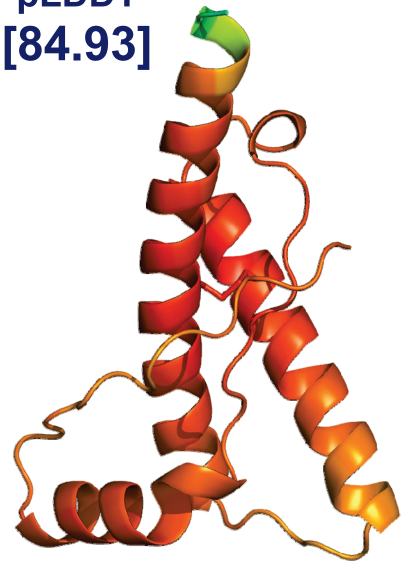
***In vitro* studies**

TgVole (1x)	**Propagate**
Dog	**Ongoing**

***In vivo* studies**

TgVole (1x)	**Infectious**
TgDog	**Ongoing**

pLDDT
[84.93]



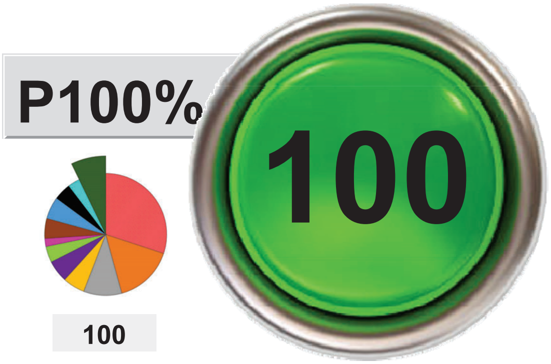
Protein code: 0139

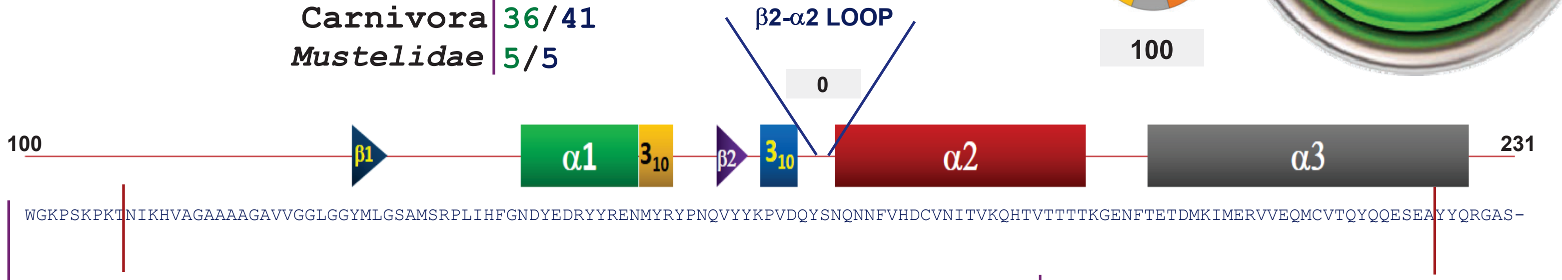
Ferret

GenBank: BK064943

Mustela putorius

Carnivora	36/41
Mustelidae	5/5





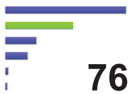
WGKPSKPKTNIKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQQESEAYYQRGAS-

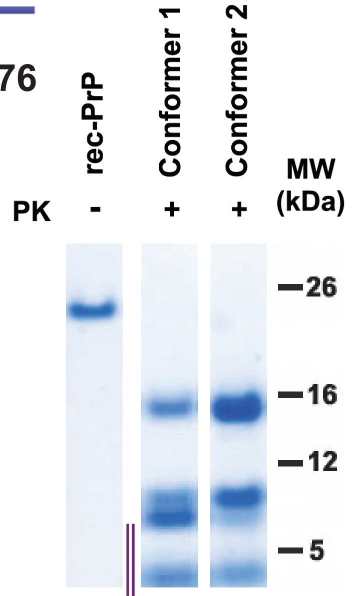
PrP sequence differs by 0 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

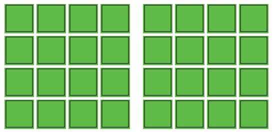
It shows polymorphic variants





213 AA

2 Conformers



Tm^{Exp}: ND

ΔΔG: -8.29

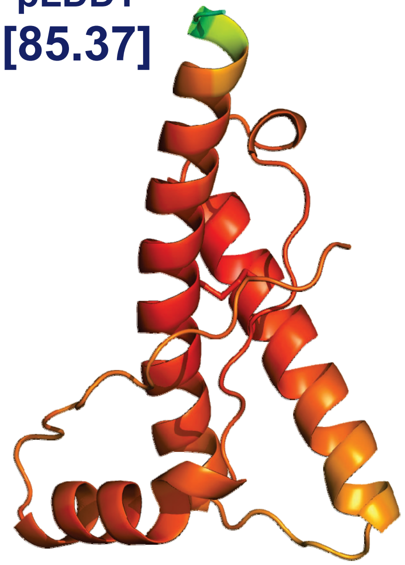
***In vitro* studies**

TgVole (1x)	Propagate
Ferret	Ongoing

***In vivo* studies**

TgVole (1x)	Ongoing
Ferret	Not tested

pLDDT [85.37]



Protein code: 1072

Red panda

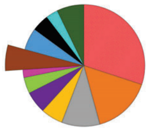
GenBank: EU341495

Ailurus fulgens

Carnivora 36/41
Ailuridae 1/1

Distinct primary sequence across species

P78%


60-70

67.9

β2-α2 LOOP
SNQNNF
273

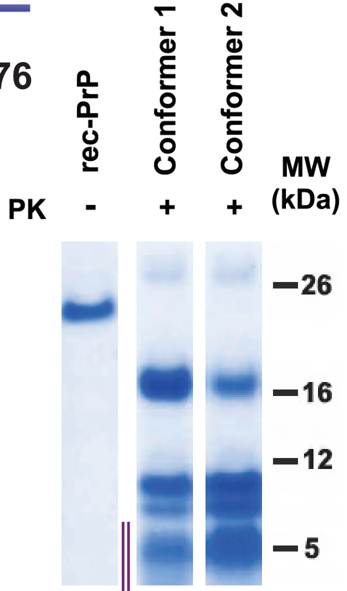
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQREAEAYYQRGAS-

N I M W N R N I V M V K SQ EGRS

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

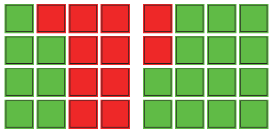
No deletions
No insertions
No polymorphic variants found


76



213 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -12.32

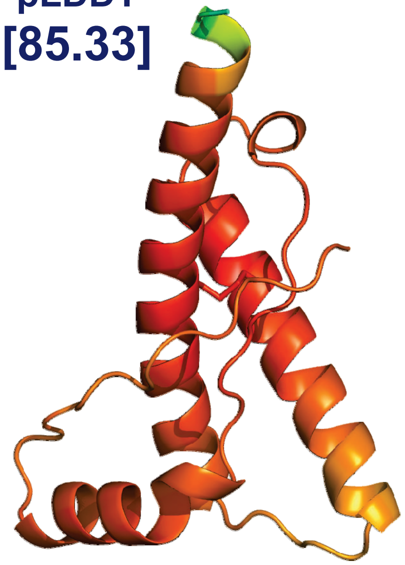
In vitro studies

TgVole (1x)	Not tested
Red panda	Not tested

In vivo studies

TgVole (1x)	Not tested
Red panda	Not tested

pLDDT
[85.33]



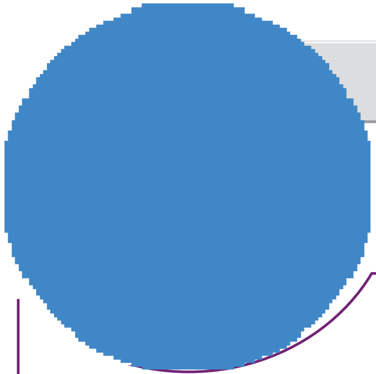
Protein code: 0948

Binturong

GenBank: JX218945

Arctictis binturong

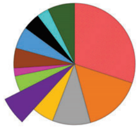
Carnivora	36/41
Viverridae	1/1



Asian palm civet
Paradoxurus hermaphroditus

1 species sharing the same primary sequence

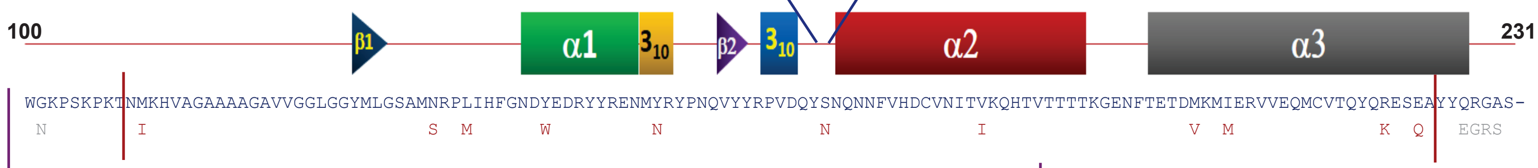
P64%



30-40

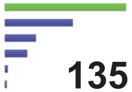
35.7

β2-α2 LOOP
SNQNNF
273

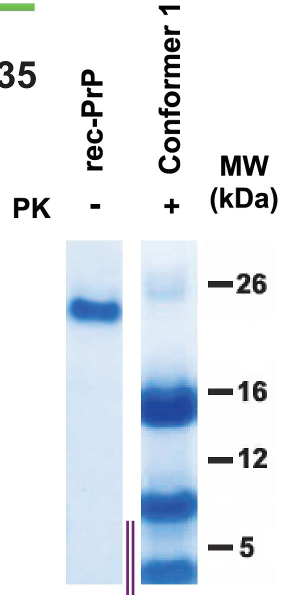


PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

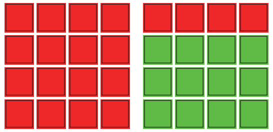


135



213 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -5.22

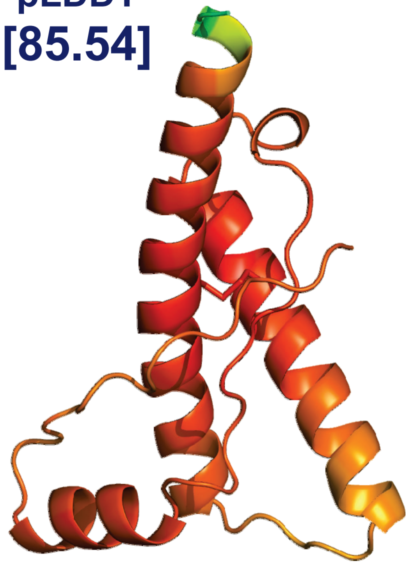
In vitro studies

TgVole (1x)	Not tested
Binturong	Not tested

In vivo studies

TgVole (1x)	Not tested
Binturong	Not tested

pLDDT
[85.54]



Protein code: 0925

Antarctic fur seal

GenBank: BK064071

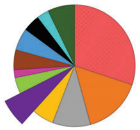
Arctocephalus gazella

Carnivora	36/41
Otariidae	1/1

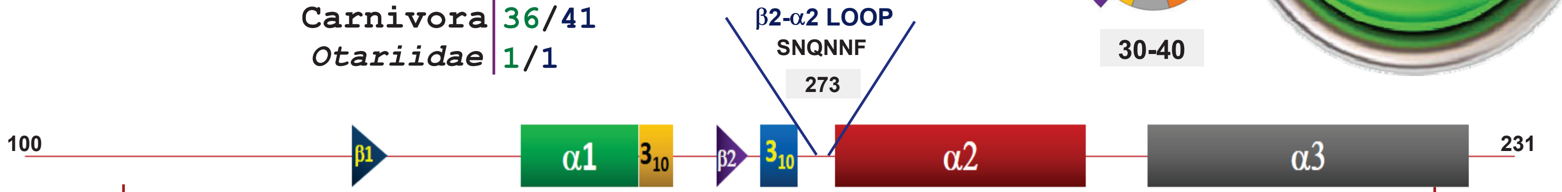
Distinct primary sequence across species

P62%

32.5



30-40



```
WGKPQKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQRGAS-
 N  S    I  V                            M      W                 R     N              I                  V M               K  Q  EGRS
```

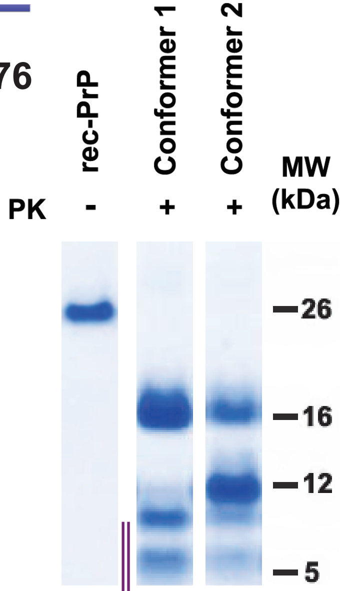
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

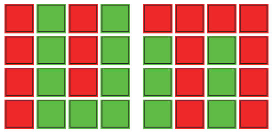
76



215 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: -11.5

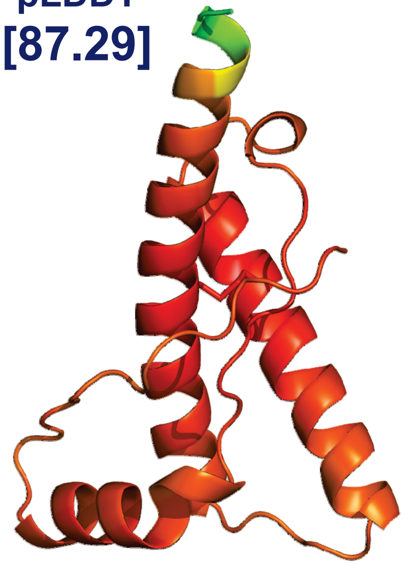
***In vitro* studies**

TgVole (1x)	Not tested
Antarctic fur seal	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Antarctic fur seal	Not tested

pLDDT [87.29]



Protein code: 3248

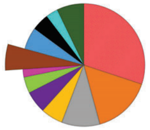
Coyote

GenBank: JX218953

Canis latrans

Carnivora	36/41
Canidae	5/5

P76%



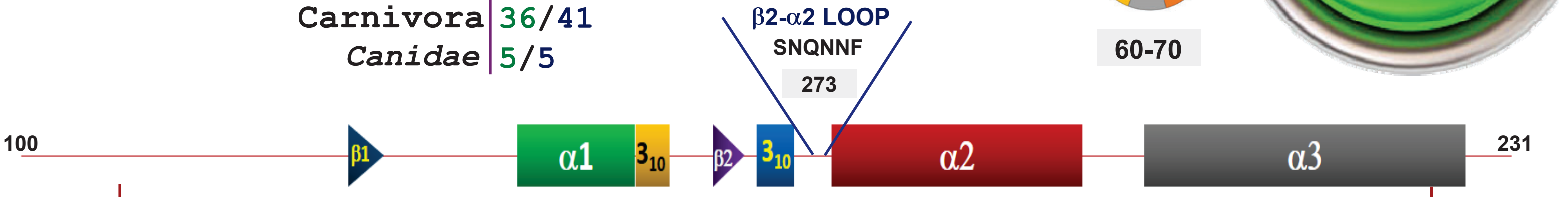
60-70

64.3

2 species sharing the same primary sequence

Maned wolf
Chrysocyon brachyurus

Bush dog
Speothos venaticus

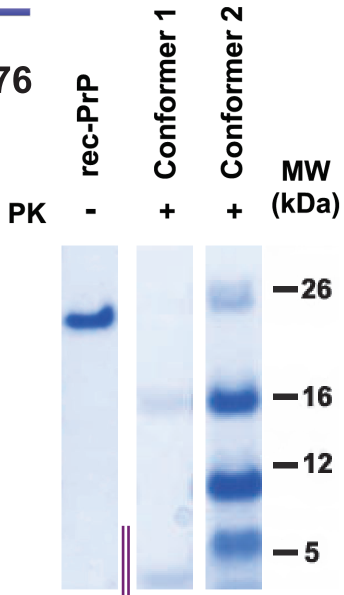


```
WGKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPDQVYYRPVDQYSNQNNFVRDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N S  I  M  W  N  N  N  H  I  V M  Q  EGRS
```

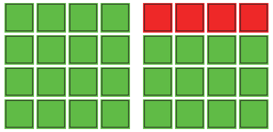
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

76



213 AA



2
Conformers

Tm^{Exp}: ND

ΔΔG: -5.73

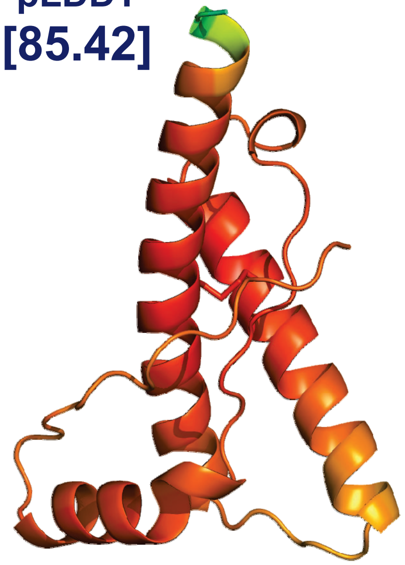
In vitro studies

TgVole (1x)	Not tested
Coyote	Not tested

In vivo studies

TgVole (1x)	Not tested
Coyote	Not tested

pLDDT
[85.42]



Protein code: 1353

Distinct primary sequence across species

Black-backed jackal

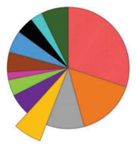
GenBank: BK064772

Canis mesomelas

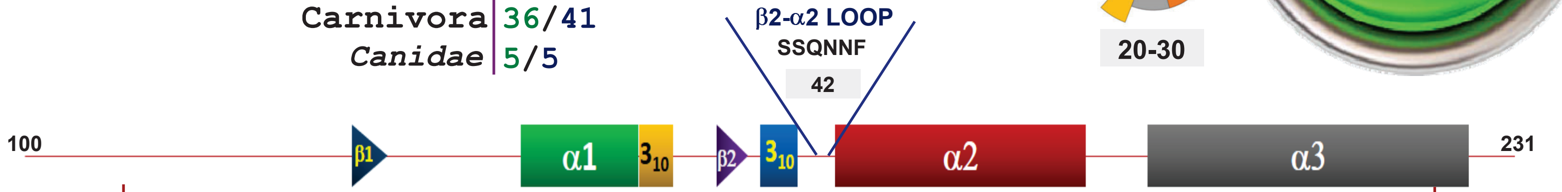
Carnivora 36/41
Canidae 5/5

P57%

23



20-30

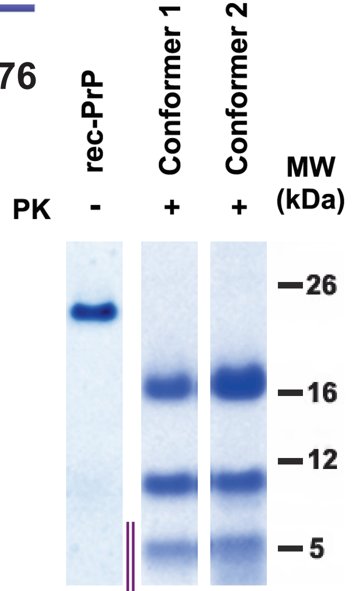


```
WGKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPDQVYYRPVDQYSSQNNFVRDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N  S     I                             M      W         N   N         NN     H      I                  V M                 Q   EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

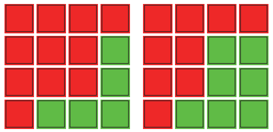
No deletions
No insertions
No polymorphic variants found

76



213 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -8.24

***In vitro* studies**

TgVole (1x) **Not tested**

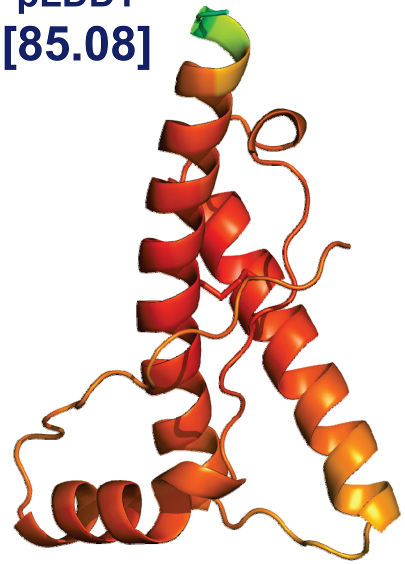
Black-backed jackal **Not tested**

***In vivo* studies**

TgVole (1x) **Not tested**

Black-backed jackal **Not tested**

pLDDT
[85.08]



Protein code: 3927

Distinct primary sequence across species

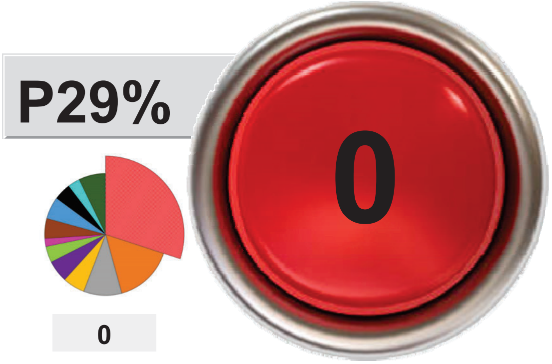
Caracal

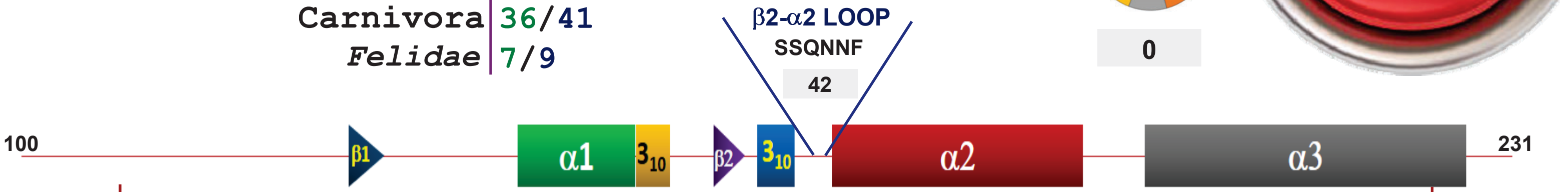
GenBank: BK063932

Caracal caracal

Carnivora	36/41
Felidae	7/9

P29%





```
WGKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMNRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSSQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N       I  V                     S  M      W         N               NN            IK                  V M                  Q  EGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

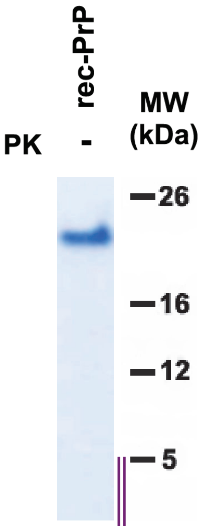
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -6.41



216 AA

NO MISFOLDING

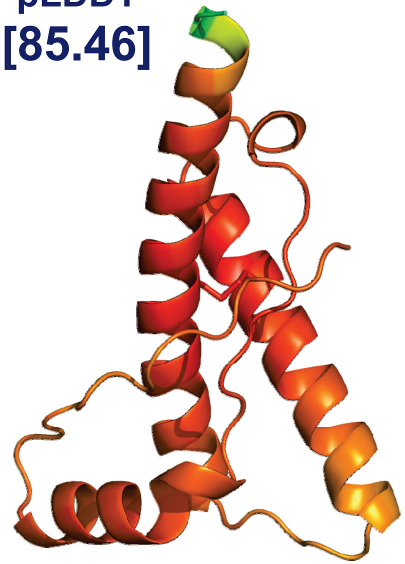
In vitro studies

NOT APPLICABLE

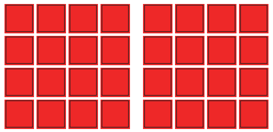
In vivo studies

NOT APPLICABLE

pLDDT
[85.46]



0
Conformers



Protein code: 3054

Distinct primary sequence across species

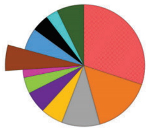
Asian golden cat

GenBank: JX218947

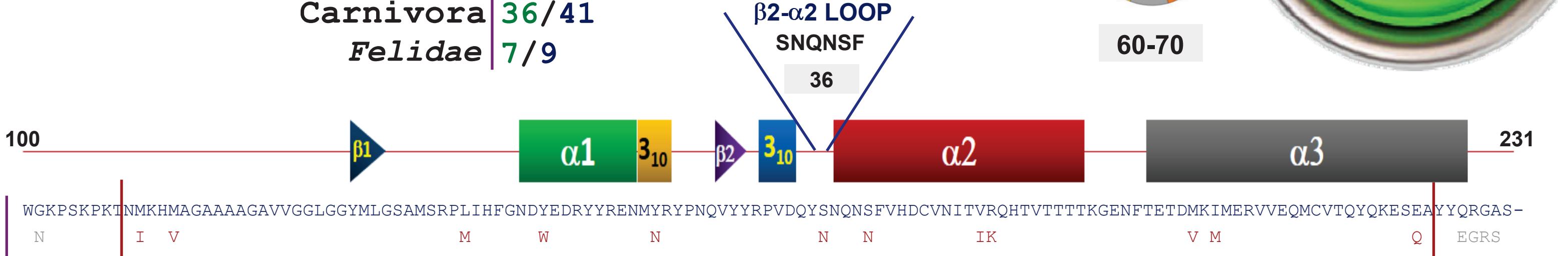
Catopuma temminckii

Carnivora 36/41
Felidae 7/9

P76%


60-70

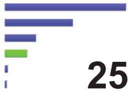
64.3



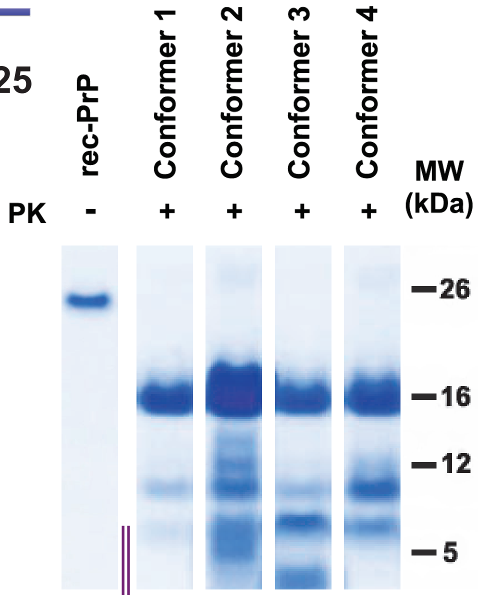
```
WGKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N        I  V                             M       W          N                  N   N           IK                       V M                    Q   EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

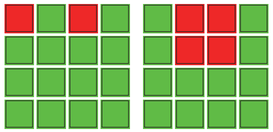


25



216 AA

4 Conformers



Tm^{Exp}: ND

ΔΔG: -12.45

***In vitro* studies**

TgVole (1x) Not tested

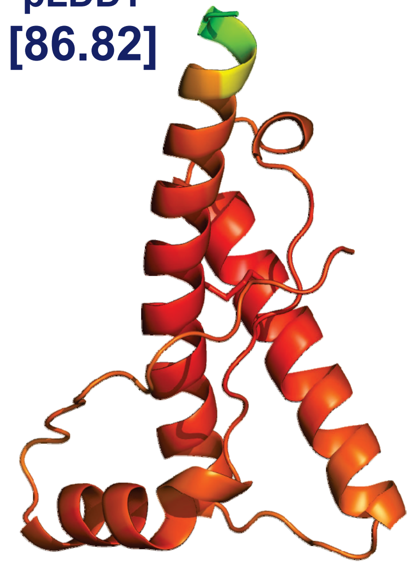
Asian golden cat Not tested

***In vivo* studies**

TgVole (1x) Not tested

Asian golden cat Not tested

pLDDT [86.82]

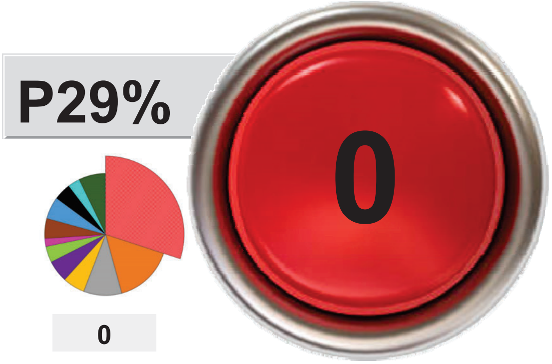


Protein code: 1408

Spotted hyena

GenBank: JX218985

P29%



Crocuta crocuta

Carnivora	36/41
Hyaenidae	1/2

Striped hyena
Hyaena hyaena

1 species sharing the same primary sequence

β2-α2 LOOP
SSQNNF
42

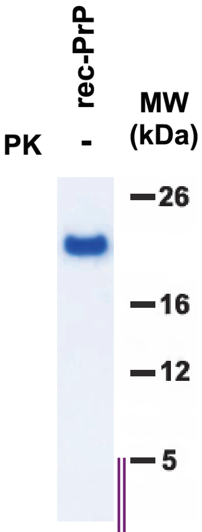
```
WGKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRQNMDRYPNQVYYKPVDQYSSQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQRGAS-
 N        I  V                          M      W      E  N         R     NN            IK                 V M               K  Q   EGRS
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

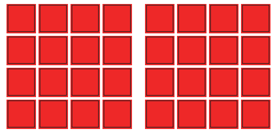
Tm^{Exp}: ND

ΔΔG: -9.33



213 AA

NO MISFOLDING



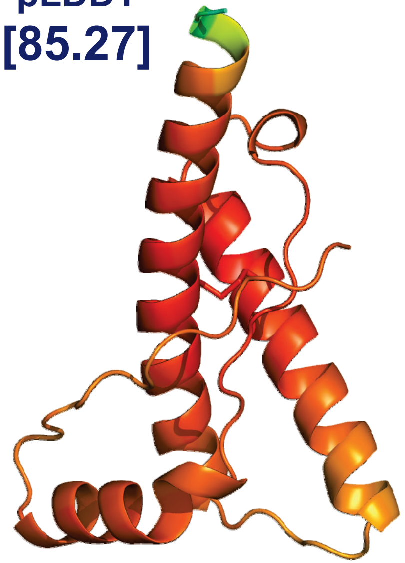
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[85.27]



Protein code: 0531

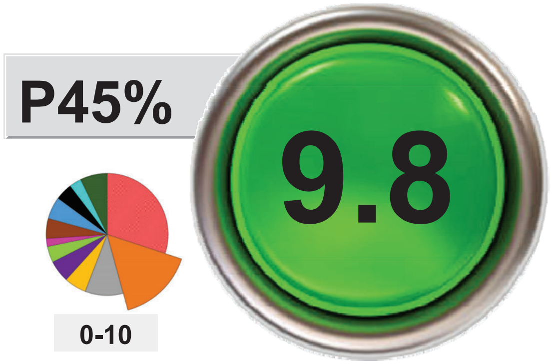
Distinct primary sequence across species

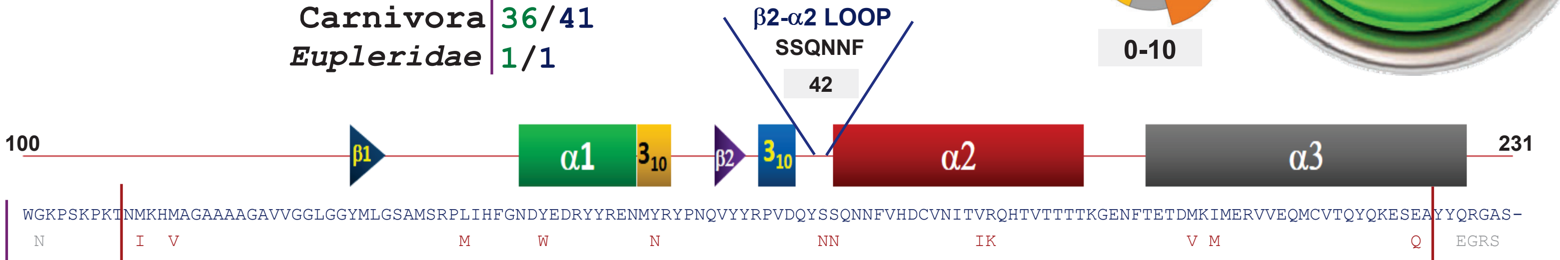
Fossa

GenBank: BK063948

Cryptoprocta ferox

Carnivora 36/41
Eupleridae 1/1

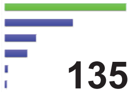


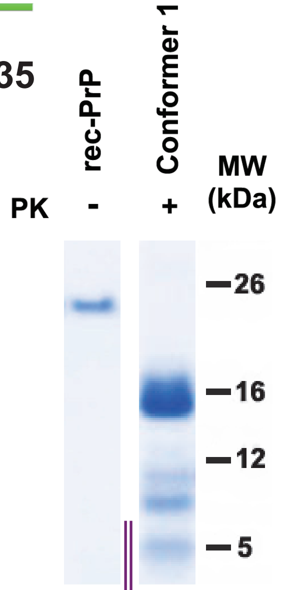


```
WGKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSSQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N         I  V                           M       W          N               NN             IK                   V M                Q   EGRS
```

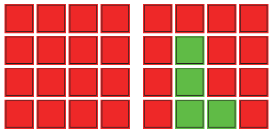
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found





213 AA



1 Conformers

Tm^{Exp}: ND

ΔΔG: -8.09

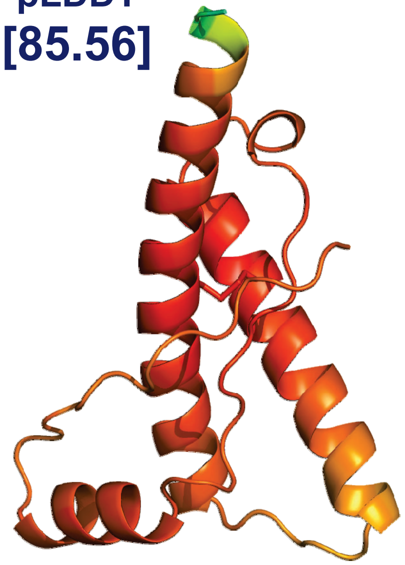
In vitro studies

TgVole (1x)	Not tested
Fossa	Not tested

In vivo studies

TgVole (1x)	Not tested
Fossa	Not tested

pLDDT [85.56]



Protein code: 3075

Distinct primary sequence across species

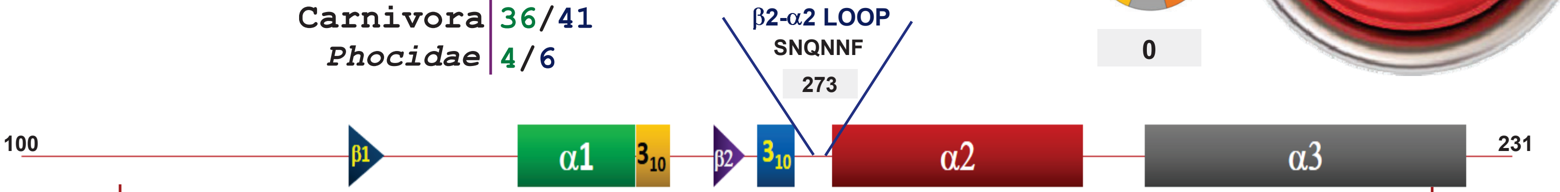
Bearded seal

GenBank: BK064769

Erignathus barbatus

Carnivora 36/41
Phocidae 4/6

P29%



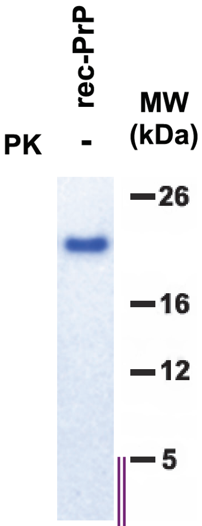
WGKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQRGAS-
N S I V M W N R N I V M K Q EGRS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

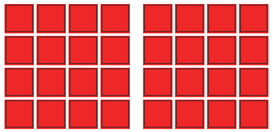
ΔΔG: -8.49



213 AA

NO MISFOLDING

0
Conformers



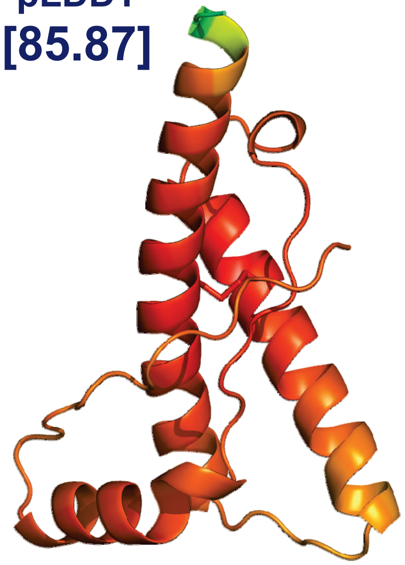
***In vitro* studies**

NOT APPLICABLE

***In vivo* studies**

NOT APPLICABLE

pLDDT
[85.87]



Protein code: 3919

Cat

GenBank: EU588730

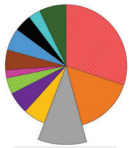
Felis silvestris catus

Carnivora	36/41
Felidae	7/9

3 species sharing the same primary sequence

- **Jungle cat** *Felis chaus*
- **Black-footed cat** *Felis nigripes*
- **Pallas's cat** *Otocolobus manul*

P49%



10-20

12.9

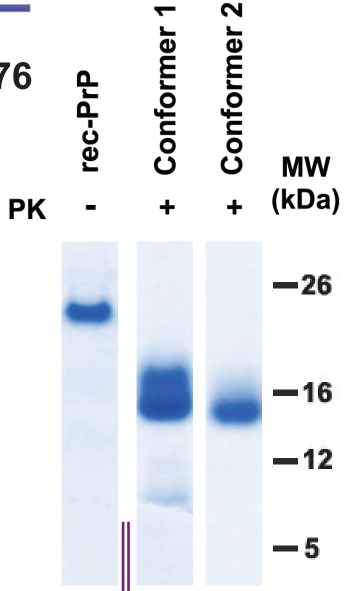
β2-α2 LOOP
SNQNNF
273

```
WGKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N         I  V                             M      W          N               N               IK                   V M                  Q  EGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

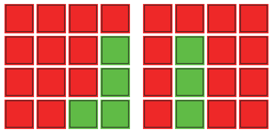
No deletions
No insertions
No polymorphic variants found

76



216 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -8.92

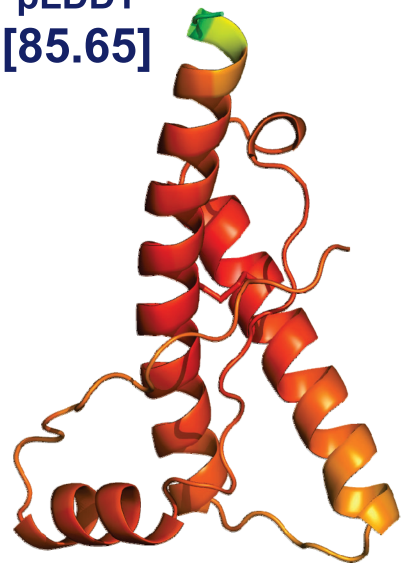
In vitro studies

TgVole (1x)	Propagate
Cat	Ongoing

In vivo studies

TgVole (1x)	Ongoing
Cat	Not tested

pLDDT
[85.65]



Protein code: 0173

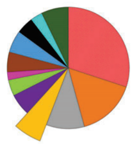
Wolverine

GenBank: EU341500

Gulo gulo

Carnivora 36/41
Mustelidae 5/5

P61%



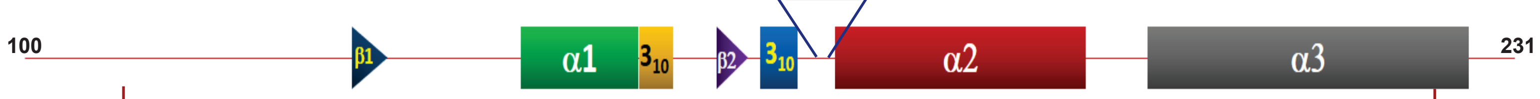
20-30

29.8

6 species sharing the same primary sequence

- **Tayra** *Eira barbara*
- **Yellow-throated marten** *Martes flavigula*
- **Beech marten** *Martes foina*
- **European pine marten** *Martes martes*
- **Sable** *Martes zibellina*
- **American badger** *Taxidea taxus jeffersonii*

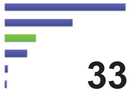
β2-α2 LOOP
SNQNNF
273



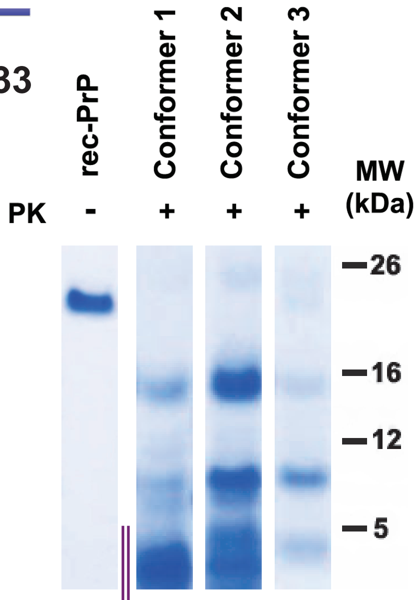
```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMHRYPDQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQRGAS-
 N       I                               M      W         N   N    R     N             I                          V M               K  Q  EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

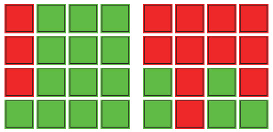


33



213 AA

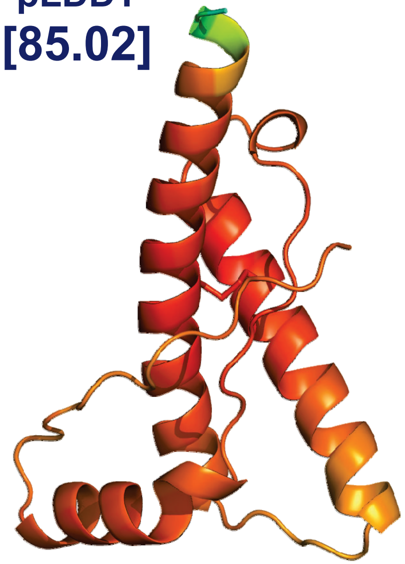
3 Conformers



Tm^{Exp}: ND

ΔΔG: -4.08

pLDDT [85.02]



In vitro studies

TgVole (1x)	Not tested
Wolverine	Not tested

In vivo studies

TgVole (1x)	Not tested
Wolverine	Not tested

Protein code: 0123

Common dwarf mongoose

GenBank: BK064051

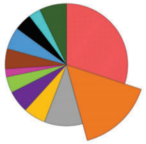
Helogale parvula

Carnivora 36/41

Herpestidae 4/4

Distinct primary sequence across species

P34%



0-10

β2-α2 LOOP
SSQNNF
42

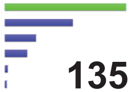
```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPIIHFGNDYEDRYYRQNMDRYPNQVYYRPVDQYSSQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYEKESQAYYQRGAS-
  N         I                             M     W       E  N                   NN                   IK                         V M                Q     EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

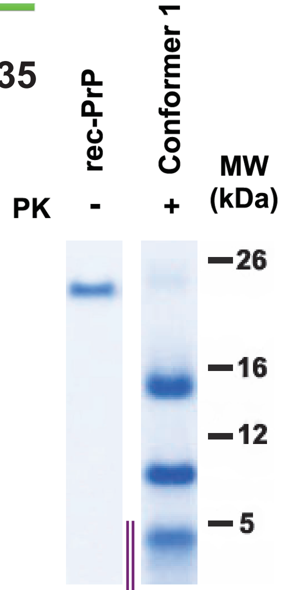
No deletions

No insertions

No polymorphic variants found



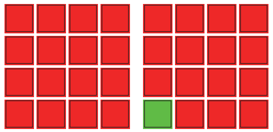
135



217 AA

1

Conformers



Tm^{Exp}: ND

ΔΔG: -11.52

In vitro studies

Not tested
TgVole (1x)

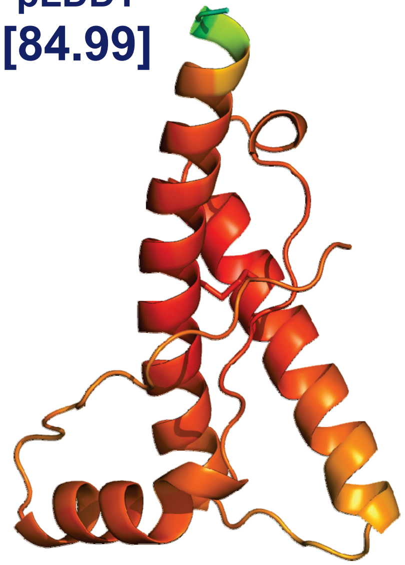
Not tested
Common dwarf mongoose

In vivo studies

Not tested
TgVole (1x)

Not tested
Common dwarf mongoose

pLDDT
[84.99]



Protein code: 3220

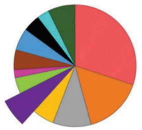
Javan mongoose

GenBank: EU341501

Herpestes javanicus

Carnivora **36/41**
Herpestidae **4/4**

P66%



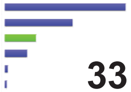
30-40

39.6

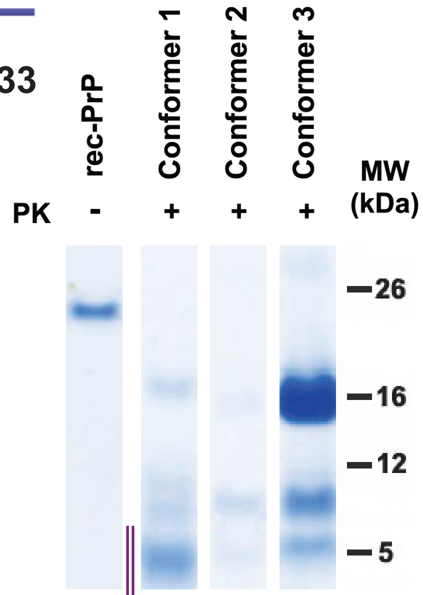
β2-α2 LOOP
SNQNNF
273

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



33



217 AA

3
Conformers

🟥	🟥	🟥	🟥	🟩	🟥	🟩	🟥
🟥	🟥	🟥	🟥	🟩	🟥	🟩	🟥
🟥	🟥	🟥	🟥	🟩	🟥	🟩	🟩
🟥	🟩	🟥	🟥	🟩	🟥	🟩	🟩

Tm^{Exp}: ND

ΔΔG: -6.95

***In vitro* studies**

TgVole (1x) **Not tested**

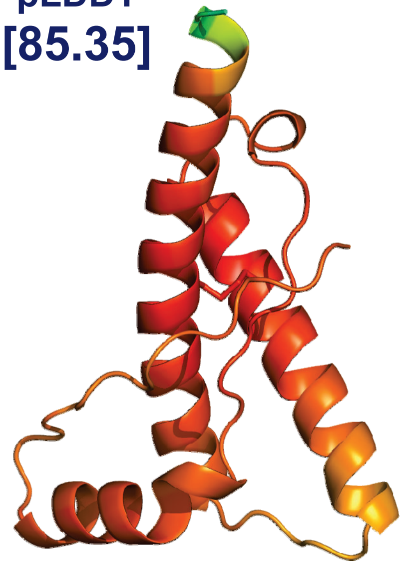
Javan mongoose **Not tested**

***In vivo* studies**

TgVole (1x) **Not tested**

Javan mongoose **Not tested**

pLDDT
[85.35]



Distinct primary sequence across species

Protein code: 1345

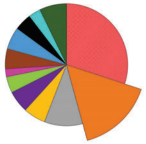
Geoffroy's cat

GenBank: BK064182

Leopardus geoffroyi

Carnivora 36/41
Felidae 7/9

P39%



0-10

3.6

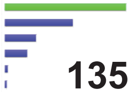
β2-α2 LOOP
SNQNNF
273

```
WGKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
  N        I  V                           M      W         N               N              IK                    V M                   Q   EGRS
```

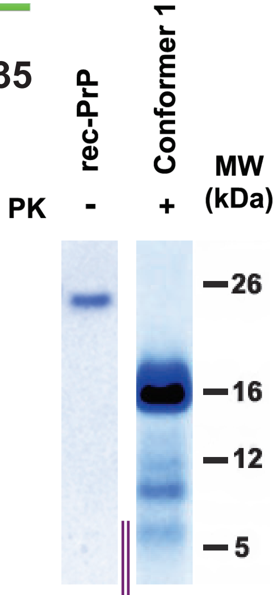
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

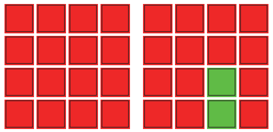


135



216 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -7.1

In vitro studies

TgVole (1x) Not tested

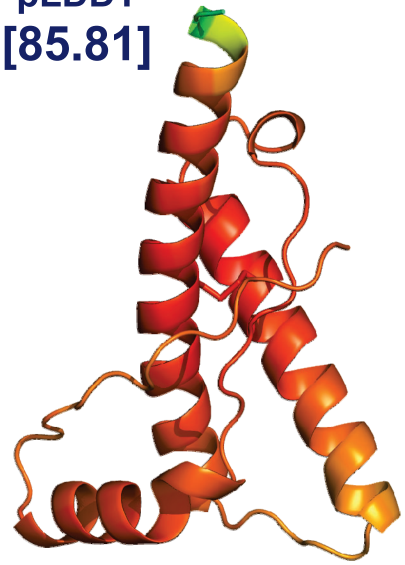
Geoffroy's cat Not tested

In vivo studies

TgVole (1x) Not tested

Geoffroy's cat Not tested

pLDDT
[85.81]



Protein code: 4011

Oncilla

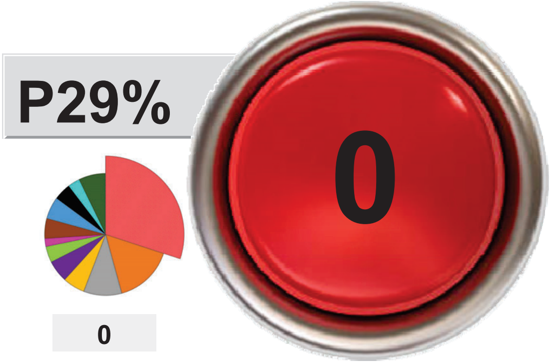
GenBank: BK064829

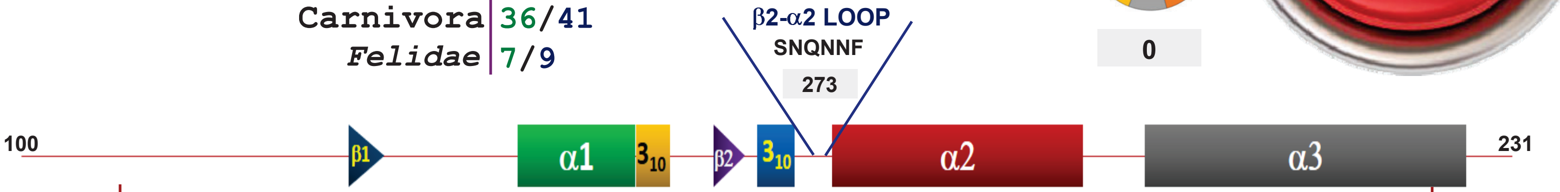
Leopardus tigrinus

Carnivora 36/41
Felidae 7/9

Distinct primary sequence across species

P29%





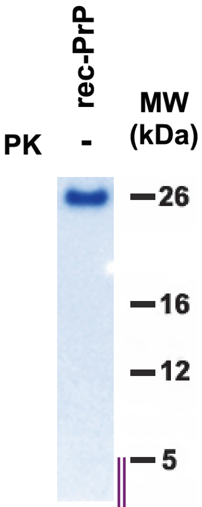
WGKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
N S I V M W N N IK V M Q EGRS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

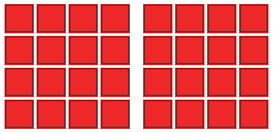
Tm^{Exp}: ND

ΔΔG: -14.52



216 AA

NO MISFOLDING



0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[93.41]

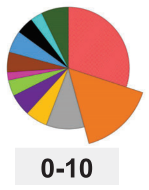
Protein code: 4815

Margay

GenBank: JX218979

Distinct primary sequence across species

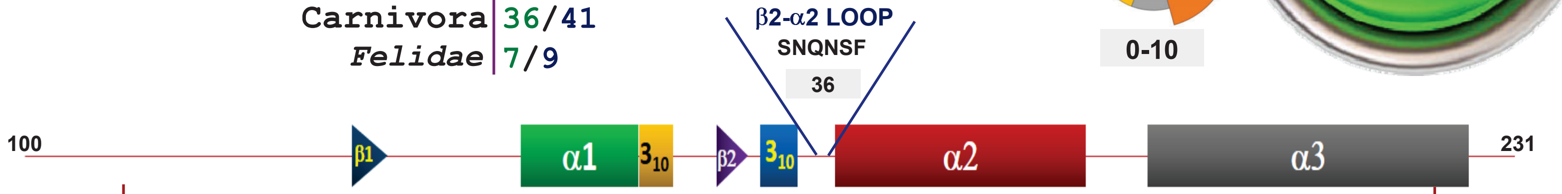
P34%



0.9

Leopardus wiedii

Carnivora	36/41
Felidae	7/9



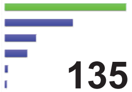
```
WGKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYYQRGAS-
 N        I  V                      M      W          N                   N   N         IK                  V M                   Q  EG SS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

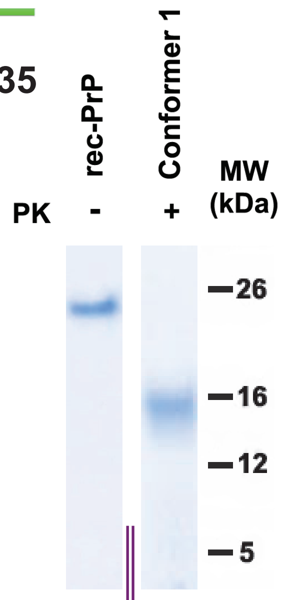
No deletions

No insertions

No polymorphic variants found

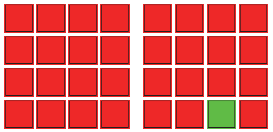


135



217 AA

1
Conformers



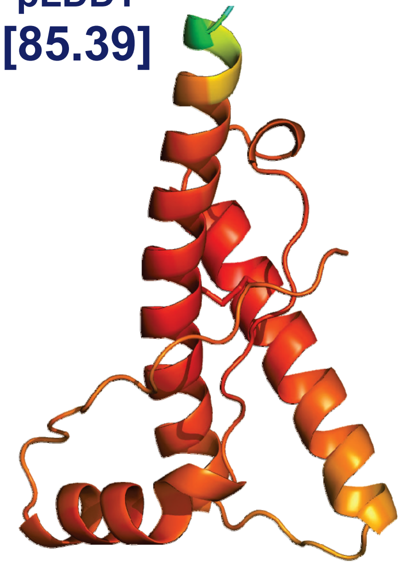
Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x)	Not tested
Margay	Not tested

pLDDT
[85.39]



In vivo studies

TgVole (1x)	Not tested
Margay	Not tested

Protein code: 1443

Distinct primary sequence across species

Weddell seal

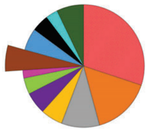
GenBank: XM_006744312

Leptonychotes weddellii

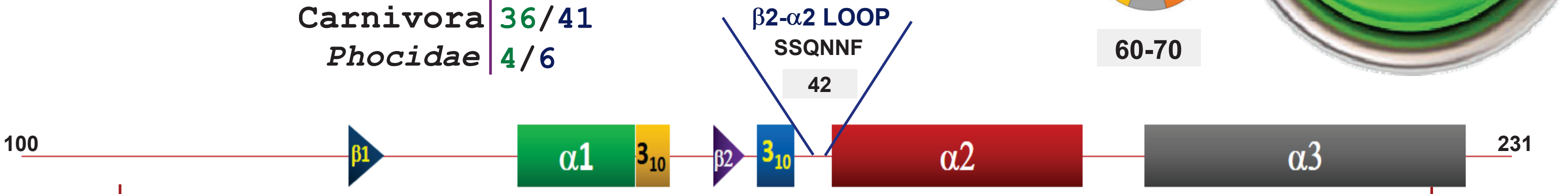
Carnivora	36/41
Phocidae	4/6

P76%

66.1



60-70



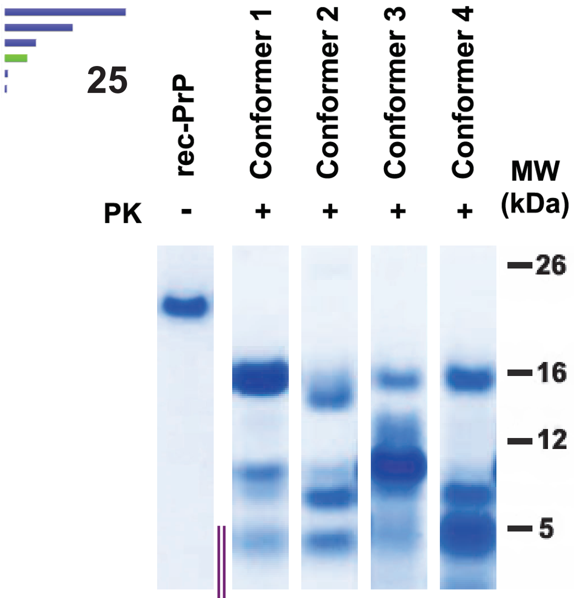
```
WGKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMHRYPNQVYYKPVDQYSSQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVSQYQRESEAYYQRGAS-
 N  S   I  V                           M       W          N         R      NN               I                     V M              T   K  Q  EGRS
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

No deletions

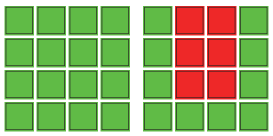
No insertions

No polymorphic variants found



213 AA

4
Conformers



Tm^{Exp}: ND

ΔΔG: -6.26

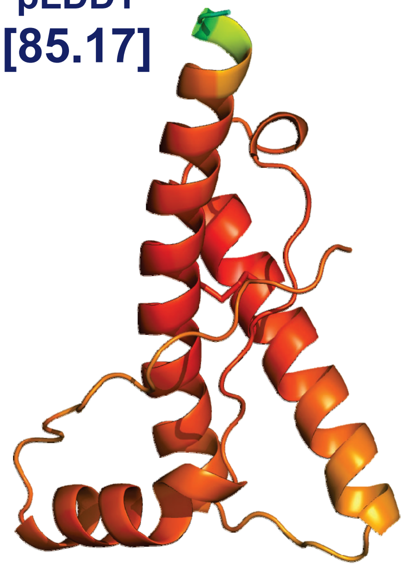
***In vitro* studies**

TgVole (1x)	**Not tested**
Weddell seal	**Not tested**

***In vivo* studies**

TgVole (1x)	**Not tested**
Weddell seal	**Not tested**

pLDDT
[85.17]

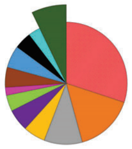


Protein code: 1081

African wild dog

GenBank: BK064019

P100%

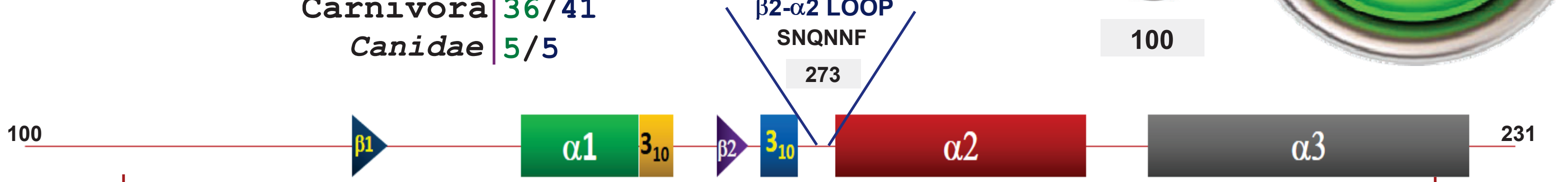


100

100

Lycaon pictus

Carnivora 36/41
Canidae 5/5



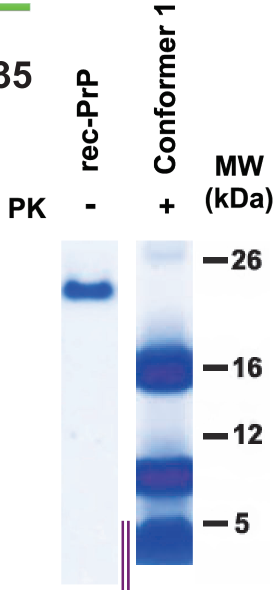
```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPDQVYYRPVDQYSNQNNFVRDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N        I                            M      W         N   N          N      H      I                  V M                 Q   EGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

135



213 AA

1
Conformers

Tm^{Exp}: ND

ΔΔG: -6.06

In vitro studies

TgVole (1x) — Not tested

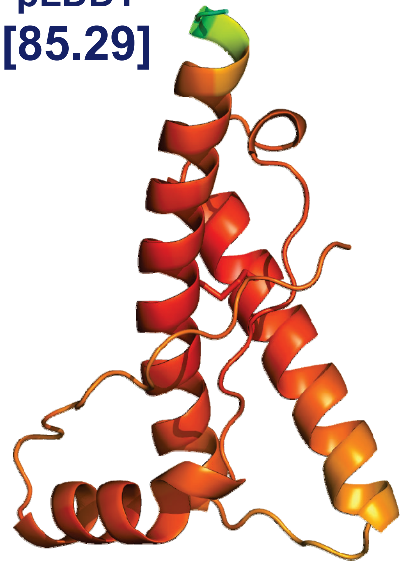
African wild dog — Not tested

In vivo studies

TgVole (1x) — Not tested

African wild dog — Not tested

pLDDT
[85.29]



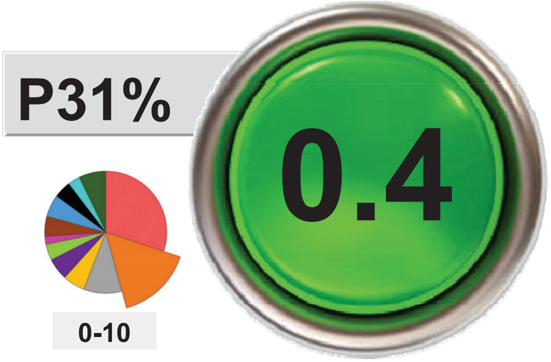
Protein code: 3183

Iberian lynx

GenBank: BK064941

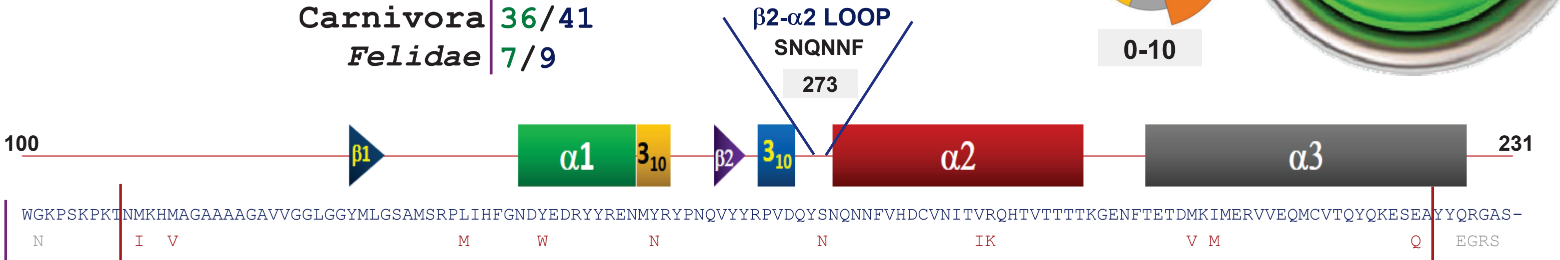
Lynx pardinus

Carnivora 36/41
Felidae 7/9



8 species sharing the same primary sequence

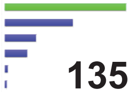
- **Cheetah** *Acinonyx jubatus*
- **Canada lynx** *Lynx canadensis*
- **Eurasian lynx** *Lynx lynx*
- **Leopard cat** *Prionailurus bengalensis euptilurus*
- **Iriomote cat** *Prionailurus iriomotensis*
- **Fishing cat** *Prionailurus viverrinus*
- **Cougar** *Puma concolor*
- **Jaguarundi** *Puma yagouaroundi*

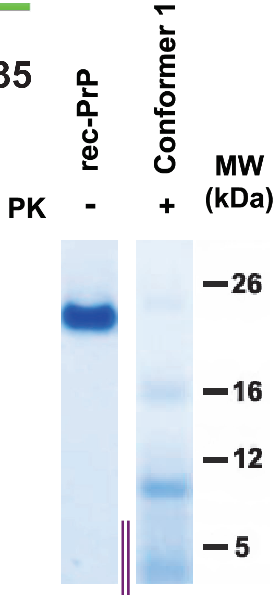


```
WGKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N         I  V                                   M     W         N              N            IK                V M                 Q  EGRS
```

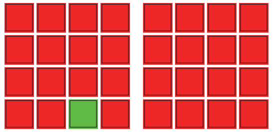
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found





207 AA



1
Conformers

Tm^{Exp}: ND

ΔΔG: -8.12

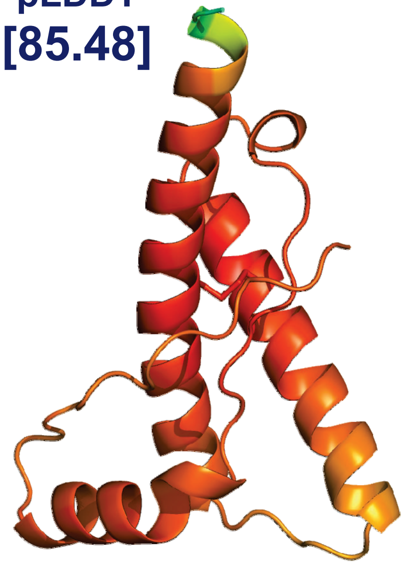
In vitro studies

TgVole (1x)	Not tested
Iberian lynx	Not tested

In vivo studies

TgVole (1x)	Not tested
Iberian lynx	Not tested

pLDDT
[85.48]



Protein code: 0977

Distinct primary sequence across species

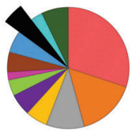
Bobcat

GenBank: EU341503

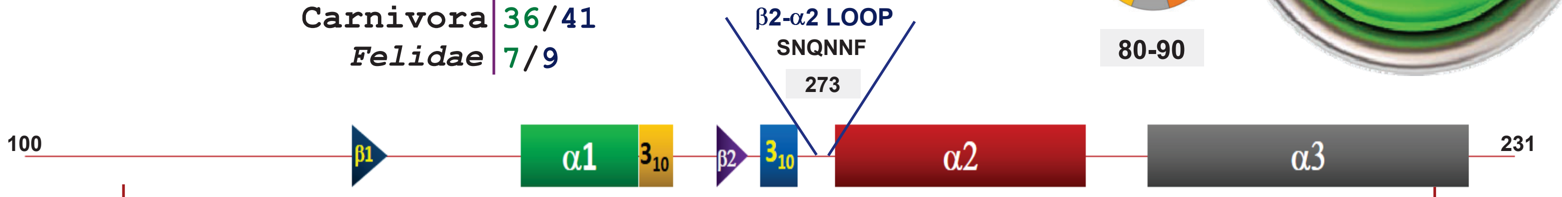
Lynx rufus

Carnivora 36/41
Felidae 7/9

P87%



80-90

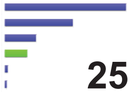


WGKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKEAEAYYQRGAS-

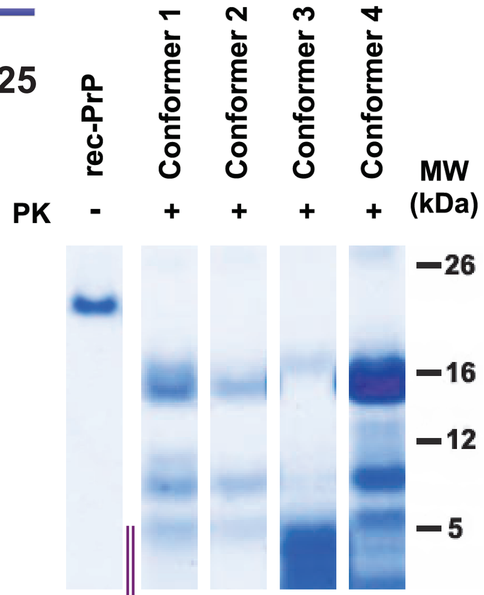
N I V M W N N IK V M SQ EGRS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

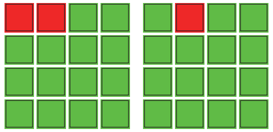


25



216 AA

4
Conformers



Tm^{Exp}: ND

ΔΔG: -6.74

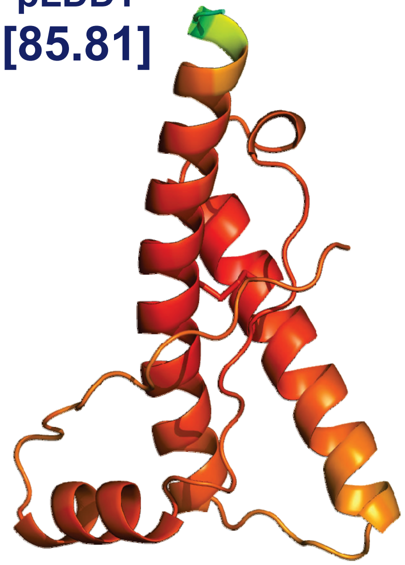
In vitro studies

TgVole (1x)	Not tested
Bobcat	Not tested

In vivo studies

TgVole (1x)	Not tested
Bobcat	Not tested

pLDDT
[85.81]



Protein code: 1333

Honey badger

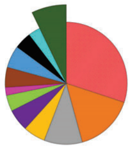
GenBank: BK064009

Mellivora capensis

Carnivora	36/41
Mustelidae	5/5

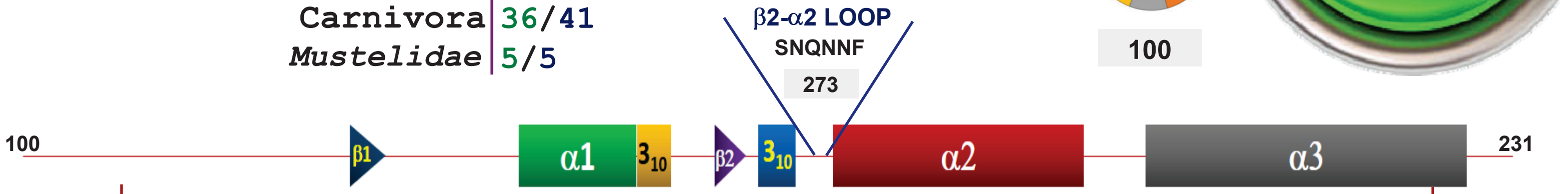
Distinct primary sequence across species

P100%



100

100



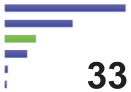
```
WGKPSKPKTNIKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMHRYPDQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQRGAS-
 N           V                         M      W         N   N    R    N             I                  V M              K  Q  EGRS
```

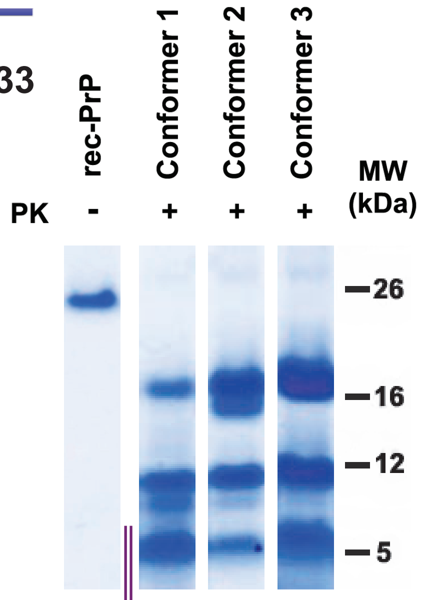
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found





213 AA

3 Conformers

Tm^{Exp}: ND

ΔΔG: -6.43

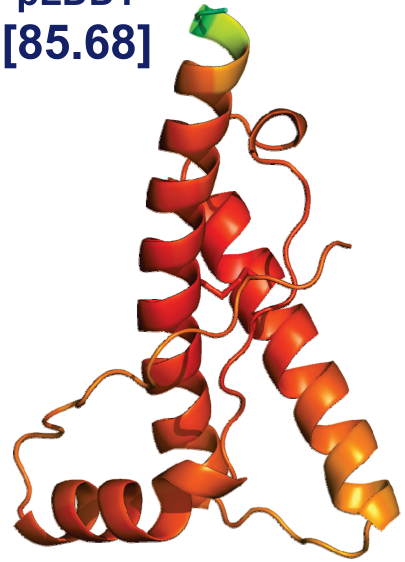
In vitro studies

TgVole (1x)	Not tested
Honey badger	Not tested

In vivo studies

TgVole (1x)	Not tested
Honey badger	Not tested

pLDDT [85.68]



Protein code: 3170

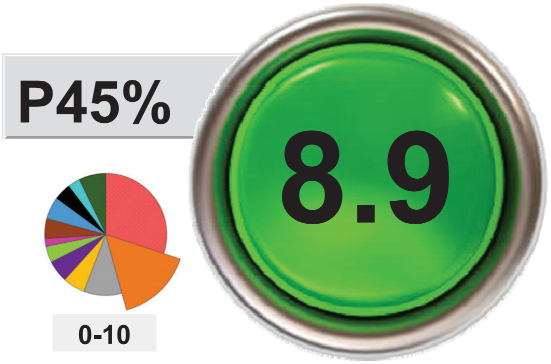
Skunk

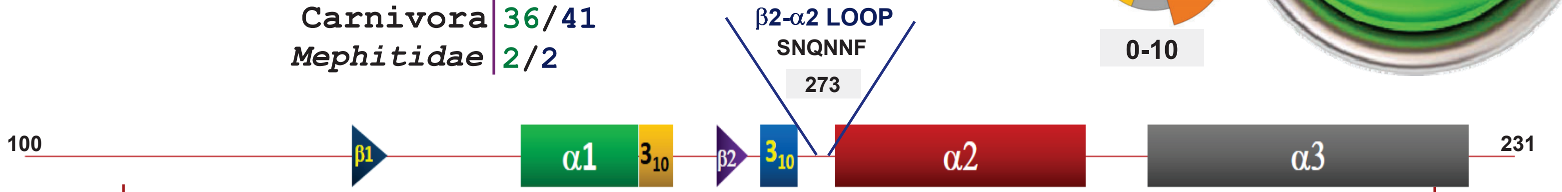
GenBank: EU341504

Mephitis mephitis

Carnivora	36/41
Mephitidae	2/2

P45%

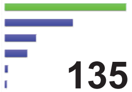


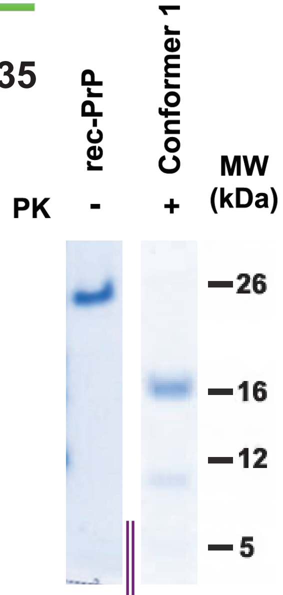


```
WGKPSKPKTNIKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRDNMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQRGAS-
 N        V                       M      W      E  N        R     N          IK                 V M               K  Q  EGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

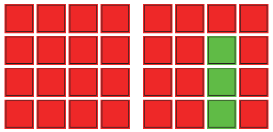
No deletions
No insertions
No polymorphic variants found





213 AA

1 Conformers



Tm^{Exp}: ND

ΔΔG: -4.03

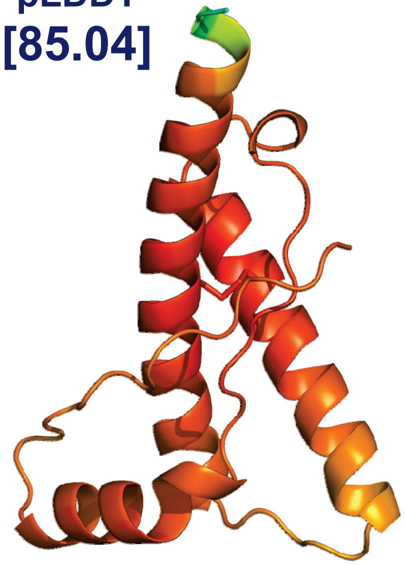
***In vitro* studies**

TgVole (1x)	Ongoing
Skunk	Ongoing

***In vivo* studies**

TgVole (1x)	Ongoing
Skunk	Not tested

pLDDT [85.04]



Distinct primary sequence across species

Protein code: 0538

Southern elephant seal

GenBank: XM_035005902

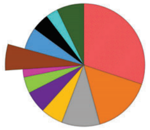
Mirounga leonina

Carnivora 36/41
Phocidae 4/6

1 species sharing the same primary sequence

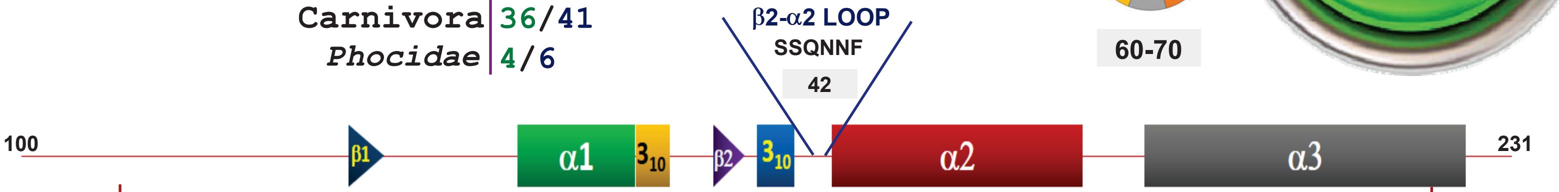
Northern elephant seal
Mirounga angustirostris

P75%



60-70

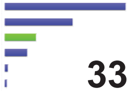
62.5



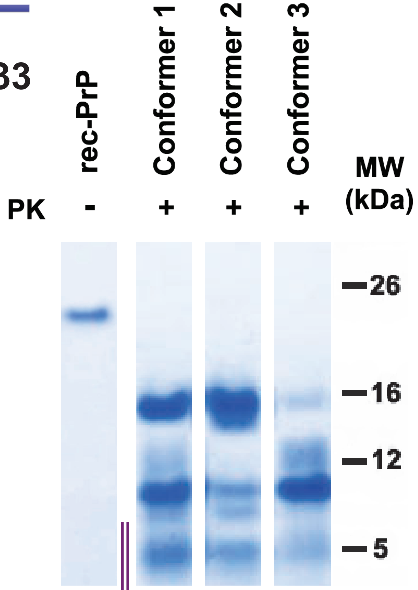
```
WGKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYYKPVDQYSSQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVSQYQRESEAYYQRGAS-
 N  S    I  V                          M       W          N         R      NN             I                   V M           T   K  Q   EGRS
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

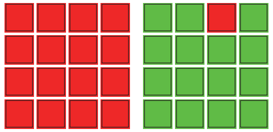


33



213 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: -12.06

***In vitro* studies**

TgVole (1x) Not tested

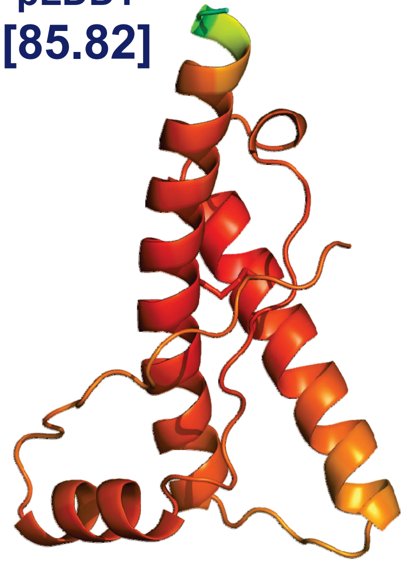
Southern elephant seal Not tested

***In vivo* studies**

TgVole (1x) Not tested

Southern elephant seal Not tested

pLDDT
[85.82]



Protein code: 2188

Hawaiian monk seal

GenBank: XM_021689157

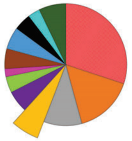
Monachus schauinslandi

Carnivora 36/41
Phocidae 4/6

Distinct primary sequence across species

P58%

24.6



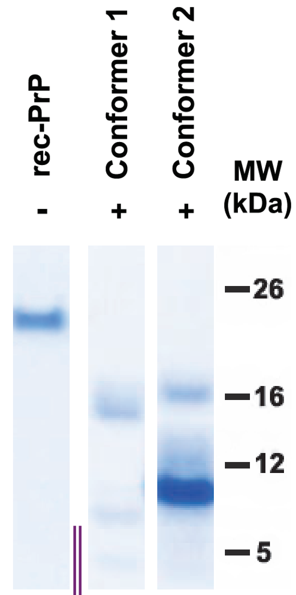
β2-α2 LOOP
SSQNNF
42

```
WGKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSSQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVSQYQRESEAYYQRGAS-
 N        I  V                         M      W         N        R     NN            I                  V M          T   K  Q   EGRS
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

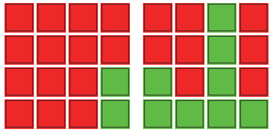
No deletions
No insertions
No polymorphic variants found

76



213 AA

2
Conformers



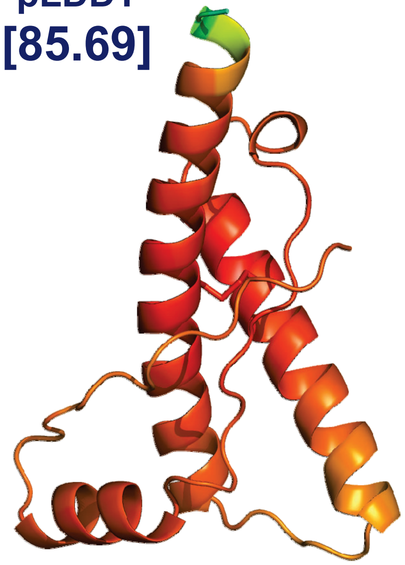
Tm^Exp: ND

ΔΔG: -10.71

***In vitro* studies**

TgVole (1x)	**Not tested**
Hawaiian monk seal	**Not tested**

pLDDT
[85.69]



***In vivo* studies**

TgVole (1x)	**Not tested**
Hawaiian monk seal	**Not tested**

Protein code: 1112

Banded mongoose

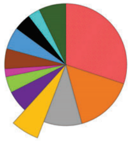
GenBank: BK064099

Mungos mungo

Carnivora 36/41
Herpestidae 4/4

P57%

23.6



20-30

Distinct primary sequence across species

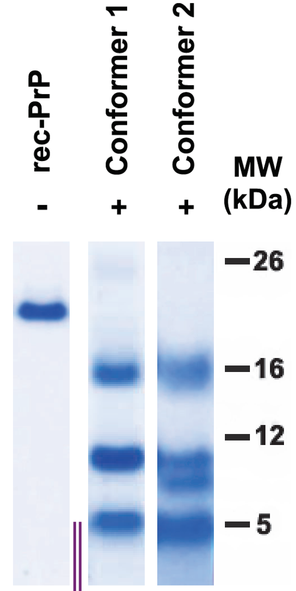
β2-α2 LOOP
SSQNNF
42

```
WGKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPIIHFGNDYEDRYYRQNMDRYPNQVYYRPVDQYSSQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYEKESQAYYQRGAS-
 N       NI                            M      W      E  N              NN            IK                 V M             Q       EGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

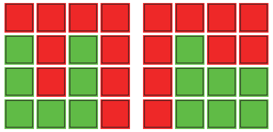
No deletions
No insertions
No polymorphic variants found

76



209 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -9.1

***In vitro* studies**

TgVole (1x) **Not tested**

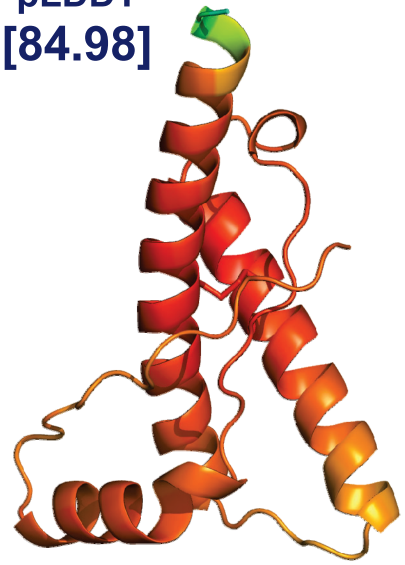
Banded mongoose **Not tested**

***In vivo* studies**

TgVole (1x) **Not tested**

Banded mongoose **Not tested**

pLDDT
[84.98]



Protein code: 3278

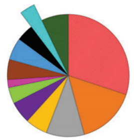
Stoat

GenBank: EU341505

Mustela erminea

Carnivora	36/41
Mustelidae	5/5

P92%



90-100

94.3

β2-α2 LOOP
SNQNNF
273

WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQRGAS-

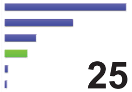
N I M W N R N I V M K Q EGRS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

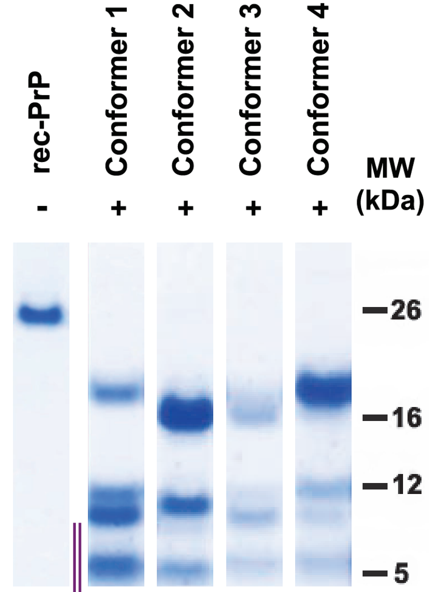
14 species sharing the same primary sequence

- ● **Raccoon** *Procyon lotor*
- ● **Stoat** *Mustela erminea*
- ● **Sea otter** *Enhydra lutris*
- ● **European otter** *Lutra lutra*
- ● **North American river otter** *Lontra canadensis*
- ● **Giant otter** *Pteronura brasiliensis*
- ● **European mink** *Mustela lutreola*
- ● **Least weasel** *Mustela nivalis*
- ● **South American coati** *Nasua nasua*
- ● **Asian small-clawed otter** *Aonyx cinerea*
- ● **Ring-tailed cat** *Bassariscus astutus*
- ● **Cacomistle** *Bassariscus sumichrasti*
- ● **White-nosed coati** *Nasua narica*
- ● **Black-footed ferret** *Mustela nigripes*



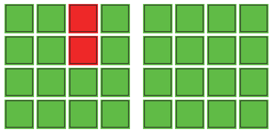
25

PK



213 AA

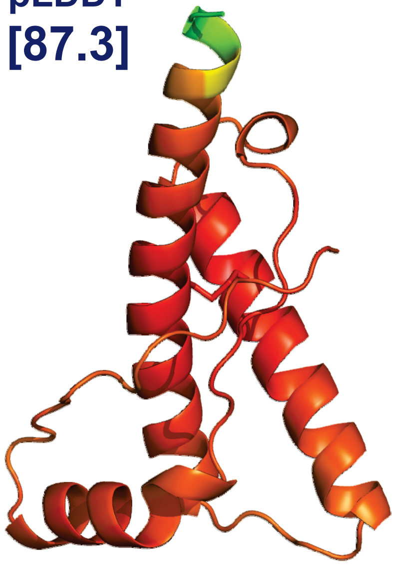
4 Conformers



Tm^{Exp}: ND

ΔΔG: -8.8

pLDDT [87.3]



In vitro studies

TgVole (1x)	Not tested
Stoat	Not tested

In vivo studies

TgVole (1x)	Not tested
Stoat	Not tested

Protein code: 0549

American mink

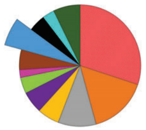
GenBank: EF508270

Neovison vison

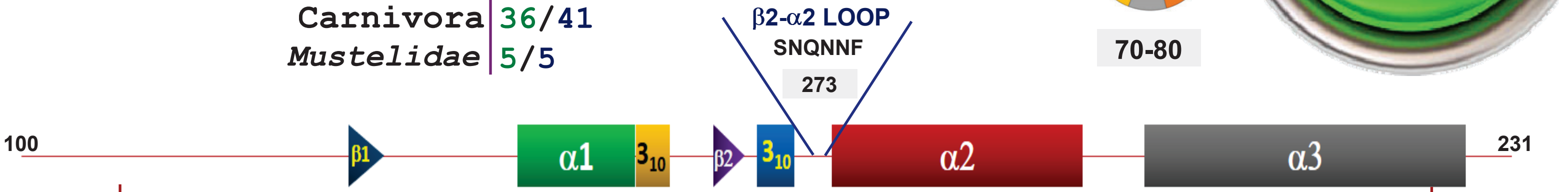
Carnivora	36/41
Mustelidae	5/5

P81%

71.4



70-80

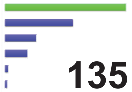


```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQKGAS-
 N        I                       M      W         N        R     N          I                   V M               K  Q  EGRS
```

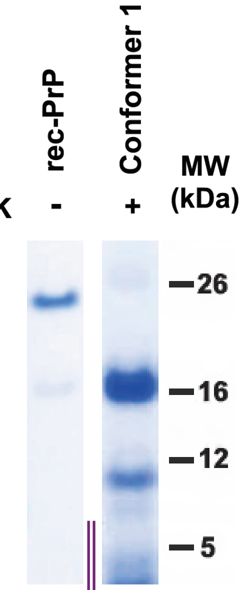
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

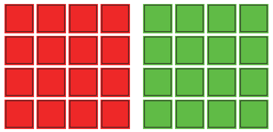


135



213 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -6.64

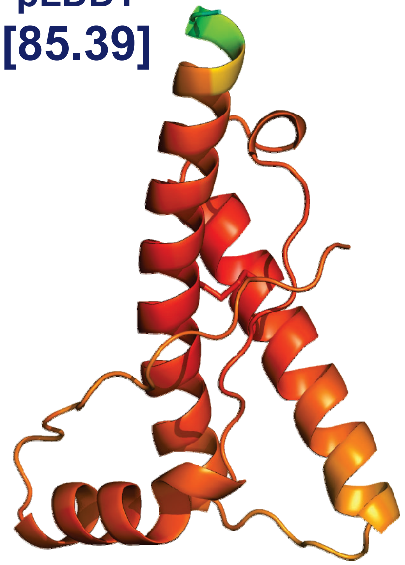
In vitro studies

TgVole (1x)	Propagate
TgAmerican mink	Ongoing

In vivo studies

TgVole (1x)	Infectious
TgAmerican mink	Not tested

pLDDT
[85.39]

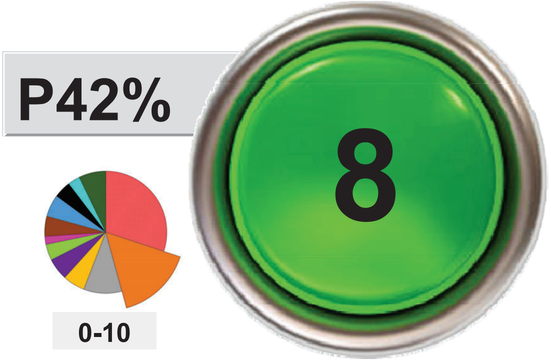


Walrus

GenBank: EU341508

Odobenus rosmarus

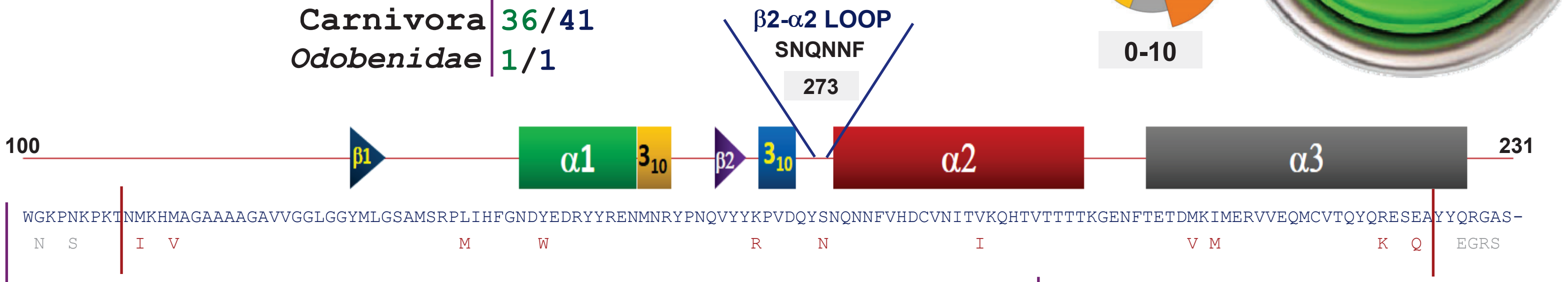
Carnivora	36/41
Odobenidae	1/1



P42%

7 species sharing the same primary sequence

- ● **Australasian fur seal** *Arctocephalus forsteri*
- ● **Brown fur seal** *Arctocephalus pusillus*
- ● **Guadalupe fur seal** *Arctocephalus townsendi*
- ● **Northern fur seal** *Callorhinus ursinus*
- ● **Steller sea lion** *Eumetopias jubatus*
- ● **Sea lion** *Otaria flavescens*
- ● **California sea lion** *Zalophus californianus*



WGKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQRGAS-

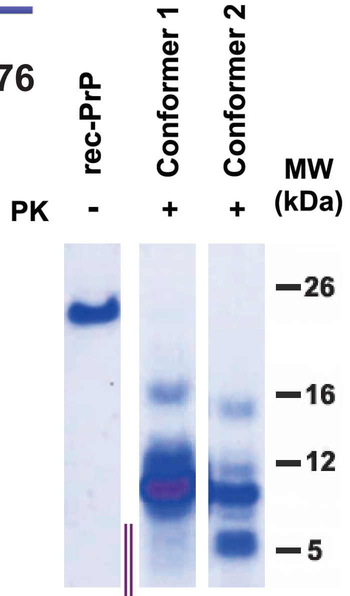
N S I V M W R N I V M K Q EGRS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

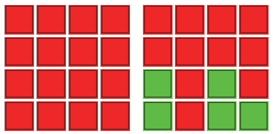
No deletions

No insertions

No polymorphic variants found



213 AA



2 Conformers

Tm^{Exp}: ND

ΔΔG: -12.13

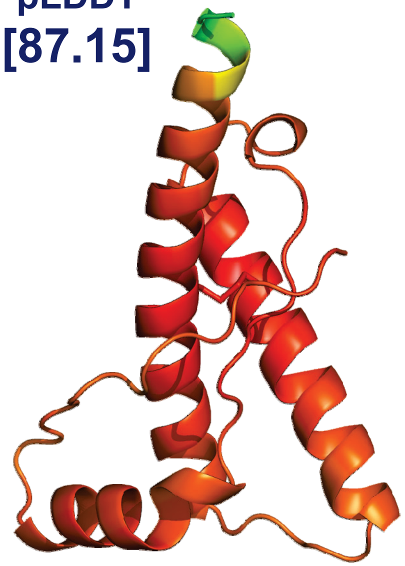
In vitro studies

TgVole (1x)	Not tested
Walrus	Not tested

In vivo studies

TgVole (1x)	Not tested
Walrus	Not tested

pLDDT [87.15]



Protein code: 0547

Lion

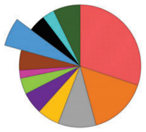
GenBank: EU236260

Panthera leo

Carnivora 36/41
Felidae 7/9

P84%

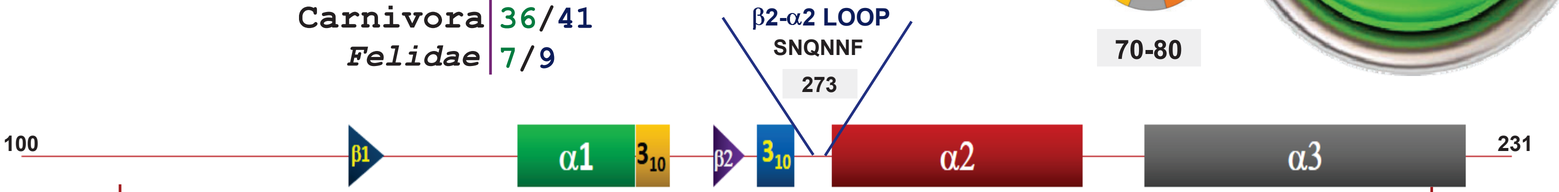
78.6



70-80

6 species sharing the same primary sequence

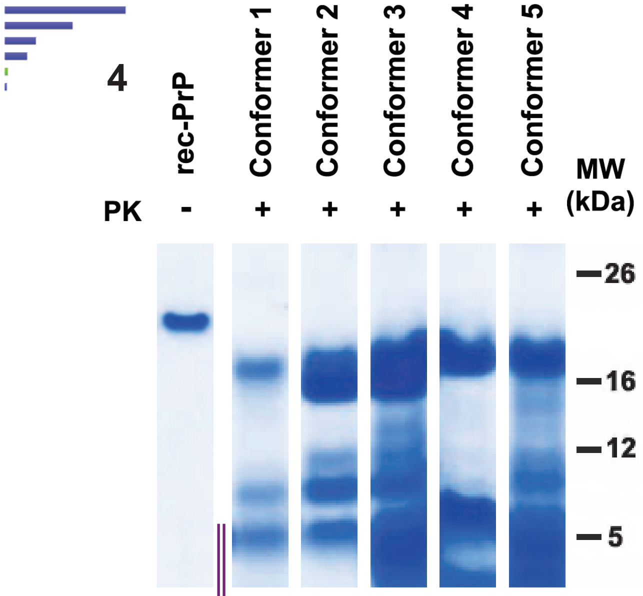
- **Sunda clouded leopard** *Neofelis diardi*
- **Clouded leopard** *Neofelis nebulosa*
- **Jaguar** *Panthera onca*
- **Leopard** *Panthera pardus*
- **Siberian tiger** *Panthera tigris*
- **Snow leopard** *Panthera uncia*



```
WGKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMNRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N        I V                          S  M     W         N              N         IK                   V M                Q  EGRS
```

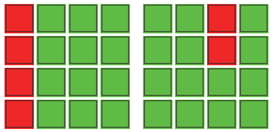
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



207 AA

5 Conformers



Tm^{Exp}: ND

ΔΔG: -6.42

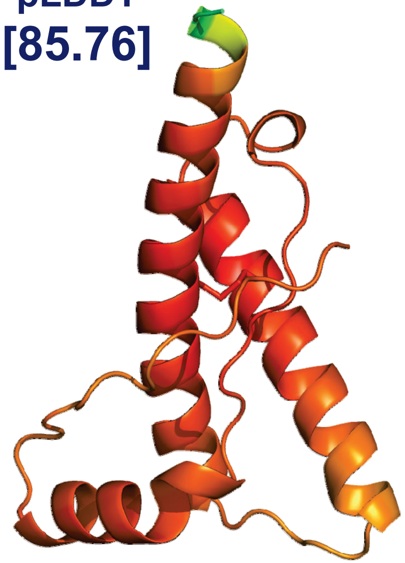
***In vitro* studies**

TgVole (1x)	Not tested
Lion	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Lion	Not tested

pLDDT [85.76]



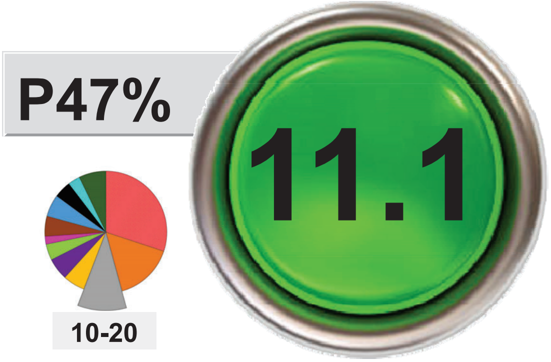
Protein code: 1085

Common seal

GenBank: EU341509

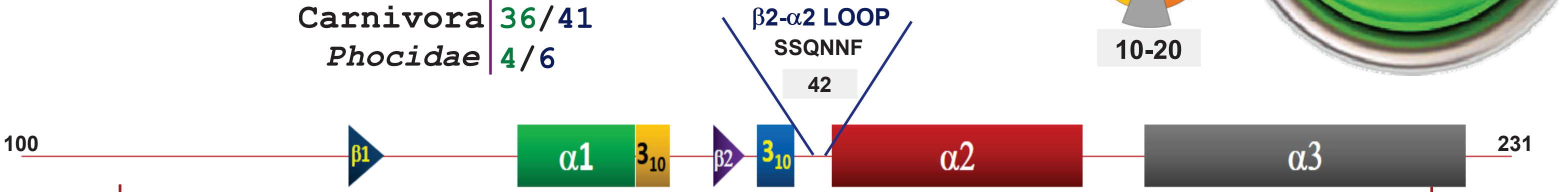
Phoca vitulina

Carnivora 36/41
Phocidae 4/6



5 species sharing the same primary sequence

- **Hooded seal** *Cystophora cristata*
- **Grey seal** *Halichoerus grypus*
- **Harp seal** *Pagophilus groenlandicus*
- **Spotted seal** *Phoca largha*
- **Baikal seal** *Pusa sibirica*



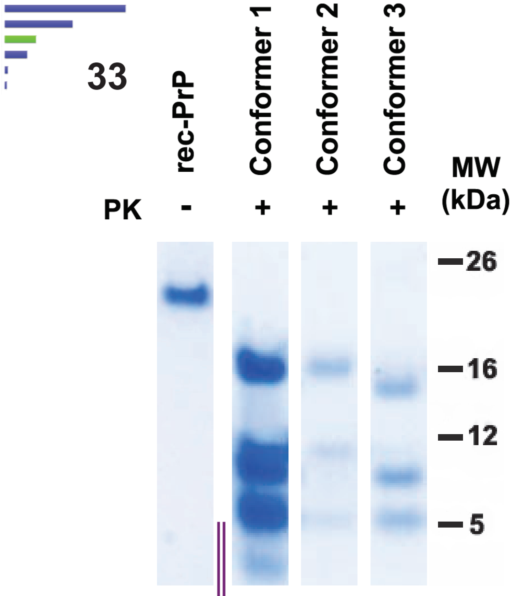
```
WGKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSSQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N  S     I  V                           M       W          N         R      NN                I                      V M                    Q  EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

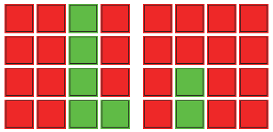
Tm^{Exp}: ND

ΔΔG: -9.87



213 AA

3 Conformers



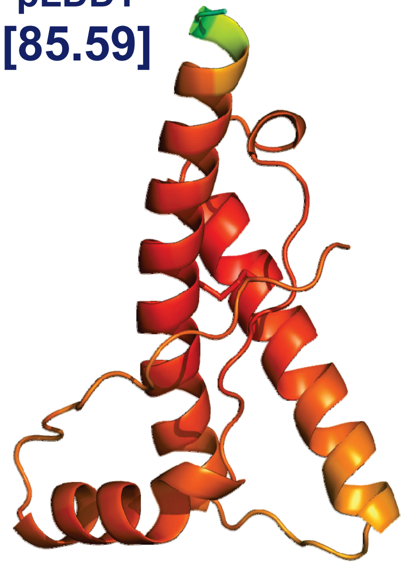
In vitro studies

TgVole (1x)	Not tested
Common seal	Not tested

In vivo studies

TgVole (1x)	Not tested
Common seal	Not tested

pLDDT [85.59]



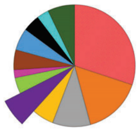
Protein code: 0929

Kinkajou

GenBank: BK063964

P64%

33.9



30-40

Potos flavus

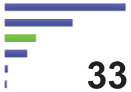
Carnivora	36/41
Procyonidae	1/1

β2-α2 LOOP
SNQNNF
273

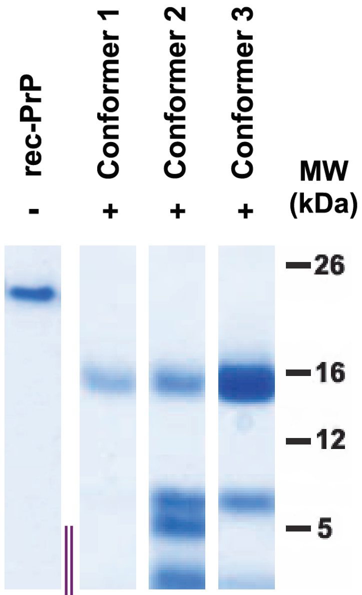
```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQRGAS-
 N        I                            M      W         N        R     N              IK                V M                    K  Q  EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

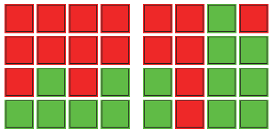


33



213 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: -6.27

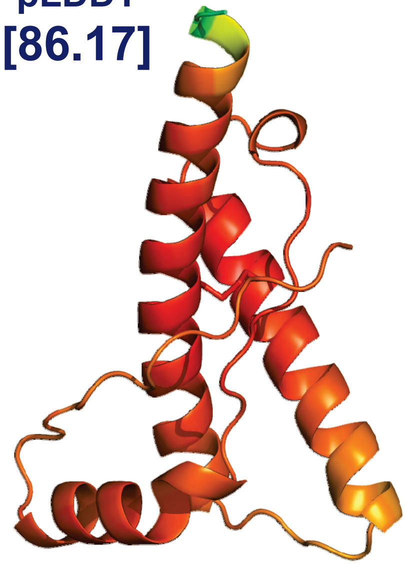
***In vitro* studies**

TgVole (1x)	Not tested
Kinkajou	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Kinkajou	Not tested

pLDDT [86.17]



Distinct primary sequence across species

Protein code: 3094

Aardwolf

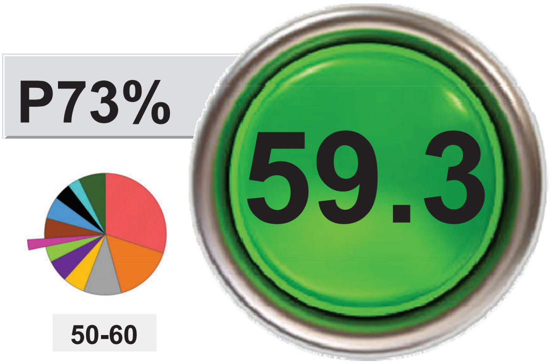
GenBank: BK064008

Proteles cristata

Carnivora 36/41
Hyaenidae 1/2

Distinct primary sequence across species

P73%

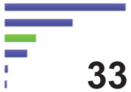


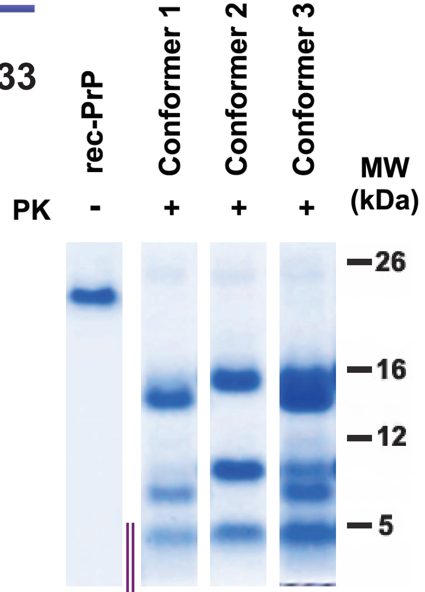
β2-α2 LOOP
SSQNNF
42

```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRQNMDRYPNQVYYKPVDQYSSQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQRGAS-
 N         I                         M       W       E  N        R      NN               IK                   V M              K  Q   EGRS
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

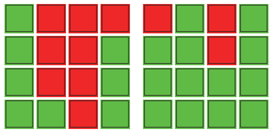
No deletions
No insertions
No polymorphic variants found





213 AA

3 Conformers



Tm^{Exp}: ND

ΔΔG: -10.08

In vitro studies

TgVole (1x) Not tested

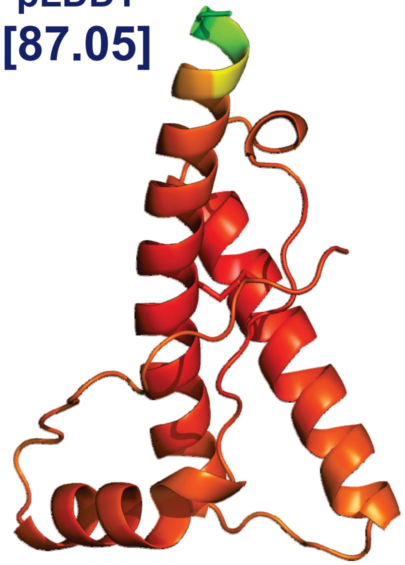
Aardwolf Not tested

In vivo studies

TgVole (1x) Not tested

Aardwolf Not tested

pLDDT
[87.05]



Ringed seal

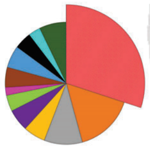
GenBank: BK064218

Pusa hispida saimensis

Carnivora 36/41
Phocidae 4/6

Distinct primary sequence across species

P29%



0

0

β2-α2 LOOP
SSQNNF
42

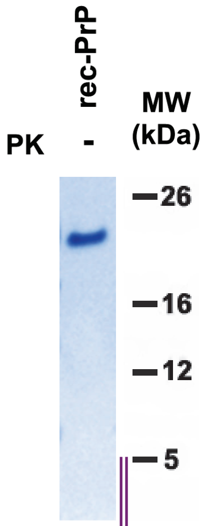
```
WGKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLVHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSSQNNFVHDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N  S     I  V                          MI    W         N        R     NN         I                 V M                  Q  EGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -14.83



213 AA

NO MISFOLDING

In vitro studies

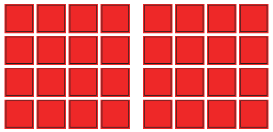
NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [92.7]

0
Conformers



Protein code: 4786

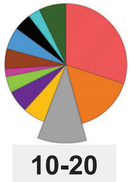
Western spotted skunk

GenBank: BK064000

Spilogale gracilis

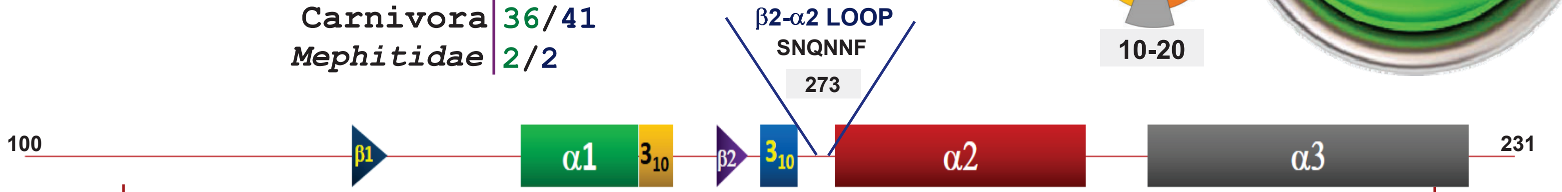
Carnivora 36/41
Mephitidae 2/2

P53% **18.2**



1 species sharing the same primary sequence

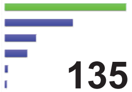
Eastern spotted skunk
Spilogale putorius interrupta

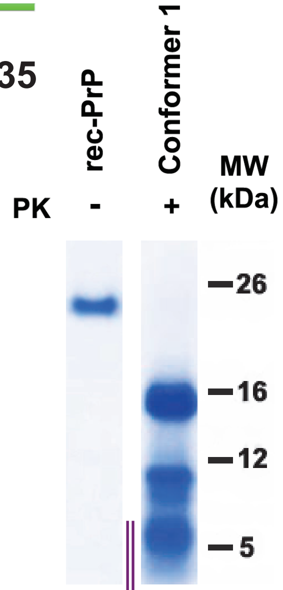


```
WGKPSKPKTNIKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRDNMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQRESEAYYQRGAS-
 N                                      M      W       E  N        R     N           IK                     V M               K  Q  EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

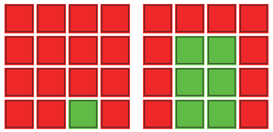
No deletions
No insertions
No polymorphic variants found





213 AA

1 Conformers



Tm^{Exp}: ND

ΔΔG: -1.74

***In vitro* studies**

TgVole (1x) Not tested

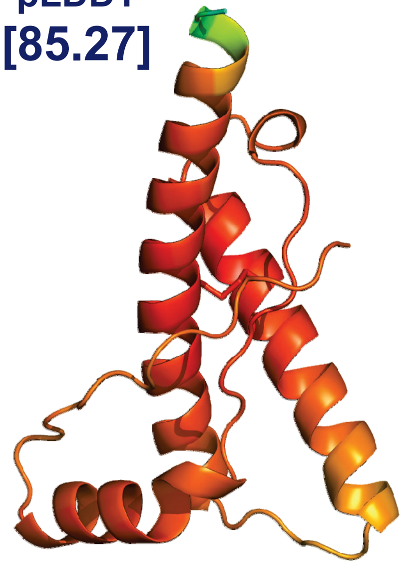
Western spotted skunk Not tested

***In vivo* studies**

TgVole (1x) Not tested

Western spotted skunk Not tested

pLDDT
[85.27]



Protein code: 3161

Meerkat

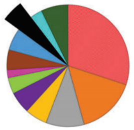
GenBank: XP_029772432

Suricata suricatta

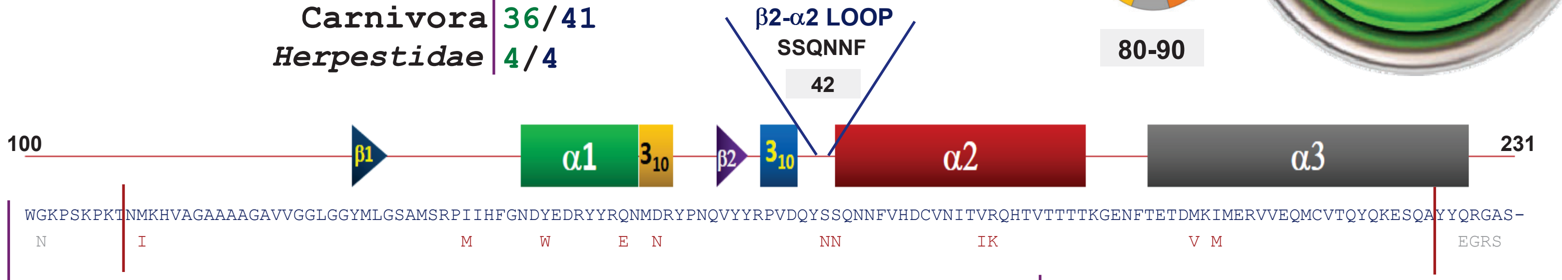
Carnivora	36/41
Herpestidae	4/4

P89%

87.5



80-90



WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPIIHFGNDYEDRYYRQNMDRYPNQVYYRPVDQYSSQNNFVHDCVNITVRQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESQAYYQRGAS-

N I M W E N NN IK V M EGRS

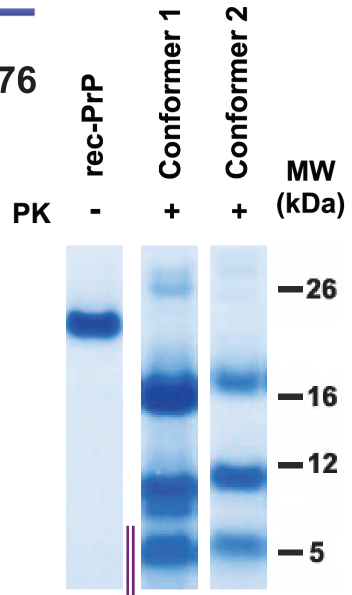
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

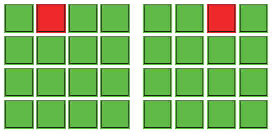
76



209 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: -9.09

In vitro studies

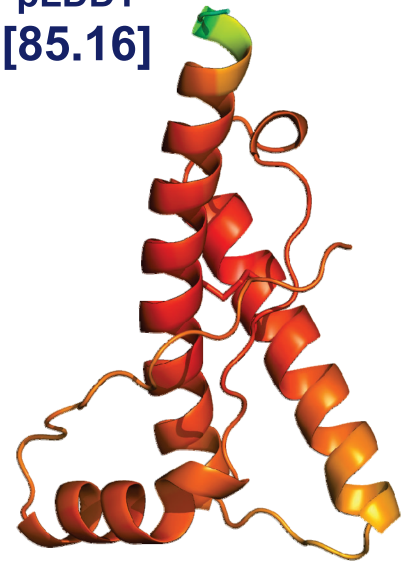
TgVole (1x)	Not tested
Meerkat	Not tested

In vivo studies

TgVole (1x)	Not tested
Meerkat	Not tested

pLDDT

[85.16]



Distinct primary sequence across species

Protein code: 0939

Spectacled bear

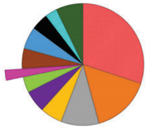
GenBank: BK064152

Tremarctos ornatus

Carnivora	36/41
Ursidae	2/2

P73%

53.6



50-60

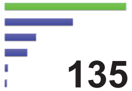
β2-α2 LOOP
SNQNSF
36

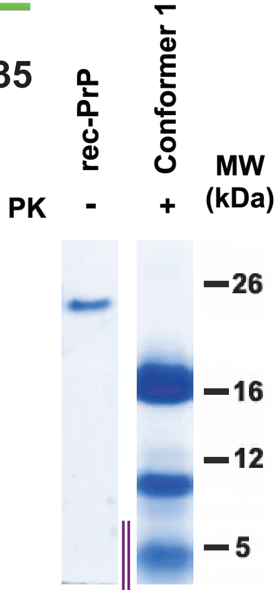
```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCVTQYQREAEAYYQRGAS-
 N         I                                   M      W          N         R      N   N          I                    V M                K SQ    EGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

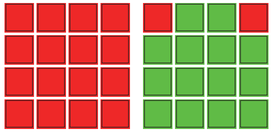
Distinct primary sequence across species





213 AA

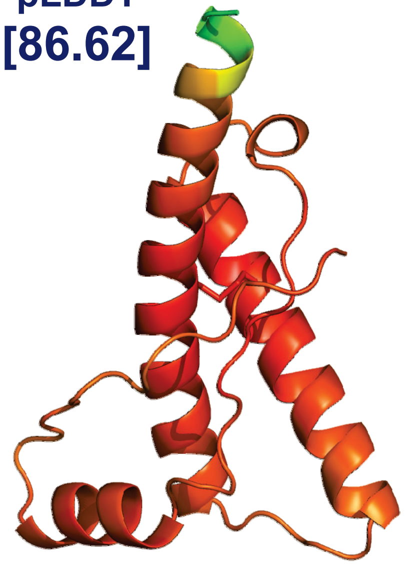
1
Conformers



Tm^{Exp}: ND

ΔΔG: -10.4

pLDDT
[86.62]



In vitro studies

TgVole (1x)	Not tested
Spectacled bear	Not tested

In vivo studies

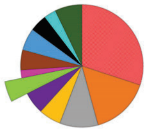
TgVole (1x)	Not tested
Spectacled bear	Not tested

Protein code: 3583

Brown bear

GenBank: JX218961

P69% **44.6**



40-50

Ursus arctos

Carnivora	36/41
Ursidae	2/2

5 species sharing the same primary sequence

Giant panda
Ailuropoda melanoleuca

Sun bear
Helarctos malayanus

American black bear
Ursus americanus

Polar bear
Ursus maritimus

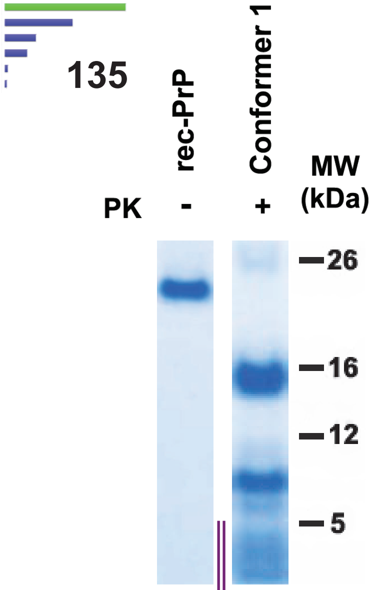
Asian black bear
Ursus thibetanus thibetanus

β2-α2 LOOP
SNQNSF
36

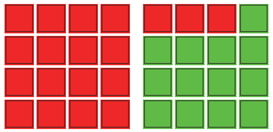
```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCVTQYQREAEAYYQRGAS-
 N        I                            M      W          N         R      N   N         I                        V M           K SQ   EGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



213 AA



1
Conformers

Tm^{Exp}: ND

ΔΔG: -10.67

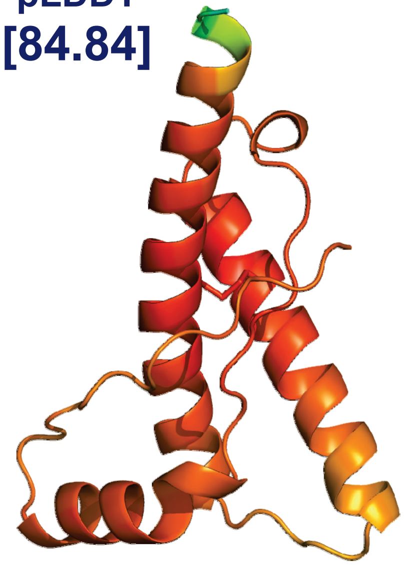
In vitro studies

TgVole (1x)	Not tested
Brown bear	Not tested

In vivo studies

TgVole (1x)	Not tested
Brown bear	Not tested

pLDDT
[84.84]



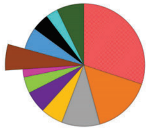
Protein code: 0927

Red fox

GenBank: XM_026012328

Vulpes vulpes

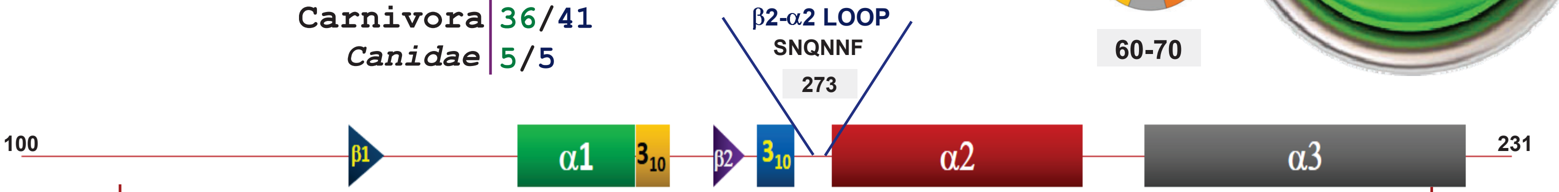
Carnivora 36/41
Canidae 5/5



60-70

9 species sharing the same primary sequence

● **Side-striped jackal** *Canis adustus*
● **Raccoon dog** *Nyctereutes procyonoides*
● **Bat-eared fox** *Otocyon megalotis*
● **Gray fox** *Urocyon cinereoargenteus*
● **Island fox** *Urocyon littoralis*
● **Corsac fox** *Vulpes corsac*
● **Arctic fox** *Vulpes lagopus*
● **Swift fox** *Vulpes velox*
● **Fennec fox** *Vulpes zerda*

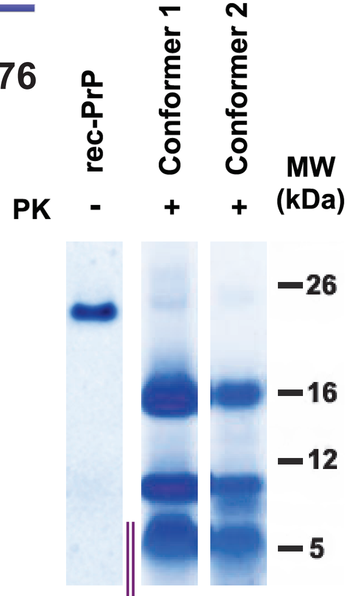


```
WGKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPDQVYYRPVDQYSNQNNFVRDCVNITVKQHTVTTTTKGENFTETDMKIMERVVEQMCVTQYQKESEAYYQRGAS-
 N  S     I                            M      W         N   N          N      H      I                  V M                  Q  EGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

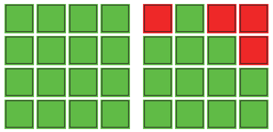
No deletions
No insertions
No polymorphic variants found

76



213 AA

2 Conformers



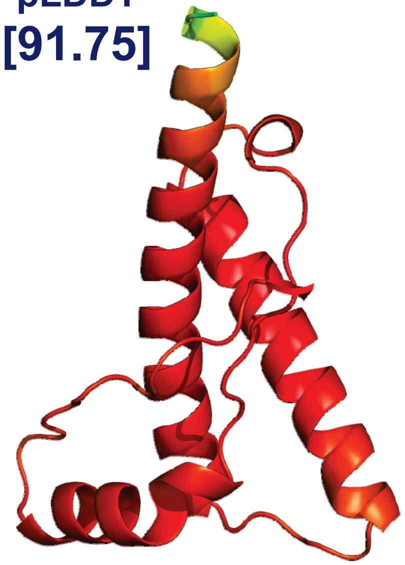
Tm^{Exp}: ND

ΔΔG: -8.8

In vitro studies

TgVole (1x)	Not tested
Red fox	Not tested

pLDDT [91.75]



In vivo studies

TgVole (1x)	Not tested
Red fox	Not tested

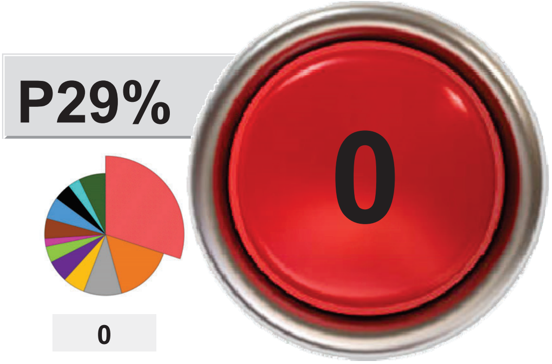
Protein code: 1114

Distinct primary sequence across species

Whale

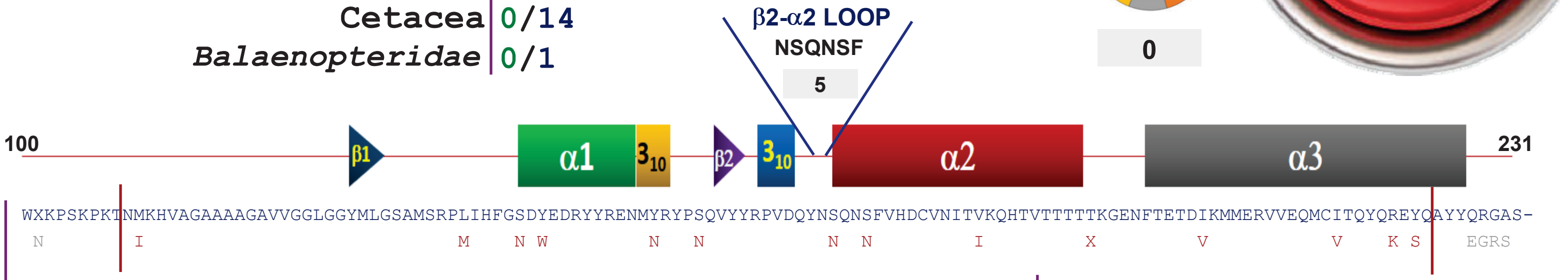
GenBank: DQ884475

P29%



Balaenoptera physalus

Cetacea	0/14
Balaenopteridae	0/1



WXKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPSQVYYRPVDQYNSQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEQMCITQYQREYQAYYQRGAS-

N I M N W N N N N I X V V K S EGRS

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

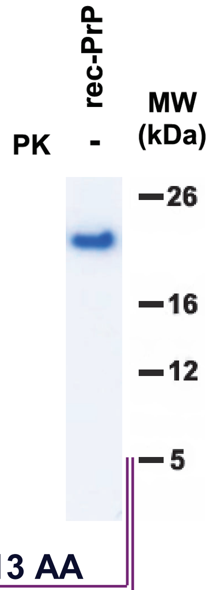
No deletions

One insertion

No polymorphic variants found

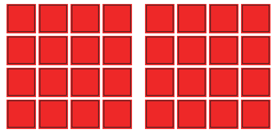
Tm^{Exp}: ND

ΔΔG: -16.96



213 AA

NO MISFOLDING



0

Conformers

In vitro studies

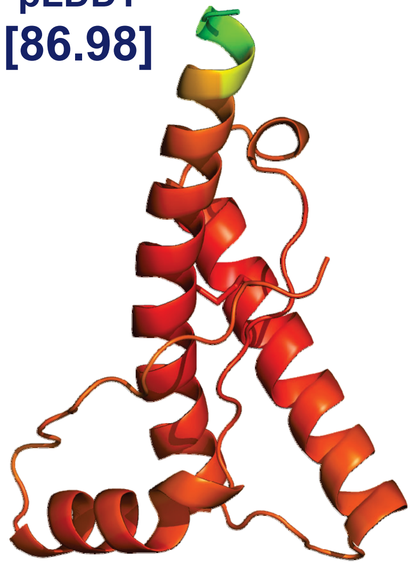
NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT

[86.98]



Protein code: 0960

Beluga whale

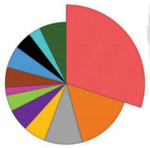
GenBank: XM_022556485

Delphinapterus leucas

Cetacea 0/14
Monodontidae 0/1

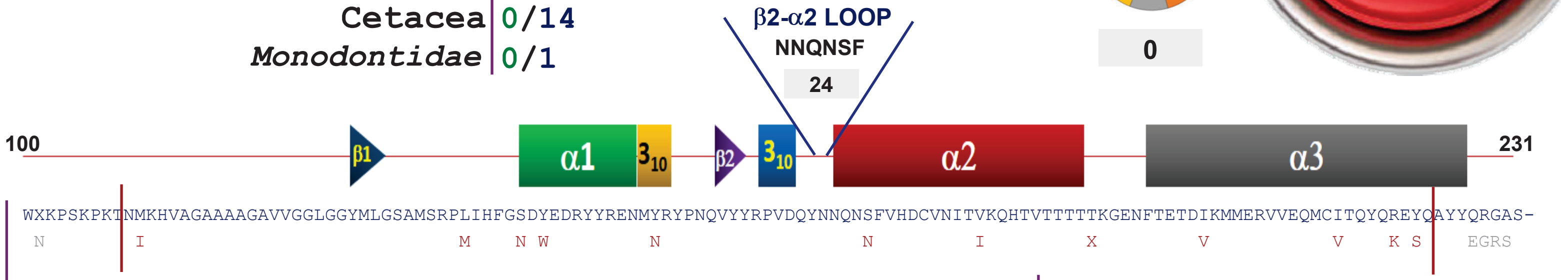
P29%

0



0

Distinct primary sequence across species



WXKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEQMCITQYQREYQAYYQRGAS-

N I M N W N N I X V V K S EGRS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

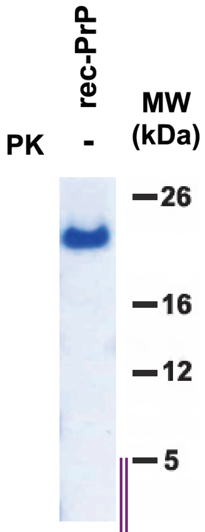
No deletions

One insertion

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -17.39



213 AA

NO MISFOLDING

0

Conformers

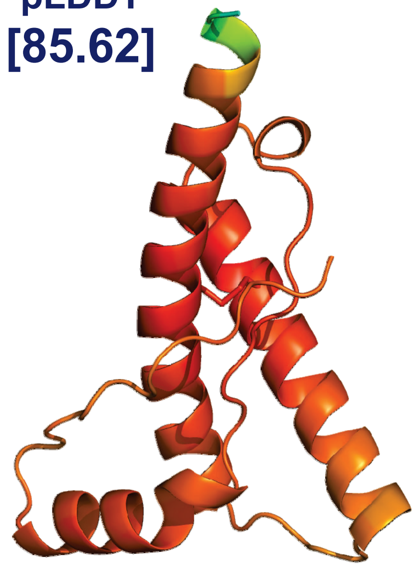
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[85.62]



Protein code: 0924

Northern bottlenose whale

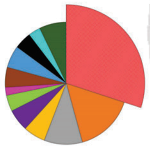
GenBank: BK064204

Hyperoodon ampullatus

Cetacea 0/14
Ziphiidae 0/4

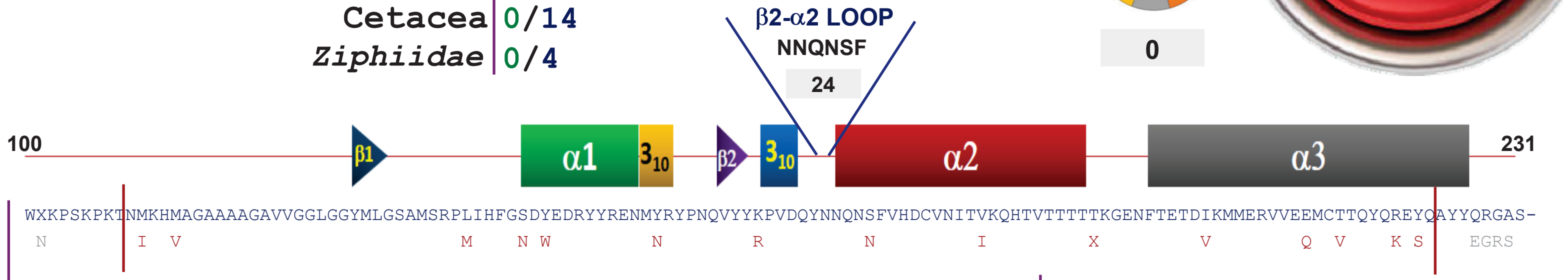
Distinct primary sequence across species

P29%



0

0



```
WXKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYKPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEEMCTTQYQREYQAYYQRGAS-
 N         I  V                              M    N W        N        R         N         I         X         V        Q  V    K S    EGRS
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

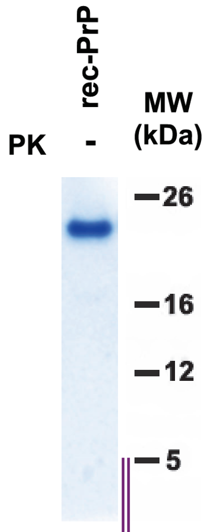
No deletions

One insertion

No polymorphic variants found

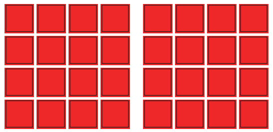
Tm^{Exp}: ND

ΔΔG: -20.25



213 AA

NO MISFOLDING



0
Conformers

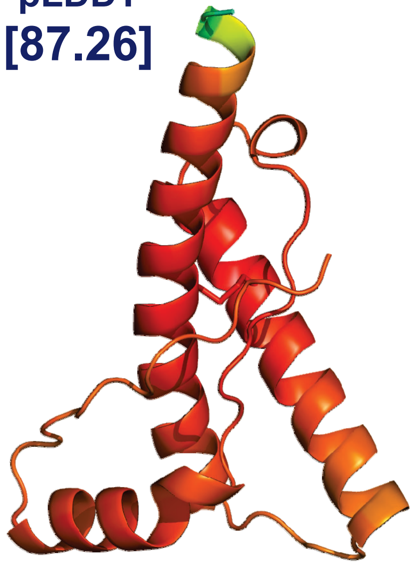
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[87.26]



Protein code: 4556

Amazon river dolphin

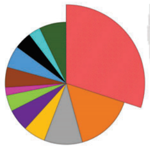
GenBank: BK064059

Inia geoffrensis

`Cetacea` 0/14
`Iniidae` 0/3

Distinct primary sequence across species

P29%



0

0

β2-α2 LOOP
NNQNSF
24

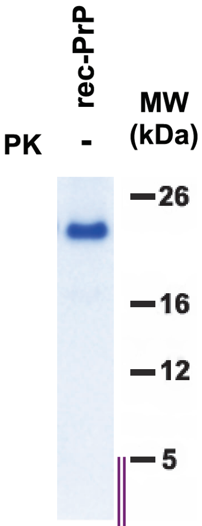
```
WXKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEQMCITQYQREYQAYYQRGAS-
 N        I                            M    N W          N                    N         I         X         V          V    K S   EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
One insertion
No polymorphic variants found

Tm^{Exp}: ND

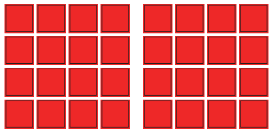
ΔΔG: -17.25



213 AA

NO MISFOLDING

0
Conformers



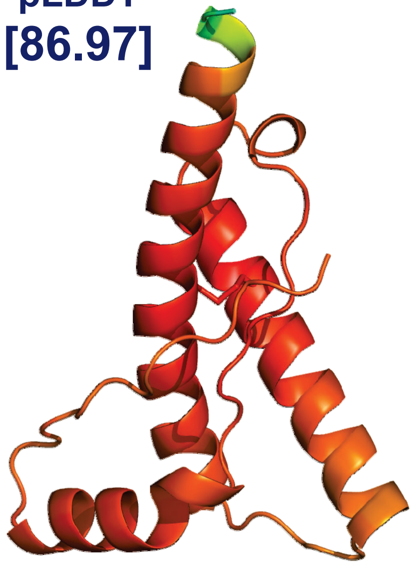
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.97]



Protein code: 3228

Distinct primary sequence across species

Pacific white-sided dolphin

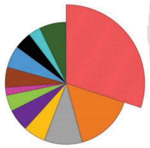
GenBank: XM_027118243

Lagenorhynchus obliquidens

Cetacea	0/14
Delphinidae	0/2

P29%

0



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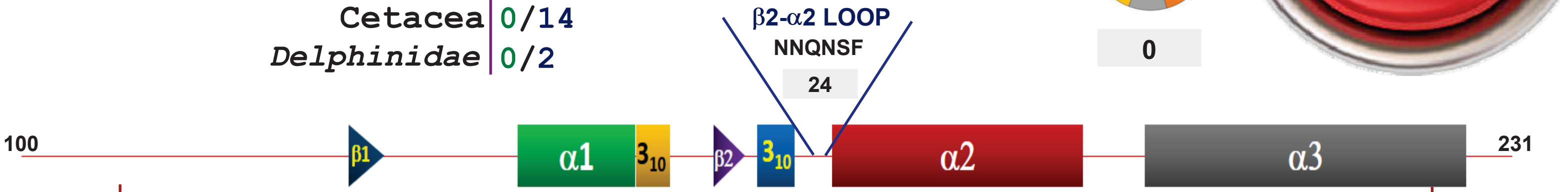


WXKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEQMCITQYQREYEAYYQRGYG-

N I M N W N N I X V V K SQ EGRSS

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

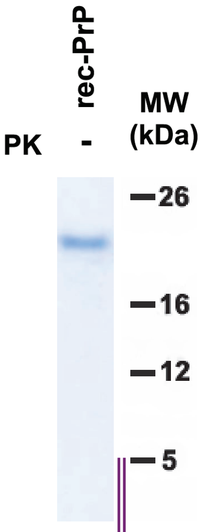
No deletions

One insertion

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -30.33

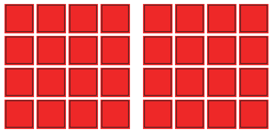


213 AA

NO MISFOLDING

0

Conformers



In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT

[87.41]

Protein code: 1416

Distinct primary sequence across species

Baiji

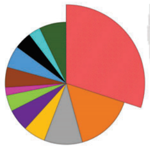
GenBank: XM_007463977

Lipotes vexillifer

Cetacea 0/14
Iniidae 0/3

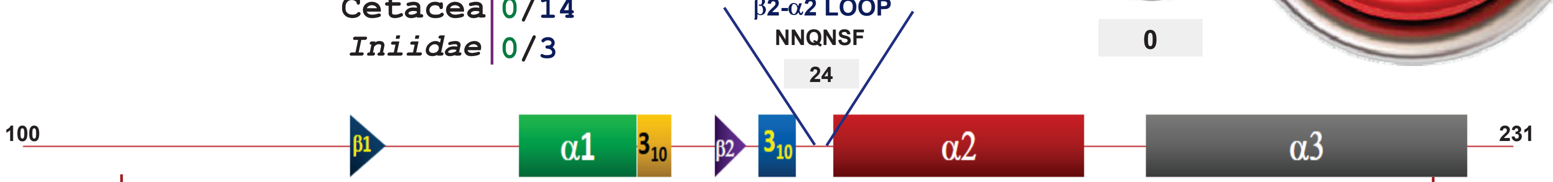
P29%

0



0

β2-α2 LOOP
NNQNSF
24



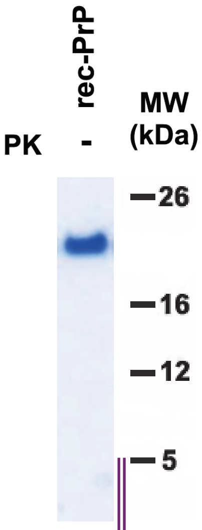
```
WXKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSATSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEQMCITQYQREYQAYYQRGAS-
 N        I                       M   M   N W     N                          N         I         X          V          V   K S     EGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
One insertion
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -10.64



213 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[85.68]

Protein code: 0922

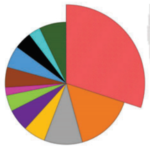
Sowerby's beaked whale

GenBank: BK064083

Mesoplodon bidens

Cetacea	0/14
Ziphiidae	0/4

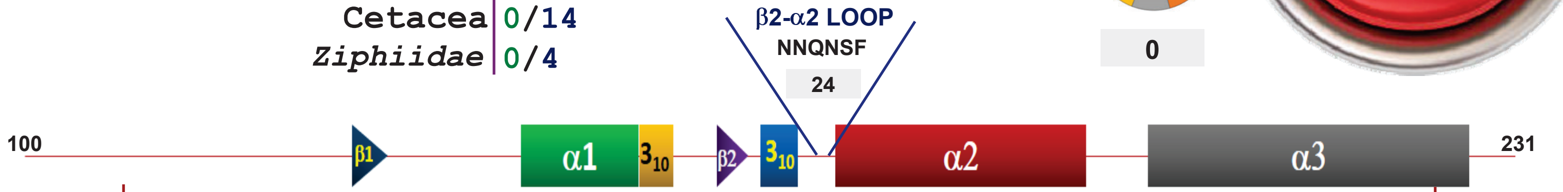
P29%



0

0

Distinct primary sequence across species



WXKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEEMCTTQYQREYQAYYQRGAS-

N I M N W N N I X V Q V K S EGRS

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

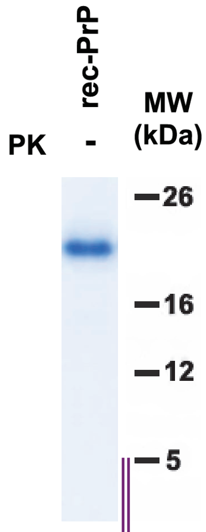
No deletions

One insertion

No polymorphic variants found

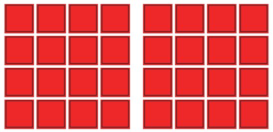
Tm^{Exp}: ND

ΔΔG: -15.45



213 AA

NO MISFOLDING



0

Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT

[87.82]

Protein code: 3262

Distinct primary sequence across species

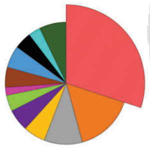
Stejneger's beaked whale

GenBank: BK064780

Mesoplodon stejnegeri

Cetacea	0/14
Ziphiidae	0/4

P29%



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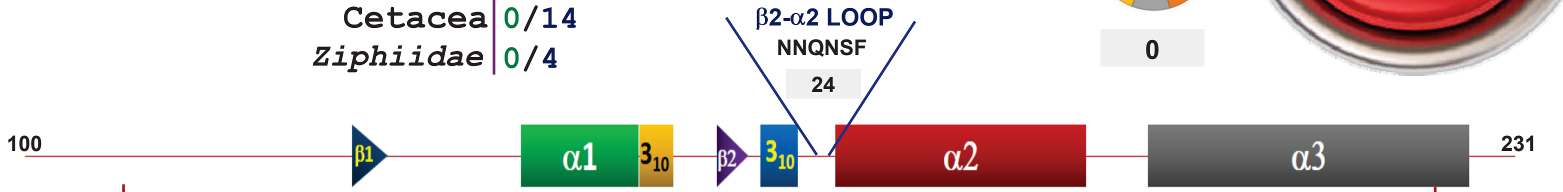


```
WXKPGKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEEMCTTQYQREYQAYYQRGAS-
 N  S     I                            M    N W         N                  N         I         X         V        Q  V    K S   EGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

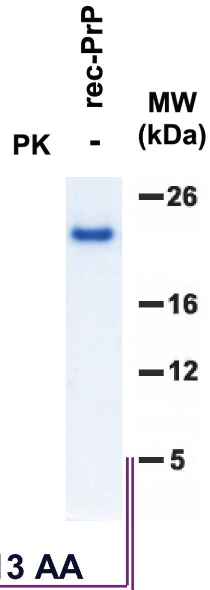
No deletions

One insertion

No polymorphic variants found

Tm^{Exp}: ND

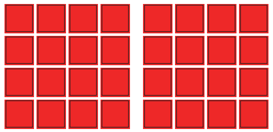
ΔΔG: -16.57



213 AA

NO MISFOLDING

0
Conformers



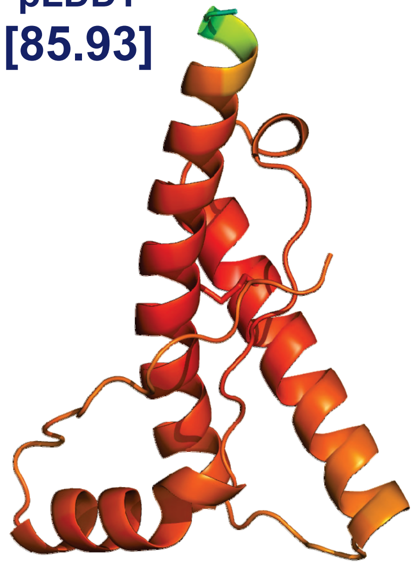
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[85.93]



Protein code: 3937

Narrow-ridged finless porpoise

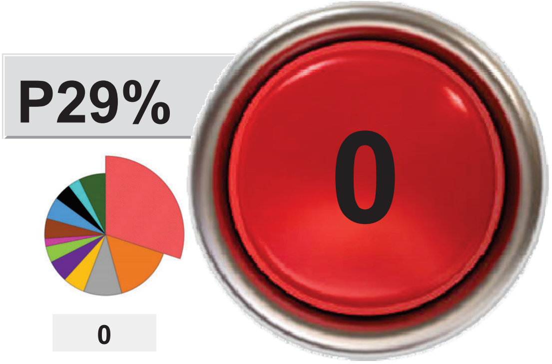
GenBank: XM_024764249

Neophocaena phocaenoides

Cetacea	0/14
Phocoenidae	0/1

Distinct primary sequence across species

P29%



0

β2-α2 LOOP
NNQNSF
24

```
WXKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEQMCITQYQREYQAYYQRGYG-
 N        I                                M    N W      N                   N         I         X         V           V    K S   EGRSS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

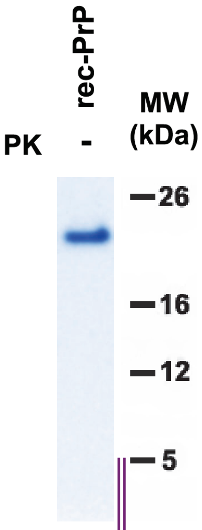
No deletions

One insertion

No polymorphic variants found

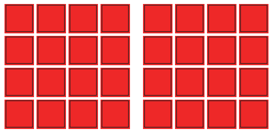
Tm^{Exp}: ND

ΔΔG: -24.72



213 AA

NO MISFOLDING



0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.94]

Protein code: 1126

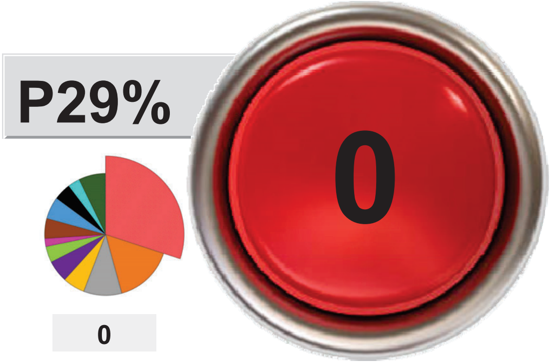
Distinct primary sequence across species

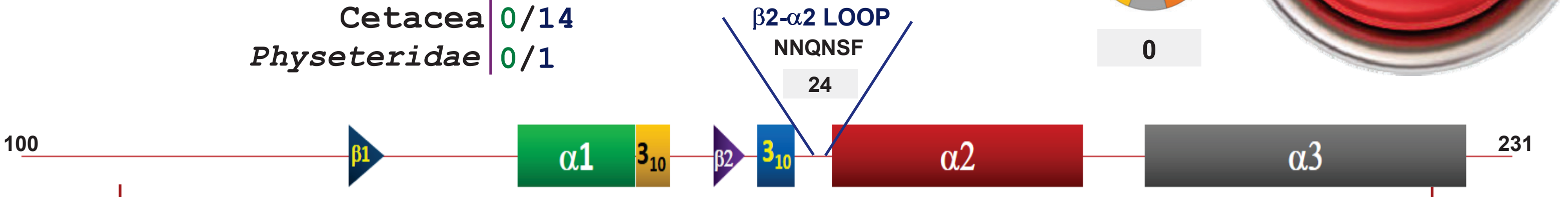
Sperm whale

GenBank: XM_007123285

Physeter catodon

Cetacea 0/14
Physeteridae 0/1





WXKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEQMCITQYQREYQAYYQRGAS-

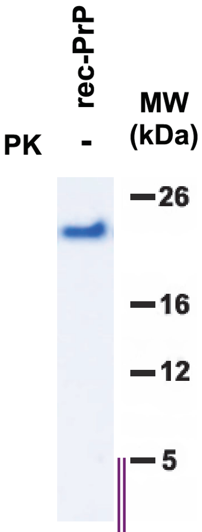
N I M N W N N I X V V K S EGRS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
One insertion
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -16.05



215 AA

NO MISFOLDING

0
Conformers

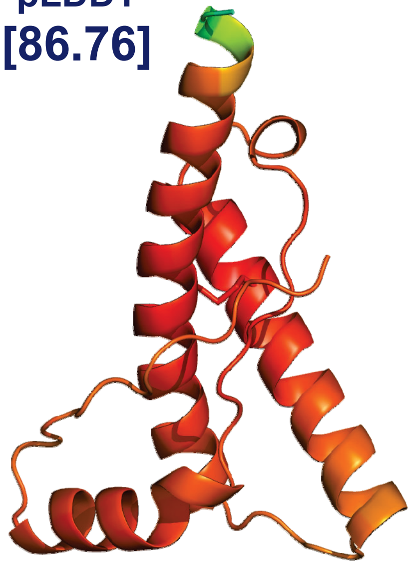
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.76]



Protein code: 0956

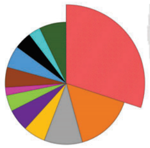
South Asian river dolphin

GenBank: BK064007

Platanista gangetica

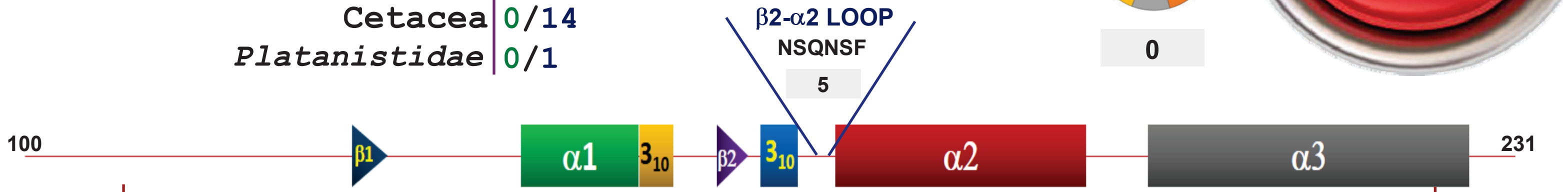
Cetacea 0/14
Platanistidae 0/1

P29%



0

0



WXKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNSQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEQMCITQYQREYQAYYQRGAS-

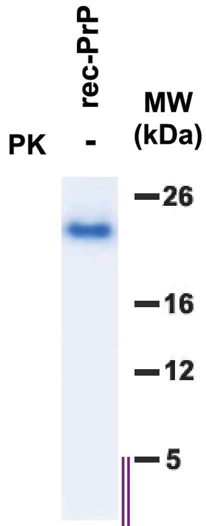
N I M N W N N N I X V V K S EGRS

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
One insertion
No polymorphic variants found

Tm^{Exp}: ND

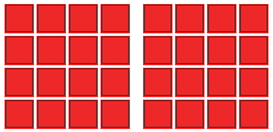
ΔΔG: -14.99



213 AA

NO MISFOLDING

0
Conformers



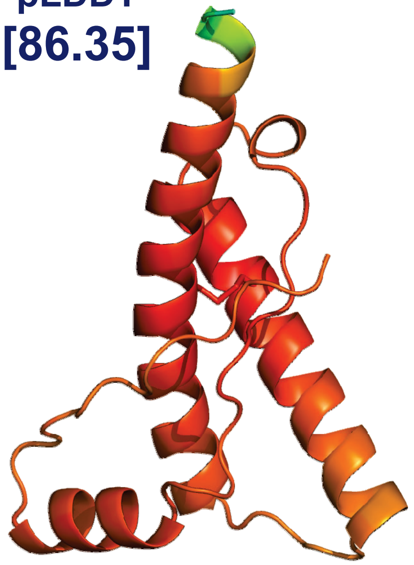
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.35]



Distinct primary sequence across species

Protein code: 3168

Distinct primary sequence across species

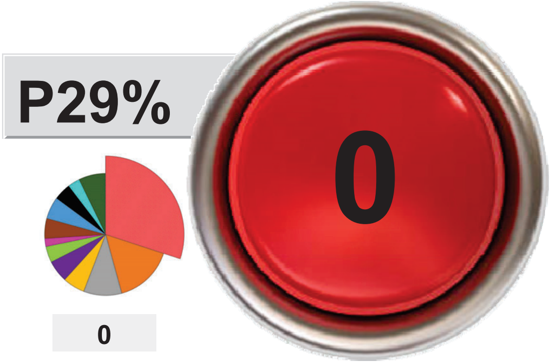
La Plata dolphin

GenBank: BK064129

Pontoporia blainvillei

Cetacea 0/14
Iniidae 0/3

P29%



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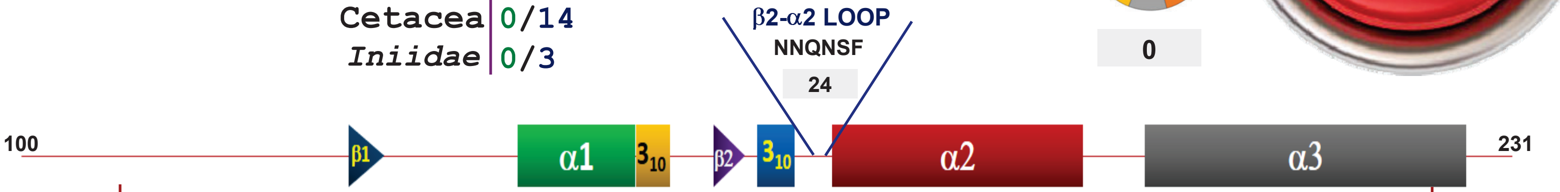


WXKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYKPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEQMCITQYQREYQAYYQRGAS-

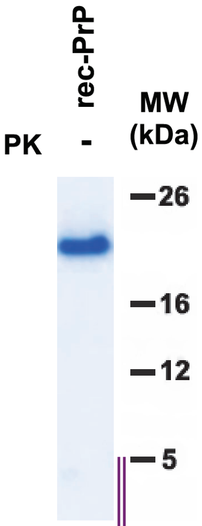
N I M N W N R N I X V V K S EGRS

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
One insertion
No polymorphic variants found

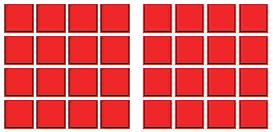
Tm^{Exp}: ND

ΔΔG: -13.69



213 AA

NO MISFOLDING



0
Conformers

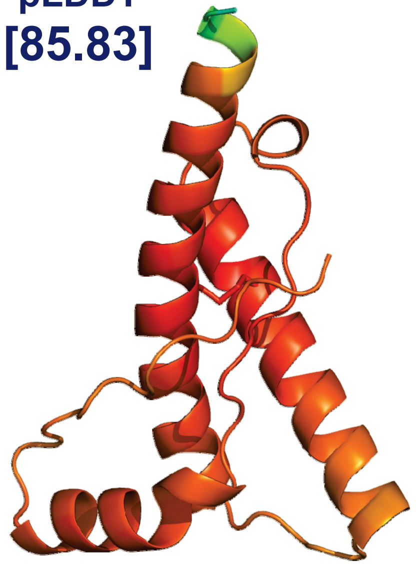
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[85.83]



Protein code: 3311

Distinct primary sequence across species

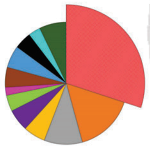
Common bottlenose dolphin

GenBank: XM_019941481

Tursiops truncatus

Cetacea	0/14
Delphinidae	0/2

P29%



0

0

WXKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEQMCITQYQREYEAYYQRGAS-

N I M N W N N I X V V K SQ EGRS

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

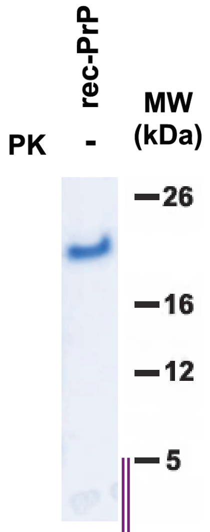
No deletions

One insertion

It shows polymorphic variants

Tm^{Exp}: 68.6 ºC

ΔΔG: -19.79



213 AA

NO MISFOLDING

0

Conformers

In vitro studies

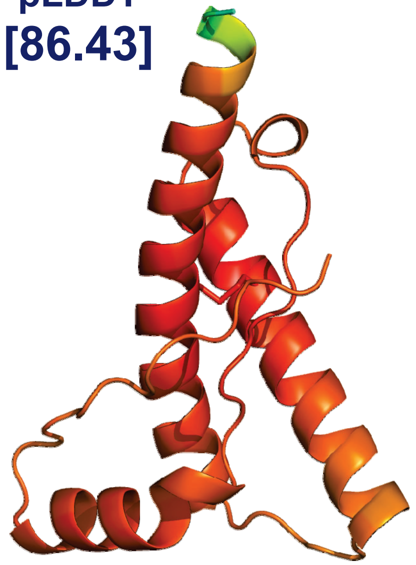
NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT

[86.43]



Protein code: 0409

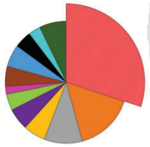
Ziphius

GenBank: DQ884467

Ziphius cavirostris

Cetacea	0/14
Ziphiidae	0/4

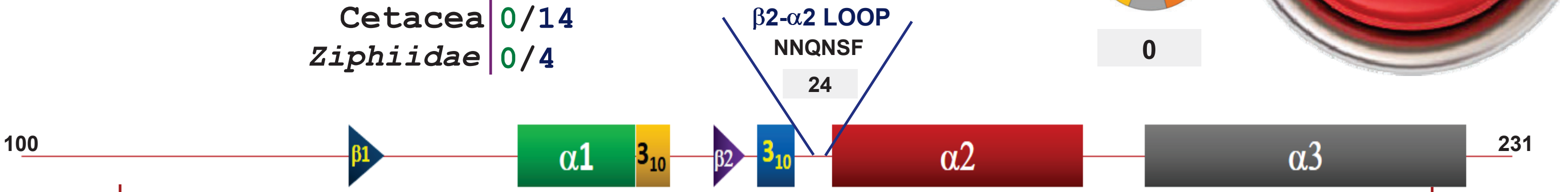
P29%



0

0

Distinct primary sequence across species



```
WXKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTTKGENFTETDIKMMERVVEEMCTTQYQREYQAYYQRGAS-
 N        I  V                             M    N W        N                  N         I         X         V        Q  V     K S    EGRS
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

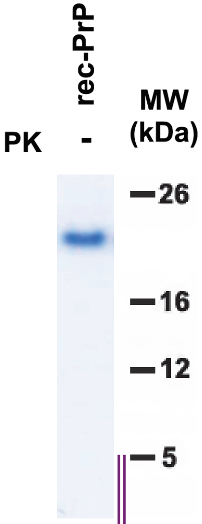
No deletions

One insertion

No polymorphic variants found

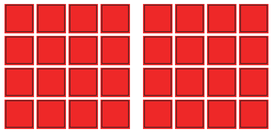
Tm^{Exp}: ND

ΔΔG: -21.45



213 AA

NO MISFOLDING



0 Conformers

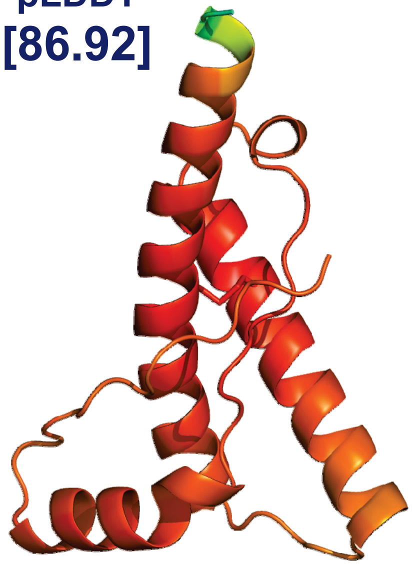
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [86.92]



Protein code: 0961

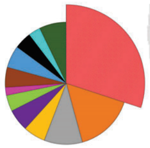
Tailed tailless bat

GenBank: **BK064067**

Anoura caudifer

Chiroptera 23/45
Phyllostomidae 2/10

P29%



0

0

β2-α2 LOOP
SNQNNF
273

GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMNRFPNQVYYRPVDQYSNQNNFVRDCVNITVKEHTVTTTTKGENFTETDVKIMERVVEEMCTIQYQREYQAYQRGAS-

WN I M N W Y N H I Q M Q VT K S YE R S

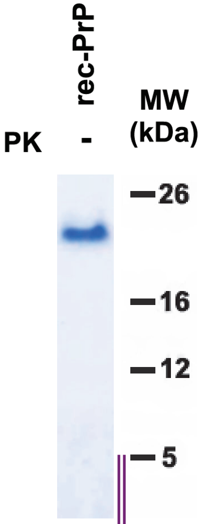
PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

ΔΔG: ND



214 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [87.61]

Protein code: 3243

Pallid bat

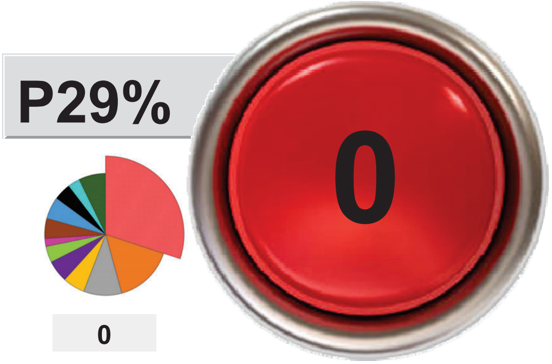
GenBank: BK064069

Antrozous pallidus

Chiroptera	23/45
Vespertilionidae	7/16

Distinct primary sequence across species

P29%



β2-α2 LOOP
SNKNNF
1

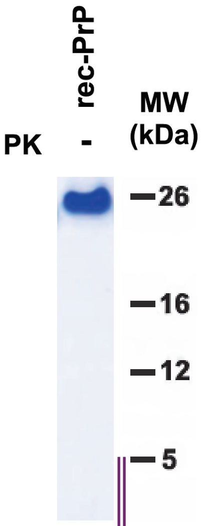
```
NKPNKPPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPAMHFGNEYEDRYYRENMNRFPEHVYYKPVDQYSNKNNFVRDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEEMCTTQYQKEYQAAYQRGAS-
WNKPSK    I                           MI    DW           Y NQ   R      N Q    H      I                     M      Q  V      S  Y EGRS
```

PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

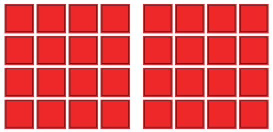
Tm^{Exp}: ND

ΔΔG: -1.85



228 AA

NO MISFOLDING



0
Conformers

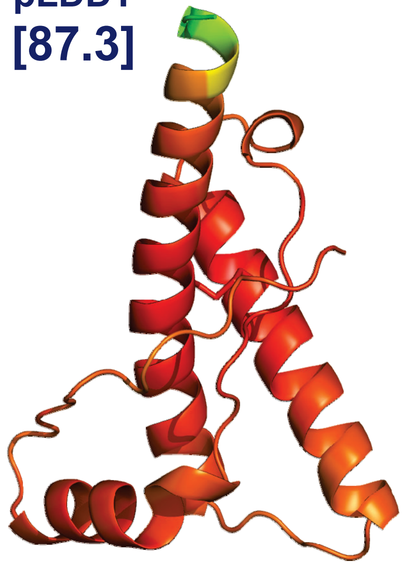
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[87.3]



Protein code: 3246

Distinct primary sequence across species

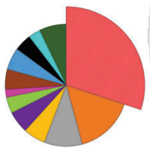
Jamaican fruit bat

GenBank: BK064072

Artibeus jamaicensis

Chiroptera	23/45
Phyllostomidae	2/10

P29%



0

0

β2-α2 LOOP
SNQNNF
273

```
GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRFPNQVYYRPVDQYSNQNNFVRDCVNITVKEHTVTTTTKGENFTSTDIKIMERVVEEMCTVQYQREYQAYQRGAS-
WN        I                            M      W           Y            N      H      I Q             E  V M      Q  VT   K S   YE R S
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

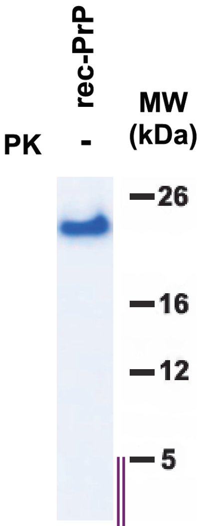
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



214 AA

NO MISFOLDING

***In vitro* studies**

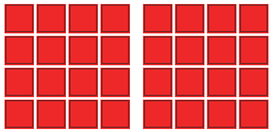
NOT APPLICABLE

***In vivo* studies**

NOT APPLICABLE

pLDDT
[86.75]

0
Conformers



Protein code: 3249

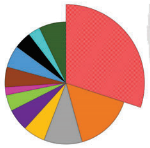
Seba's short-tailed bat

GenBank: BK063935

Carollia perspicillata

Chiroptera 23/45
Phyllostomidae 2/10

P29%



0

0

β2-α2 LOOP
SNQNNF
273

GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRFPNQVYYRPVDQYSNQNNFVRDCVNITVKEHTVTTTTKGENFTATDVKIMERVVEEMCTMQYQREYQAYQRGAS-

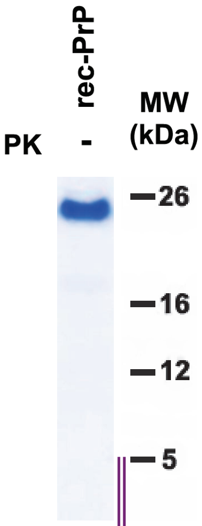
WN I M W Y N H I Q E M Q VT K S YE R S

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



226 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[87.23]

Distinct primary sequence across species

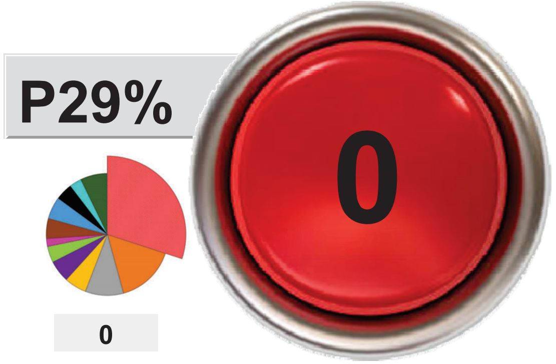
Protein code: 3058

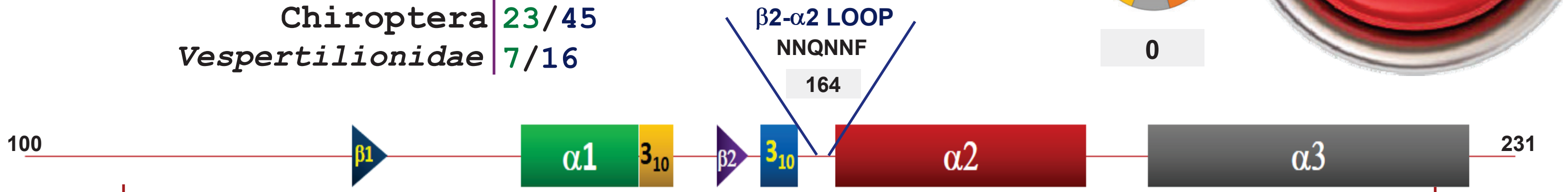
Townsend's big-eared bat

GenBank: BK064211

Corynorhinus townsendii

Chiroptera 23/45
Vespertilionidae 7/16





WSKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPAMHFGNEYEDRYYRENMNRFPEQVYYKPVDQYNNQNNFVRDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEEMCTTQYKKEYQASYQRGAS-
N S I V MI DW Y N R H I V M Q V Q S Y EGRS

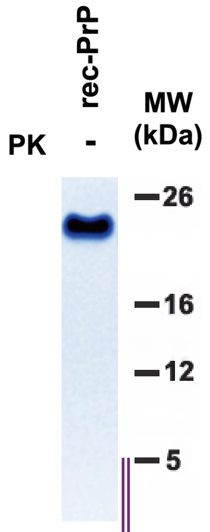
PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

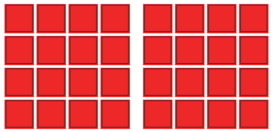
ΔΔG: -17.27



218 AA

NO MISFOLDING

0
Conformers



In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[91.52]

Protein code: 4684

Kitti's hog-nosed bat

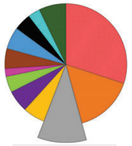
GenBank: BK063940

Craseonycteris thonglongyai

Chiroptera 23/45
Craseonycteridae 1/1

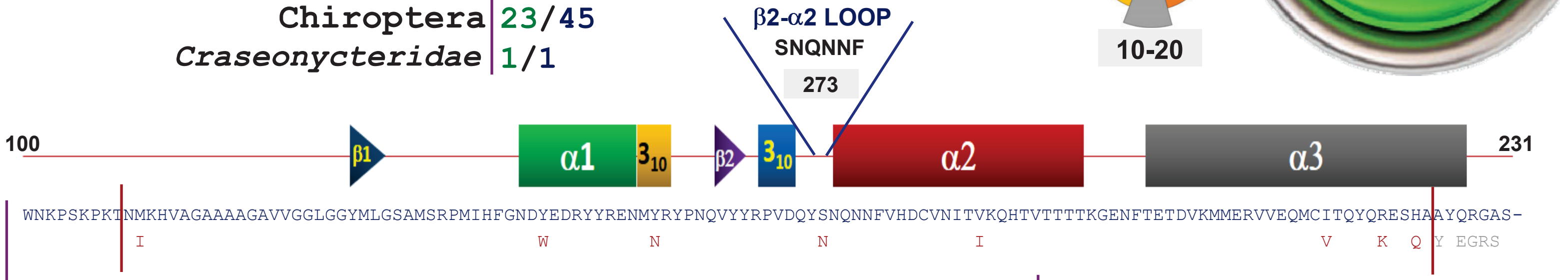
Distinct primary sequence across species

P46%



10-20

10.7

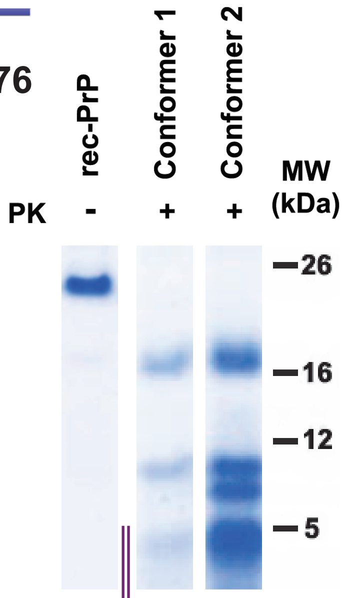


```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQRESHAAYQRGAS-
           I                                W          N               N             I                                      V     K  Q Y EGRS
```

PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

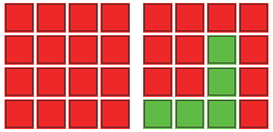
No deletions
No insertions
No polymorphic variants found

76



221 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -6.77

In vitro studies

Not tested
TgVole (1x)

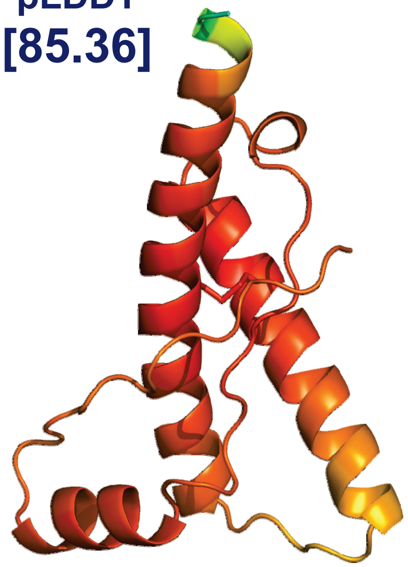
Not tested
Kitti's hog-nosed bat

In vivo studies

Not tested
TgVole (1x)

Not tested
Kitti's hog-nosed bat

pLDDT
[85.36]



Protein code: 3066

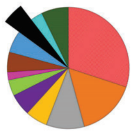
Indian short-nosed fruit bat

GenBank: AY133046

Cynopterus sphinx

Chiroptera 23/45
Pteropodidae 8/8

P89%



80-90

87.5

1 species sharing the same primary sequence

Lesser short-nosed fruit bat
Cynopterus brachyotis

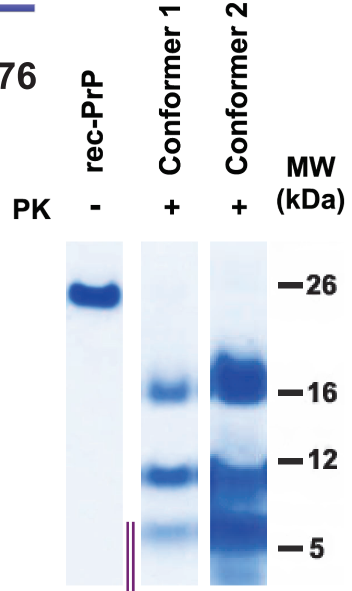
β2-α2 LOOP
SNQNSF
36

```
WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDYEDRYYRENMNRYPNQVYYYRPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQQESRAAYHRGAS-
          I                                     W                                   N   N         I                                 M         V    K  Q Y EGRS
```

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

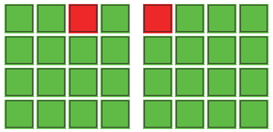
No deletions
No insertions
No polymorphic variants found

76



213 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -7.08

In vitro studies

Not tested
TgVole (1x)

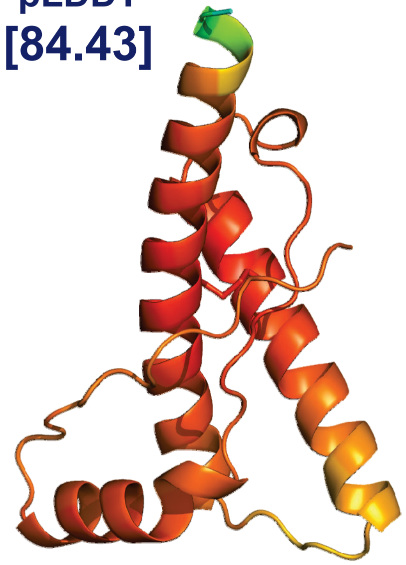
Not tested
Indian short-nosed fruit bat

In vivo studies

Not tested
TgVole (1x)

Not tested
Indian short-nosed fruit bat

pLDDT
[84.43]



Protein code: 1156

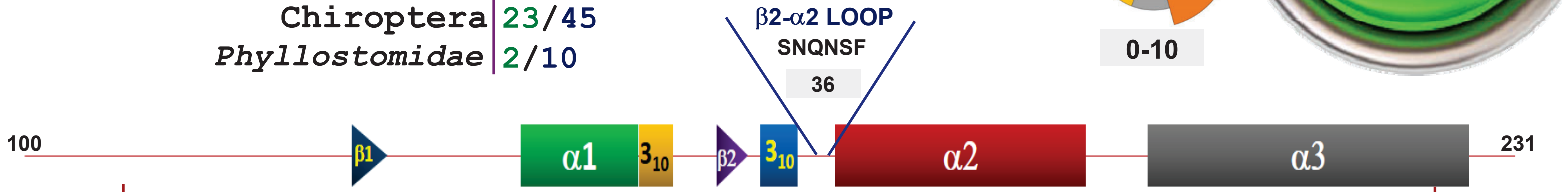
Distinct primary sequence across species

Common vampire bat

GenBank: BK064947

Desmodus rotundus

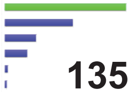
Chiroptera 23/45
Phyllostomidae 2/10

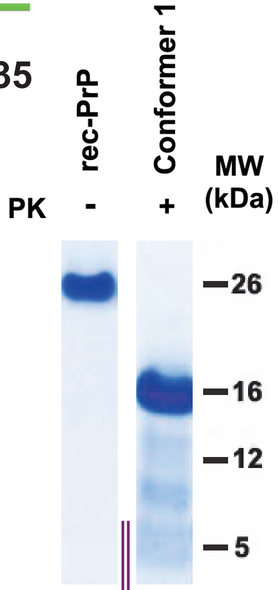


```
GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRDNMNRFPNQVYYRPVDQYSNQNSFVRDCVNITVKEHTVTTTTKGENFTETDVKIMERVVEEMCTIQYQKEYQAYQRGAS-
WN        I                            M      W      E    Y            N   N  H      I Q                  M      Q  VT     S   YE R S
```

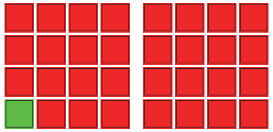
PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



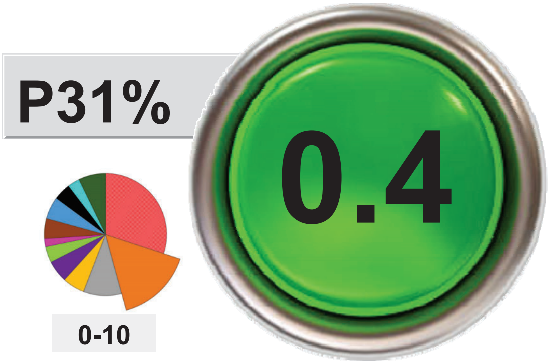


216 AA



1
Conformers

P31%



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

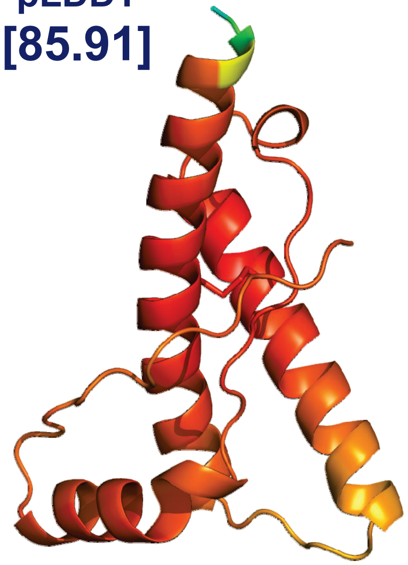
Common vampire bat Not tested

In vivo studies

TgVole (1x) Not tested

Common vampire bat Not tested

pLDDT
[85.91]



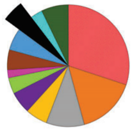
Protein code: 1472

Straw-coloured fruit bat

GenBank: BK064039

1 species sharing the same primary sequence

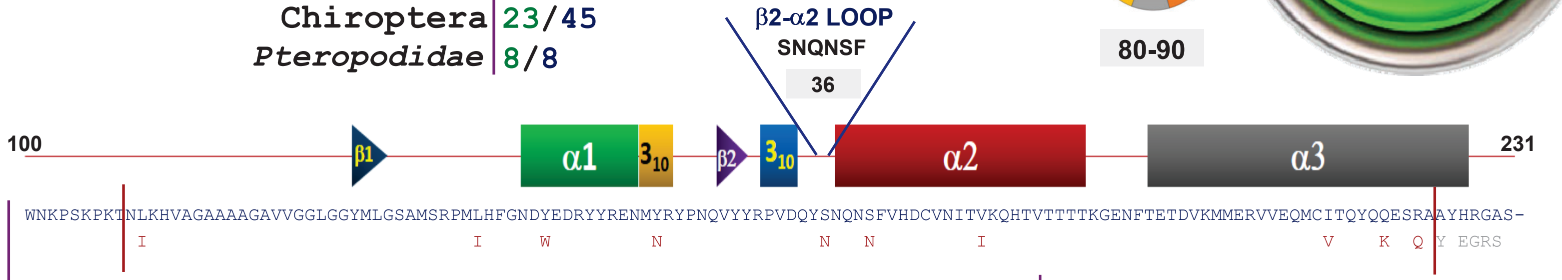
P86%



Eidolon helvum

Chiroptera 23/45
Pteropodidae 8/8

Madagascan fruit bat
Eidolon dupreanum

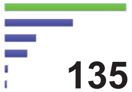


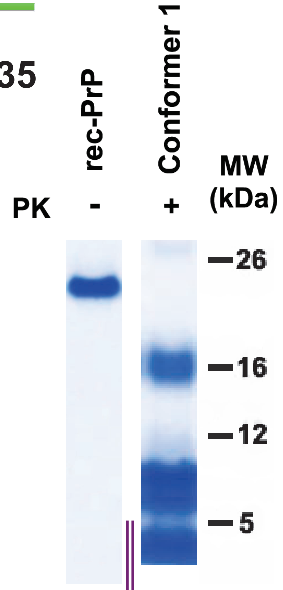
WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQQESRAAYHRGAS-

I I W N N N I V K Q Y EGRS

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

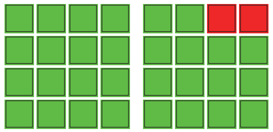
No deletions
No insertions
No polymorphic variants found





220 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -16.93

***In vitro* studies**

Not tested
TgVole (1x)

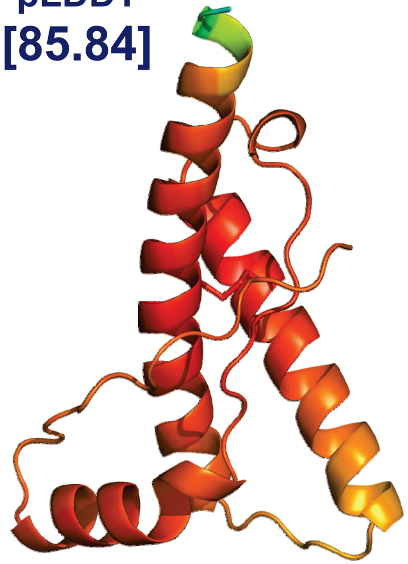
Not tested
Straw-coloured fruit bat

***In vivo* studies**

Not tested
TgVole (1x)

Not tested
Straw-coloured fruit bat

pLDDT
[85.84]



Protein code: 3205

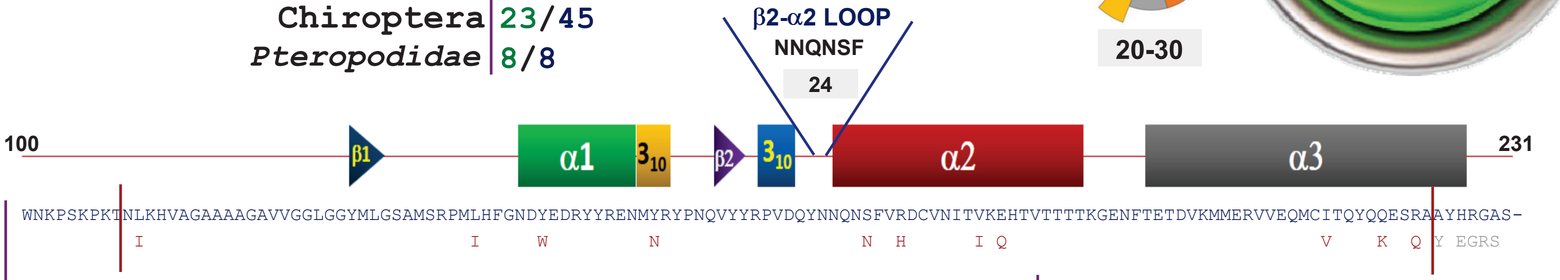
Cave nectar bat

GenBank: BK064041

Eonycteris spelaea

Chiroptera 23/45
Pteropodidae 8/8

Distinct primary sequence across species

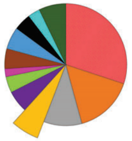


```
WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDYEDRYYRENMYRYPNQVYYYRPVDQYNNQNSFVRDCVNITVKEHTVTTTTKGENFTETDVKMMERVVEQMCITQYQQESRAAYHRGAS-
          I                            I     W         N                  N  H      I Q                           V    K  Q Y EGRS
```

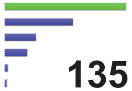
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

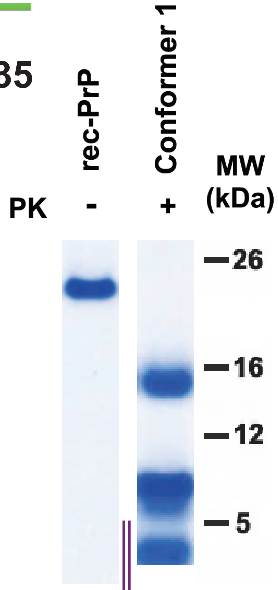
No deletions
No insertions
No polymorphic variants found

P56%

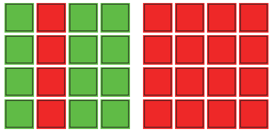


21.4





219 AA



Tm^{Exp}: ND

ΔΔG: -13.08

***In vitro* studies**

TgVole (1x) Not tested

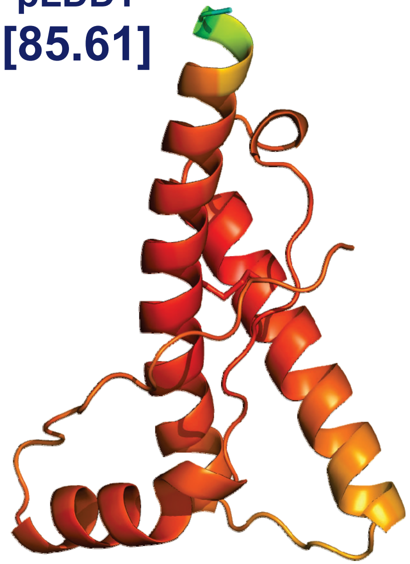
Cave nectar bat Not tested

***In vivo* studies**

TgVole (1x) Not tested

Cave nectar bat Not tested

pLDDT
[85.61]



Protein code: 3207

Big brown bat

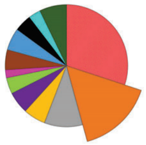
GenBank: BK064945

Eptesicus fuscus

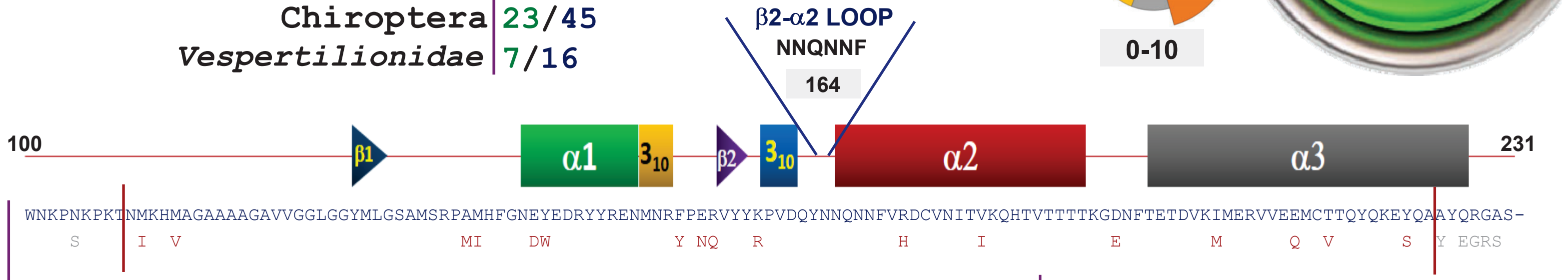
Chiroptera 23/45
Vespertilionidae 7/16

P31%

0.4



0-10

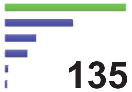


```
WNKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPAMHFGNEYEDRYYRENMNRFPERVYYKPVDQYNNQNNFVRDCVNITVKQHTVTTTTKGDNFTETDVKIMERVVEEMCTTQYQKEYQAAYQRGAS-
    S     I  V                         MI    DW            Y NQ   R           H      I           E        M      Q  V      S  Y EGRS
```

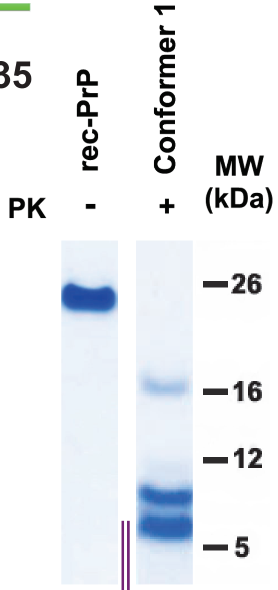
PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species



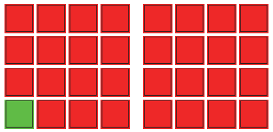
135



217 AA

1

Conformers



Tm^{Exp}: ND

ΔΔG: -0.01

In vitro studies

TgVole (1x) Not tested

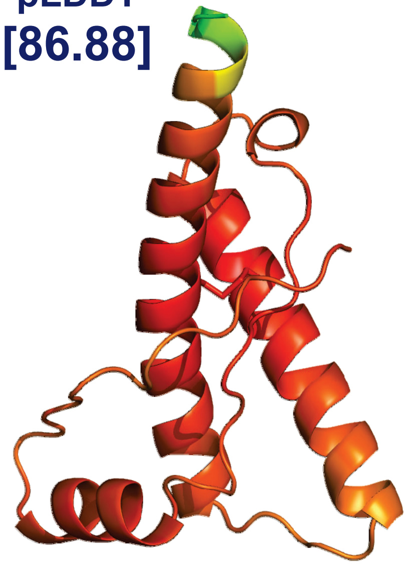
Big brown bat Not tested

In vivo studies

TgVole (1x) Not tested

Big brown bat Not tested

pLDDT
[86.88]



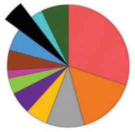
Great roundleaf bat

GenBank: XM_019644637

Hipposideros armiger

Chiroptera 23/45
Hipposideridae 2/2

P86%

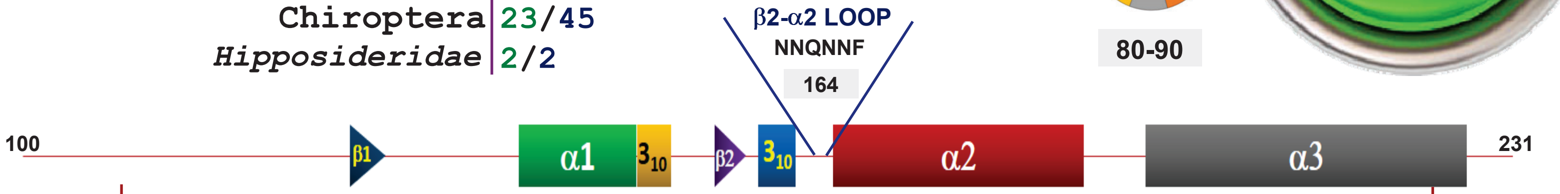


80-90

82.1

1 species sharing the same primary sequence

Pendlebury's roundleaf bat
Hipposideros turpis pendleburyi

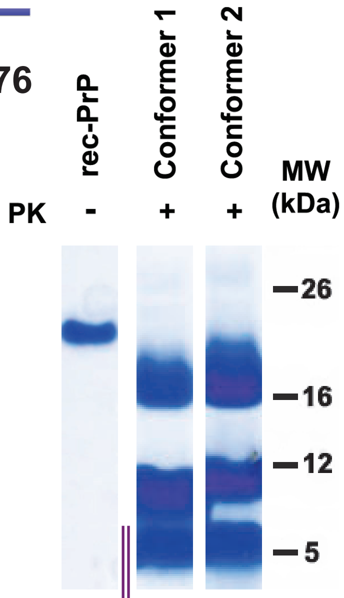


```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQKESHAAYQRDAS-
          I                               MI    W         N                                                                      V       Q Y EGRS
```

PrP sequence differs by 7 amino acids from the bank vole PrP (see in red)

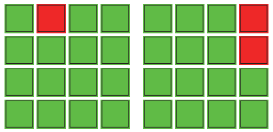
No deletions
No insertions
No polymorphic variants found

76



203 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -2.36

In vitro studies

TgVole (1x) — Not tested

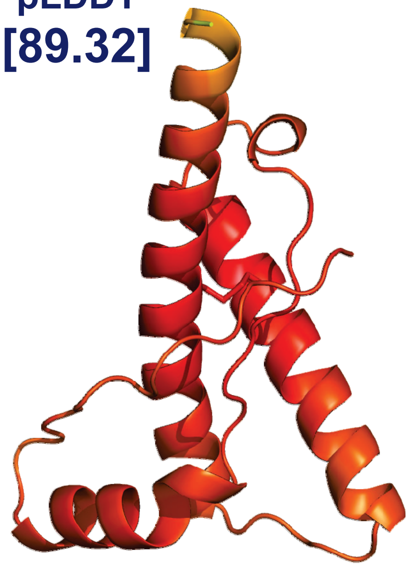
Great roundleaf bat — Not tested

In vivo studies

TgVole (1x) — Not tested

Great roundleaf bat — Not tested

pLDDT
[89.32]



Protein code: 1109

Cantor's roundleaf bat

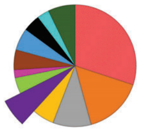
GenBank: BK064054

Distinct primary sequence across species

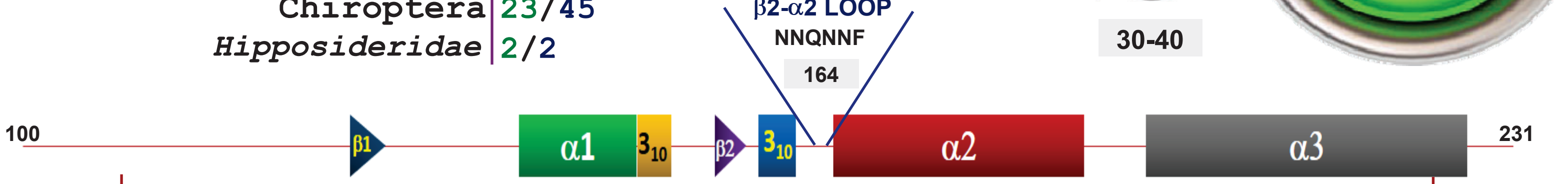
Hipposideros galeritus

Chiroptera	23/45
Hipposideridae	2/2

P65%



30-40



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQKEYQAAYQGSAS-

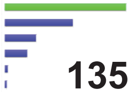
I M W N V S Y E RS

PrP sequence differs by 6 amino acids from the bank vole PrP (see in red)

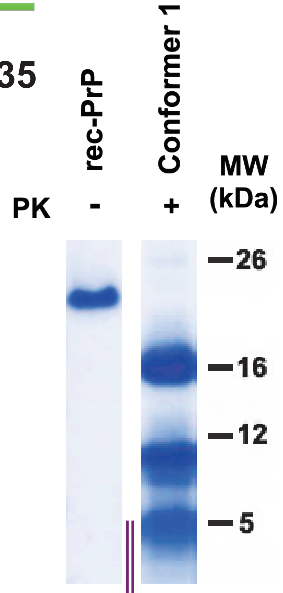
No deletions

No insertions

No polymorphic variants found



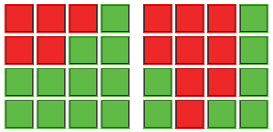
135



211 AA

1

Conformers



Tm^{Exp}: ND

ΔΔG: -8.51

In vitro studies

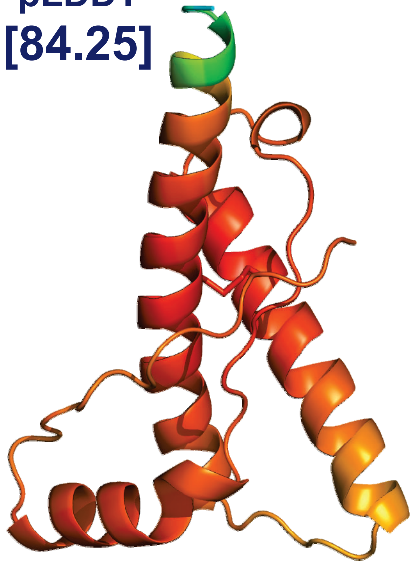
TgVole (1x)	Not tested
Cantor's roundleaf bat	Not tested

In vivo studies

TgVole (1x)	Not tested
Cantor's roundleaf bat	Not tested

pLDDT

[84.25]



Protein code: 3223

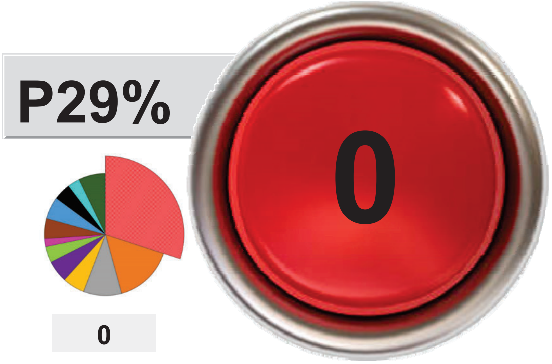
Great evening bat

GenBank: BK064208

Ia io

Chiroptera	23/45
Vespertilionidae	7/16

P29%



0

β2-α2 LOOP
SNQNNF
273

```
WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPAMHFGNEYEDRYYRENMNRFPEHVYYKPVDQYSNQNNFVRDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCTTQYQKEYQAAYQRGAS-
    S     I                            MI    DW           Y NQ   R     N      H      I                    M         V      S  Y EGRS
```

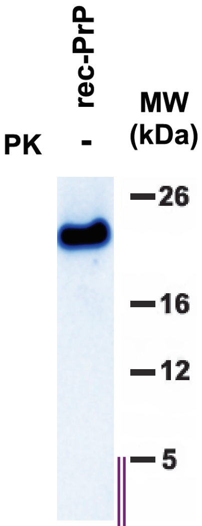
PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

ΔΔG: -13.71



NO MISFOLDING

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[92.15]

218 AA

0
Conformers

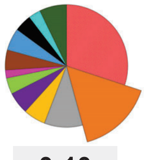
Protein code: 4617

Hoary bat

GenBank: BK063928

P39%

3.6



0-10

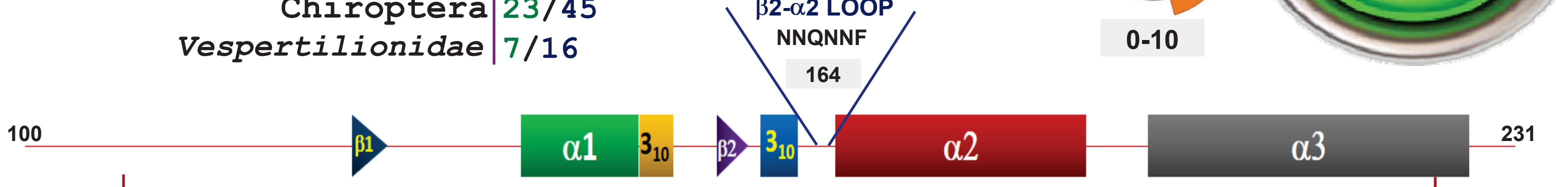
Lasiurus cinereus

Chiroptera	23/45
Vespertilionidae	7/16

2 species sharing the same primary sequence

Rafinesque's big-eared bat
Corynorhinus rafinesquii

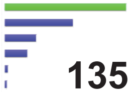
Eastern red bat
Lasiurus borealis



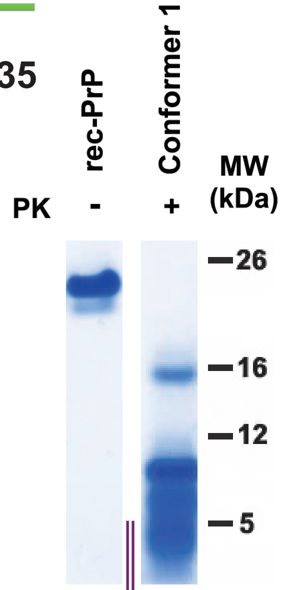
```
WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPAMHFGNEYEDRYYRENMNRFPEQVYYKPVDQYNNQNNFVRDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEEMCTTQYKKEYQASYQRGAS-
    S    I                              MI    DW             Y N    R         H      I                             V M       Q  V    Q   S  Y EGRS
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

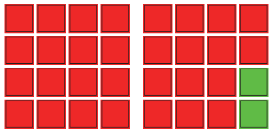


135



224 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -4.45

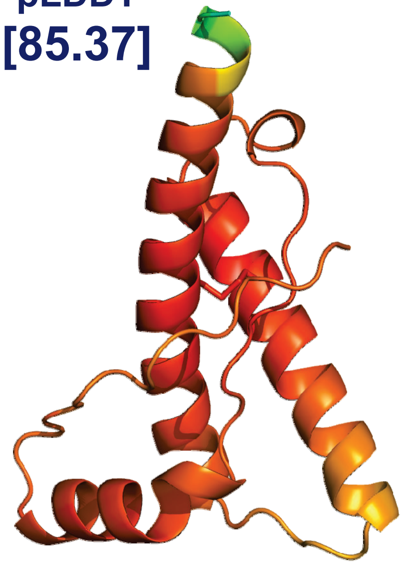
In vitro studies

TgVole (1x)	Not tested
Hoary bat	Not tested

In vivo studies

TgVole (1x)	Not tested
Hoary bat	Not tested

pLDDT
[85.37]

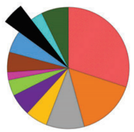


Protein code: 3046

Long-tongued fruit bat

GenBank: BK063991

P86%

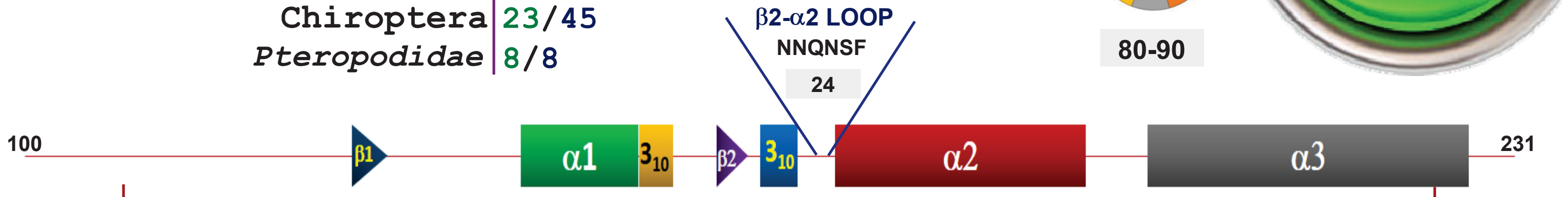


82.1

Macroglossus sobrinus

Distinct primary sequence across species

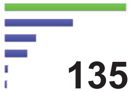
Chiroptera 23/45
Pteropodidae 8/8



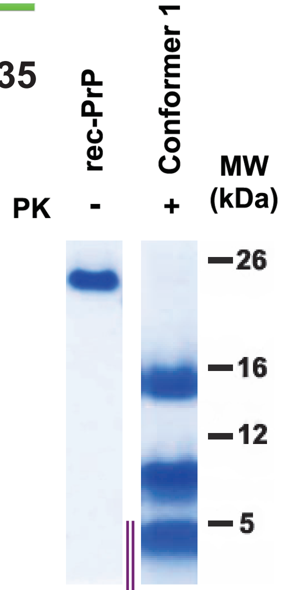
```
WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQQESRAAYHRGAS-
           I                              I     W          N                 N         I                                V    K  Q Y EGRS
```

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

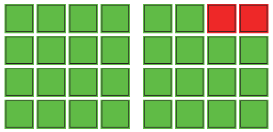


135



220 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -14.88

In vitro studies

TgVole (1x) — Not tested

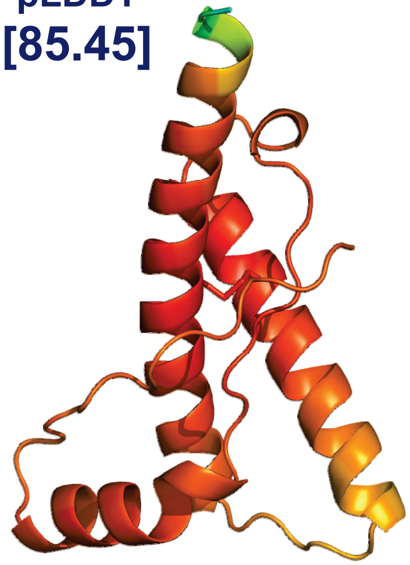
Long-tongued fruit bat — Not tested

In vivo studies

TgVole (1x) — Not tested

Long-tongued fruit bat — Not tested

pLDDT
[85.45]



Protein code: 3149

Distinct primary sequence across species

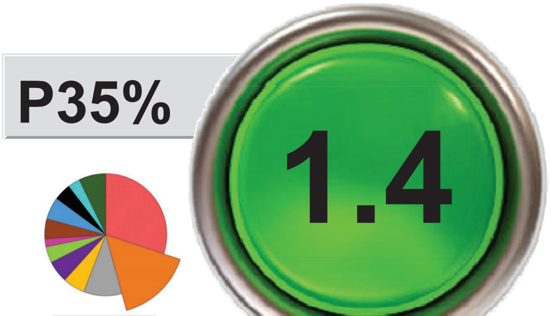
California leaf-nosed bat

GenBank: AY133049

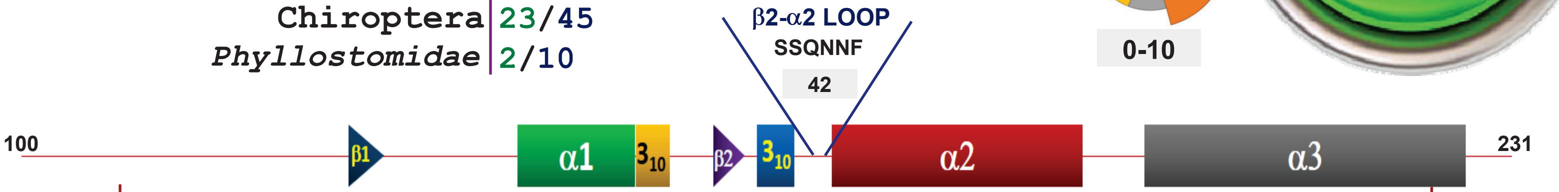
Macrotus californicus

Chiroptera	23/45
Phyllostomidae	2/10

P35%



0-10



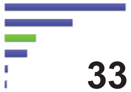
```
GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRFPNQVYYKPVDQYSSQNNFVRDCVNITVKEHTVTTTTKGENFTETDVKIMQRVVEEMCTIQYQQEFQAYQRGAS-
WN        I                            M      W           Y      R      NN    H      I Q                  M E    Q  VT   K S   YE R S
```

PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

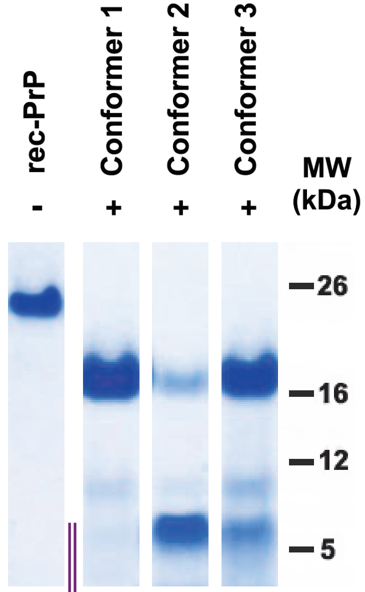
No deletions

No insertions

No polymorphic variants found



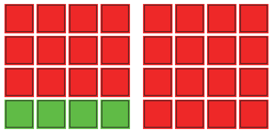
33



215 AA

3

Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x)	Not tested
California leaf-nosed bat	Not tested

In vivo studies

TgVole (1x)	Not tested
California leaf-nosed bat	Not tested

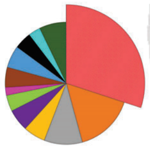
pLDDT [87.91]

Protein code: 1151

Greater false vampire bat

GenBank: BK064080

P29%



0

0

Megaderma lyra

Chiroptera 23/45
Megadermatidae 0/1

β2-α2 LOOP
SNQNNF
273

WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQRESQAAAYHRGAS-
N I W N R N I V K YYEG SS

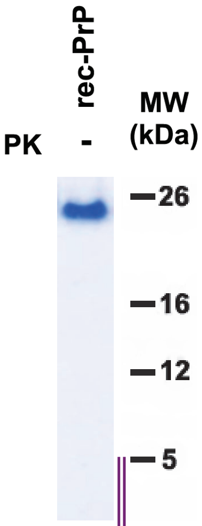
PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

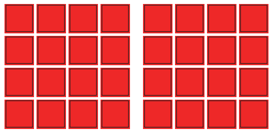
ΔΔG: ND



222 AA

NO MISFOLDING

0
Conformers



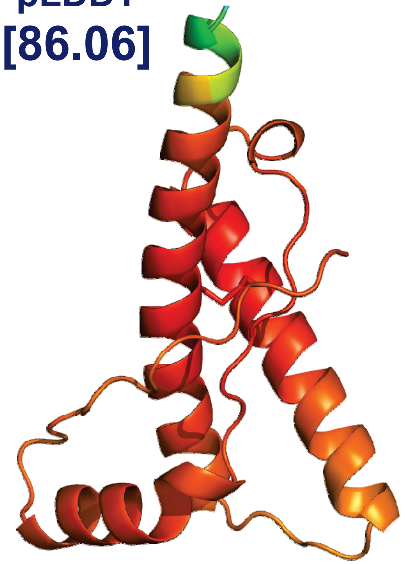
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.06]

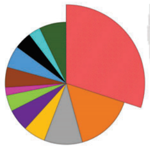


Protein code: 3258

Hairy big-eared bat

GenBank: BK064088

P29%



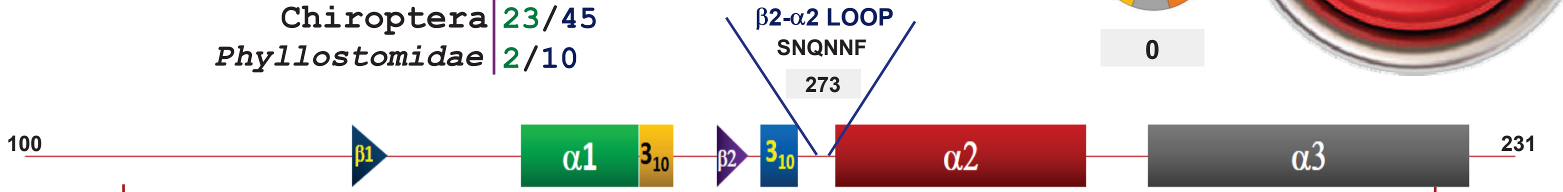
0

0

Micronycteris hirsuta

Chiroptera	23/45
Phyllostomidae	2/10

Distinct primary sequence across species



```
GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRDNMNRFPNQVYYRPVDQYSNQNNFVRDCVNITVKEHTVTTTTKGENFTETDVKIMQRVVEEMCTIQYQKEYQAYQSGAYYQRGA
WN        I                                  M       W       E    Y            N       H      I Q                       M E     Q  VT      S   YE RSS
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

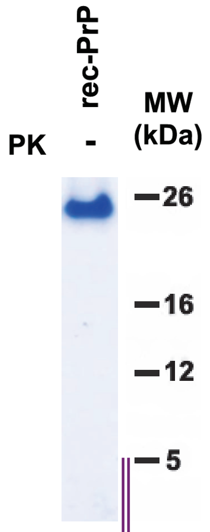
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND

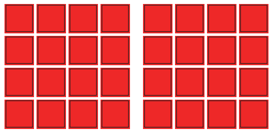


229 AA

NO MISFOLDING

0

Conformers



In vitro studies

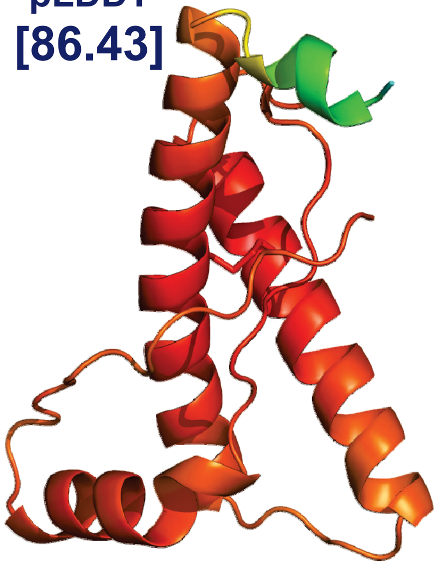
NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT

[86.43]



Protein code: 3267

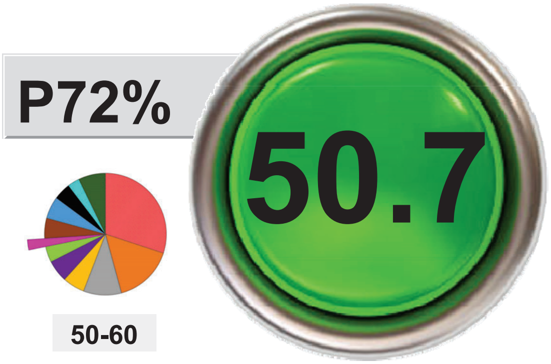
Natal long-fingered bat

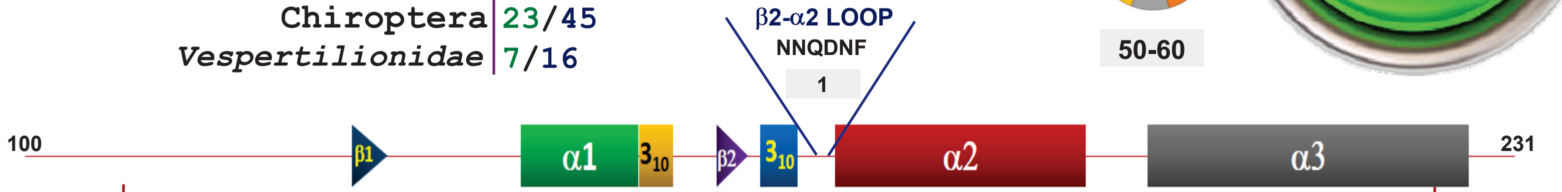
GenBank: XM_016212061

Miniopterus natalensis

Chiroptera 23/45
Vespertilionidae 7/16

Distinct primary sequence across species

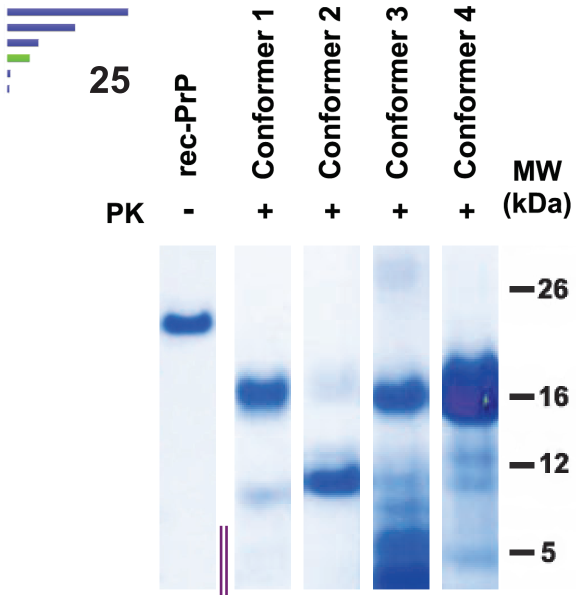




```
WNKPSKPKTNLKHMAGAAAAGAVVGGLGGYMVGSAMSRPLMHFGNDYEDRYYRENMNRFPNQVYYKPVNQYNNQDNFVRDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEEMCTTQYQKEYQAYQSYNGMS-
           I  V          L      MI    W         Y    R  D    N   H     I                    M     Q  V      S    YEGRSS
```

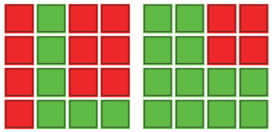
PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



207 AA

4
Conformers



Tm^{Exp}: ND

ΔΔG: ND

***In vitro* studies**

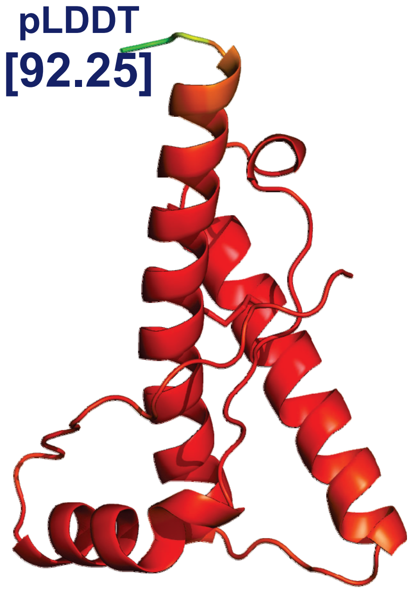
TgVole (1x) Not tested

Natal long-fingered bat Not tested

***In vivo* studies**

TgVole (1x) Not tested

Natal long-fingered bat Not tested



Protein code: 1125

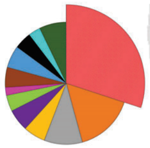
Common bent-wing bat

GenBank: BK064092

Miniopterus schreibersii

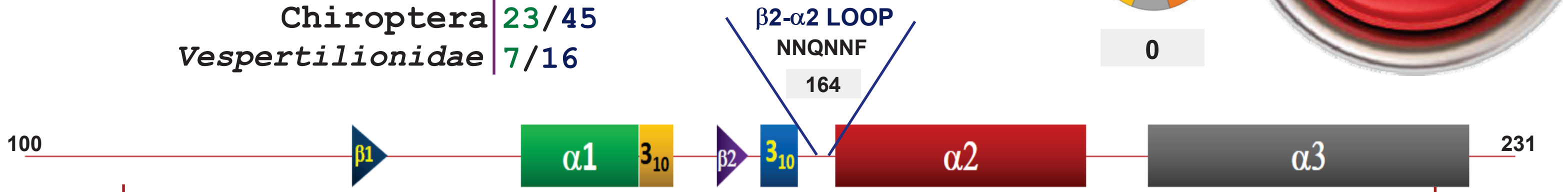
Chiroptera 23/45
Vespertilionidae 7/16

P29%



0

0



WNKPSKPKTNLKHMAGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNDYEDRYYRENMNRFPNQVYYKPVDQYNNQNNFVRDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEEMCTTQYQKEYQAYRSYNGMS-

I V MI W Y R H I M Q V S YEGRSS

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions

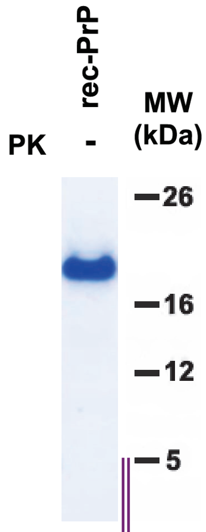
No insertions

No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

ΔΔG: ND

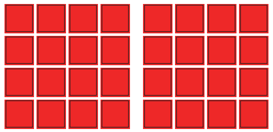


207 AA

NO MISFOLDING

0

Conformers



***In vitro* studies**

NOT APPLICABLE

***In vivo* studies**

NOT APPLICABLE

pLDDT
[92.8]

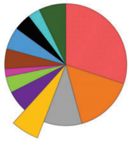
Protein code: 3271

Velvety free-tailed bat

GenBank: KAF6472180

P55%

21.1



20-30

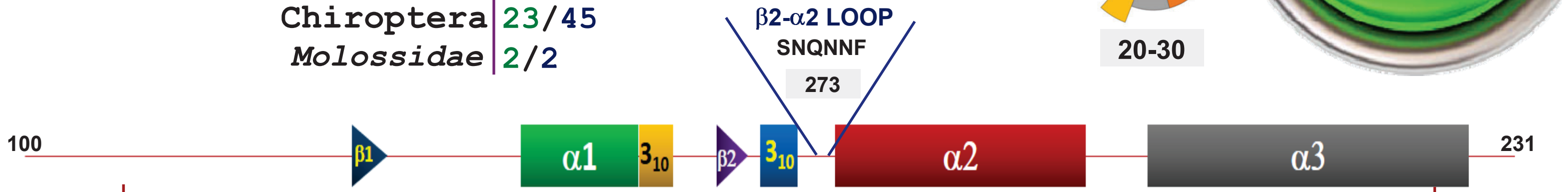
Molossus molossus

Chiroptera 23/45
Molossidae 2/2

2 species sharing the same primary sequence

Alvarez's mastiff bat
Molossus alvarezi

Northern black mastiff bat
Molossus rufus

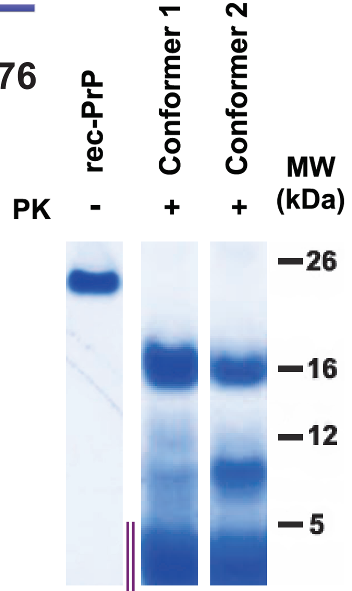


WGKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMNRFPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGDNFTETDIKIMERVVEEMCTTQYQKEYQAYYQRGAS-
N S I M N W Y R N I E V M Q V S EGRS

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

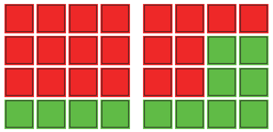
76



225 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: -7.17

In vitro studies

TgVole (1x) Not tested

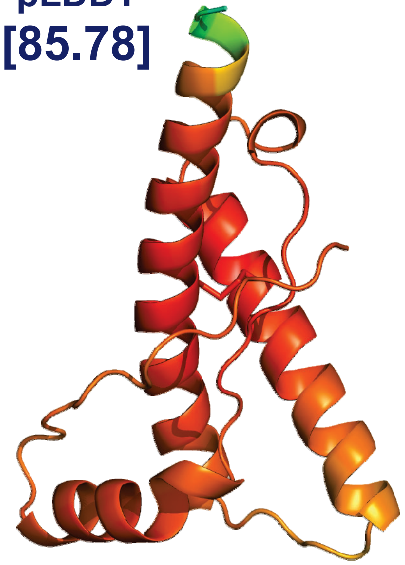
Velvety free-tailed bat Not tested

In vivo studies

TgVole (1x) Not tested

Velvety free-tailed bat Not tested

pLDDT
[85.78]

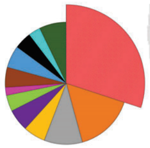


Protein code: 2386

Antillean ghost-faced bat

GenBank: BK063931

P29%



0

0

Mormoops blainvillei

Chiroptera 23/45
Mormoopidae 0/2

Distinct primary sequence across species

β2-α2 LOOP
SNQNNF
273

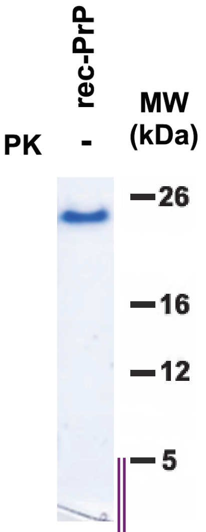
```
GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRFPNQVYYKPVDQYSNQNNFVRDCVNITVKEHTVTTTTKGENFTETDVKIMERVVEEMCTIQYQKEYQTYYQRGAS-
WN        I                            M      W           Y      R     N      H      I Q                  M      Q  VT     S A  EGRS
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

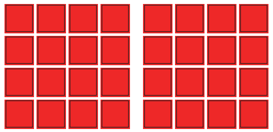
ΔΔG: -14.83



227 AA

NO MISFOLDING

0
Conformers



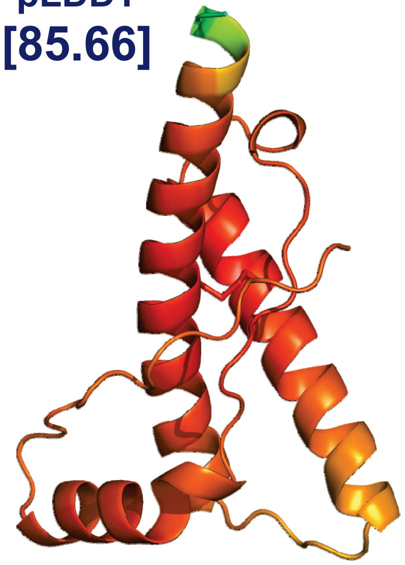
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[85.66]



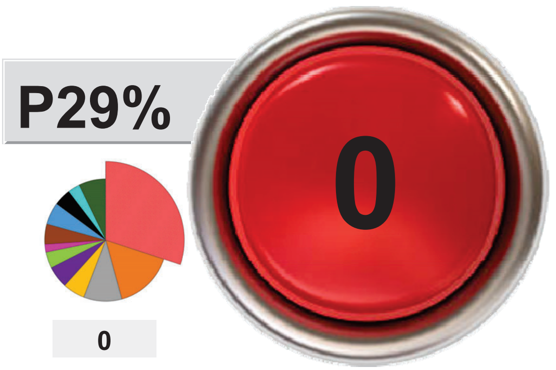
Protein code: 3049

Little tube-nosed bat

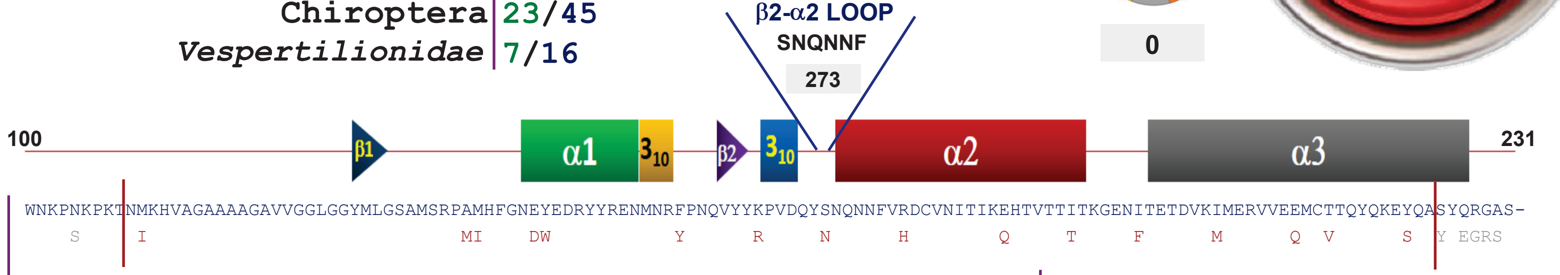
GenBank: **BK064100**

Murina aurata feae

P29%



Chiroptera 23/45
Vespertilionidae 7/16



```
WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPAMHFGNEYEDRYYRENMNRFPNQVYYKPVDQYSNQNNFVRDCVNITIKEHTVTTITKGENITETDVKIMERVVEEMCTTQYQKEYQASYQRGAS-
     S     I                             MI     DW            Y      R      N       H           Q      T      F       M      Q  V        S  Y EGRS
```

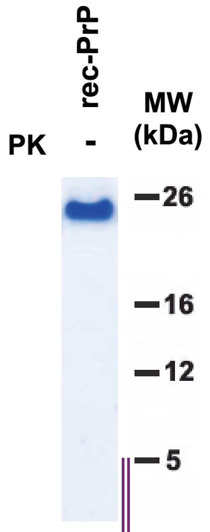
PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

ΔΔG: -7.85



224 AA

NO MISFOLDING

0 Conformers

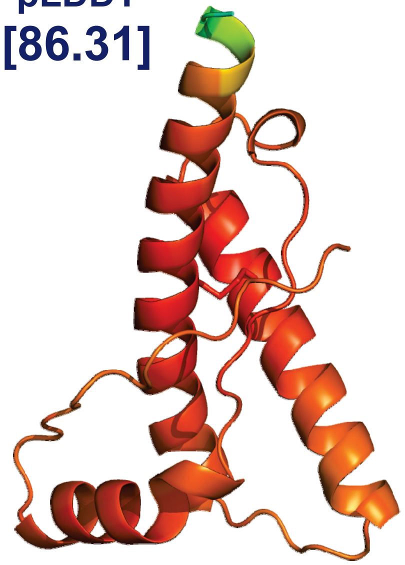
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [86.31]



Protein code: 3279

Brandt's bat

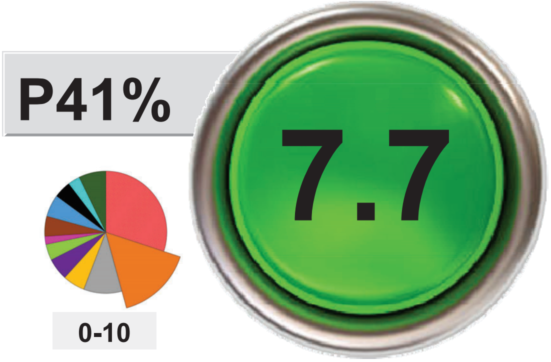
GenBank: XM_005874678

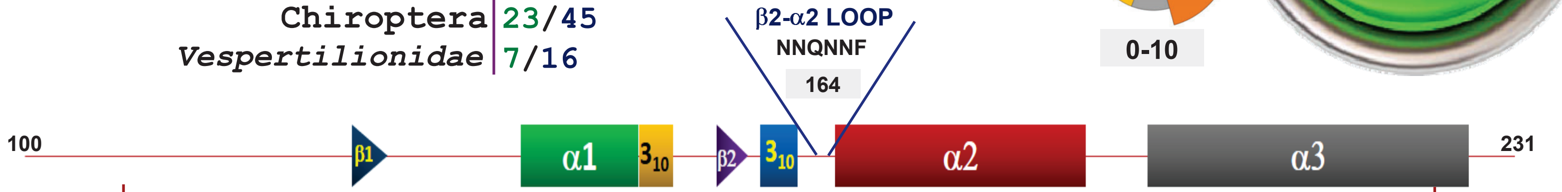
Myotis brandtii

Chiroptera 23/45
Vespertilionidae 7/16

1 species sharing the same primary sequence

Little brown bat
Myotis lucifugus





```
WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPPMHFGNEYEDRYYRENMNRFPDQVYYKPVDQYNNQNNFVRDCVNITVKQHTVTTITKGENITETDVKIMERVVEEMCTTQYQKEYQASYQRGAS-
      S    I                              MI    DW              Y N    R               H     I      T     F     M     Q  V      S  Y EGRS
```

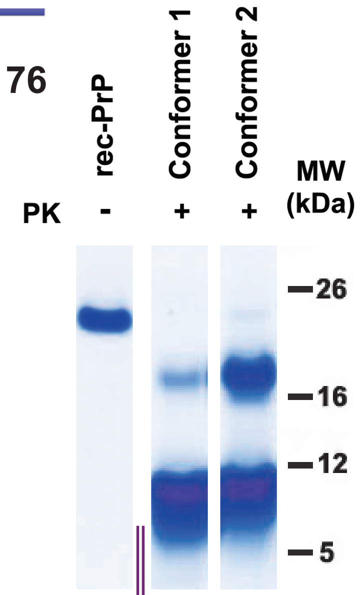
PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

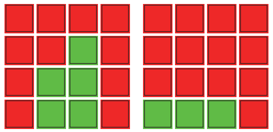
76



207 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: -12.24

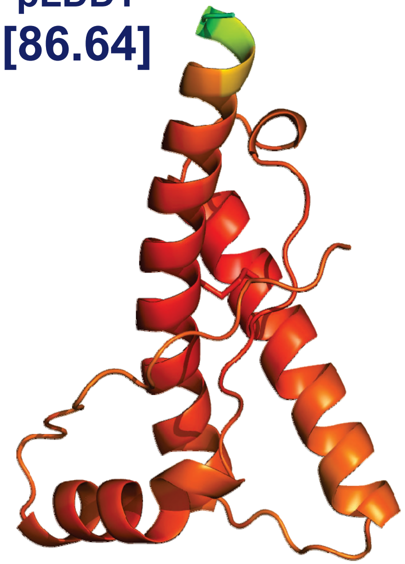
In vitro studies

TgVole (1x)	Not tested
Brandt's bat	Not tested

In vivo studies

TgVole (1x)	Not tested
Brandt's bat	Not tested

pLDDT [86.64]



Protein code: 1102

David's myotis

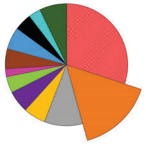
GenBank: XM_006758058

Myotis davidii

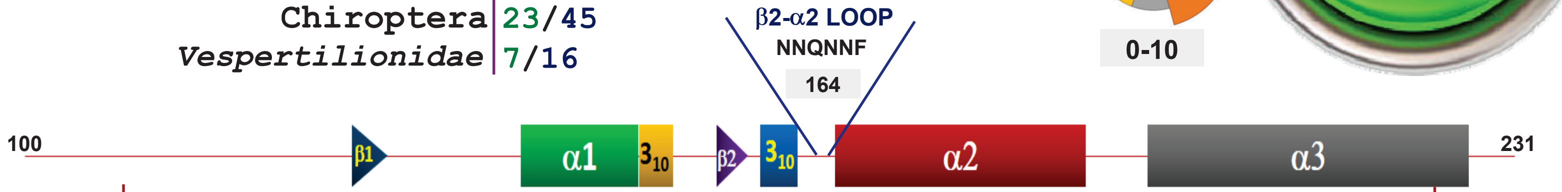
Chiroptera 23/45
Vespertilionidae 7/16

P41%

7.1



0-10



WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPPIHFGNEYEDRYYRENMNRFPNQVYYKPVDQYNNQNNFVRDCVNITVKQHTVTTITKGENITETDVKIMERVVEEMCTTQYQKEYQASYQRGAS-

S I M DW Y R H I T F M Q V S Y EGRS

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

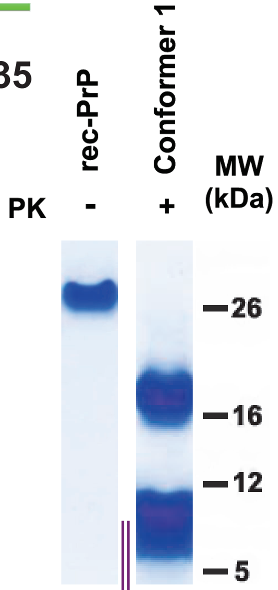
No deletions
No insertions
No polymorphic variants found

2 species sharing the same primary sequence

Daubenton's bat
Myotis daubentonii

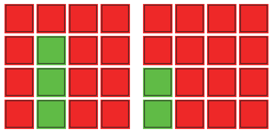
Greater mouse-eared bat
Myotis myotis

135



215 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -13.43

In vitro studies

TgVole (1x) Not tested

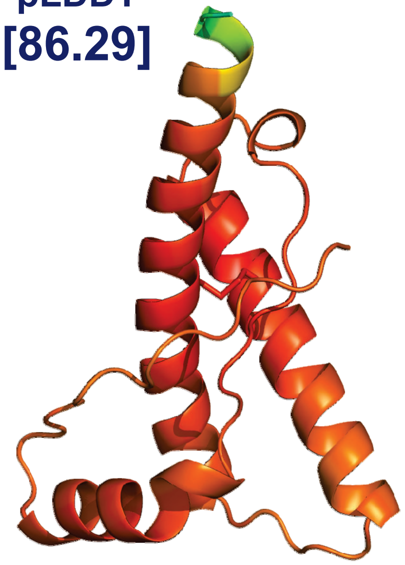
David's myotis Not tested

In vivo studies

TgVole (1x) Not tested

David's myotis Not tested

pLDDT
[86.29]



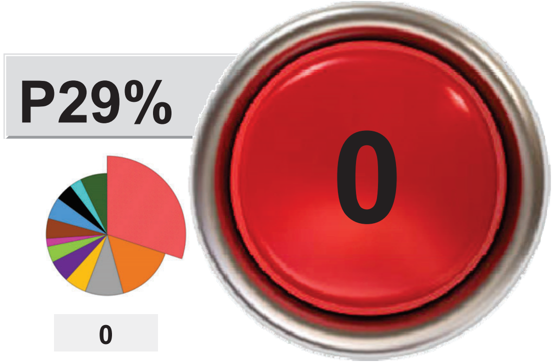
Protein code: 1132

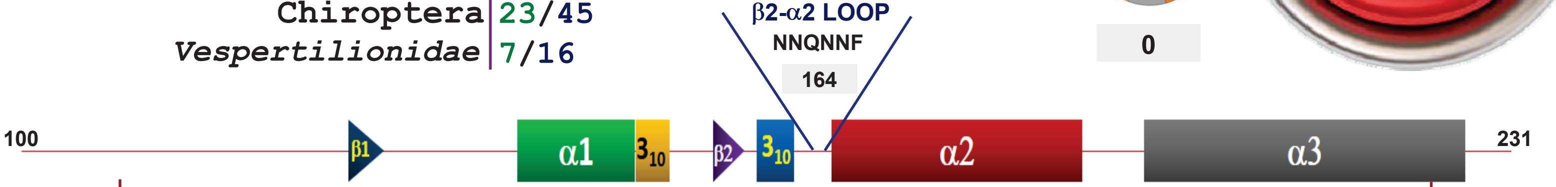
Rickett's big-footed bat

GenBank: BK064146

Myotis ricketti

Chiroptera	23/45
Vespertilionidae	7/16





```
WNKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPPIHFGNEYEDRYYRENMNRFPNQVYYKPVDQYNNQNNFVRDCVNITVKQHTVTTITKGENITETDVKIMERVVEEMCTTQYQKEYQASYQRGAS-
    S     I  V                         M     DW           Y      R            H      I       T     F      M      Q  V      S  Y EGRS
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

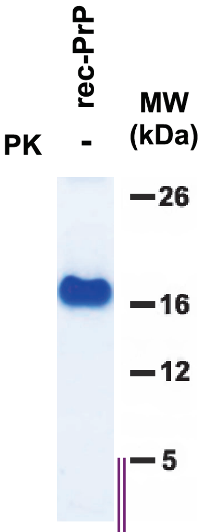
No deletions

No insertions

No polymorphic variants found

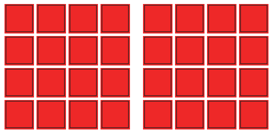
Tm^{Exp}: ND

ΔΔG: -12.32



188 AA

NO MISFOLDING



0

Conformers

In vitro studies

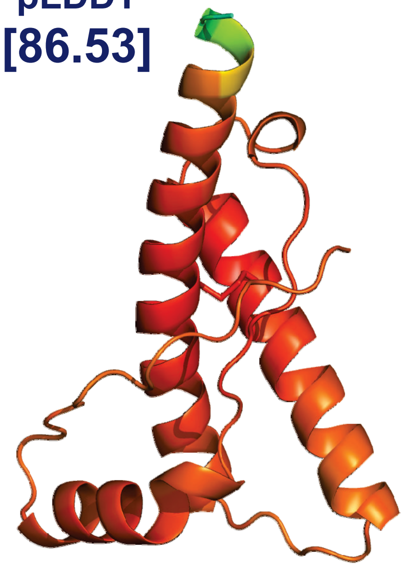
NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT

[86.53]



Distinct primary sequence across species

Protein code: 3338

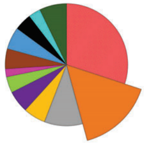
Northern long-eared bat

GenBank: BK064803

Myotis septentrionalis

Chiroptera 23/45
Vespertilionidae 7/16

P45%



0-10

8.9

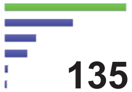
β2-α2 LOOP
NNQNNF
164

WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPPMHFGNEYEDRYYRENMNRFPNQVYYKPVDQYNNQNNFVRDCVNITVKQHTVTTITKGENITETDVKIMERVVEEMCTTQYQKEYQASYQRGAS-
S I MI DW Y R H I T F M Q V S Y EGRS

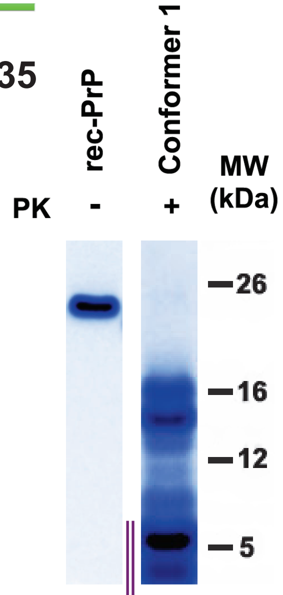
PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

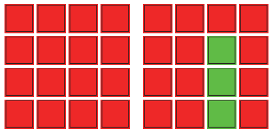


135



216 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -10.06

In vitro studies

Not tested
TgVole (1x)

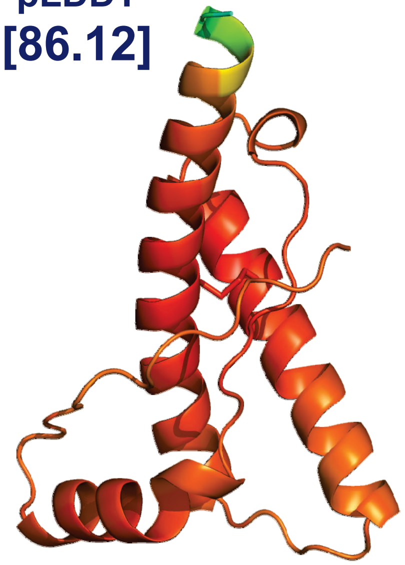
Not tested
Northern long-eared bat

In vivo studies

Not tested
TgVole (1x)

Not tested
Northern long-eared bat

pLDDT
[86.12]



Protein code: 3970

Yuma myotis

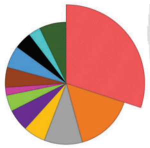
GenBank: BK064222

Myotis yumanensis

Chiroptera 23/45
Vespertilionidae 7/16

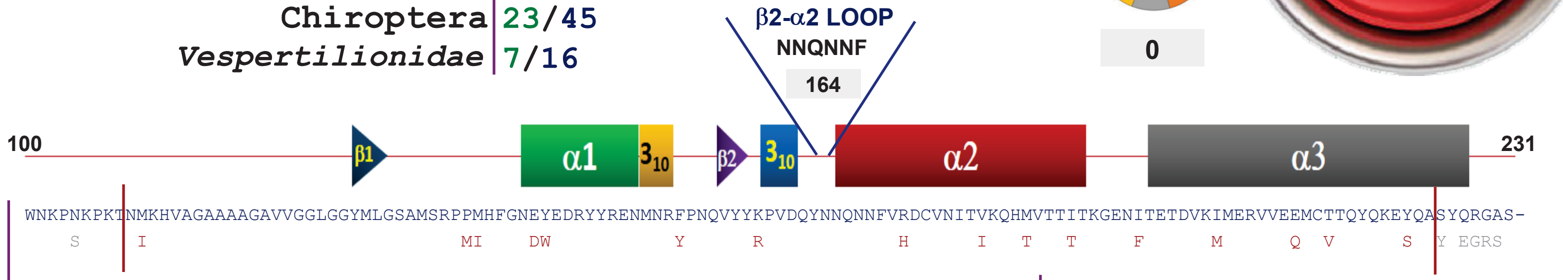
Distinct primary sequence across species

P29%



0

0



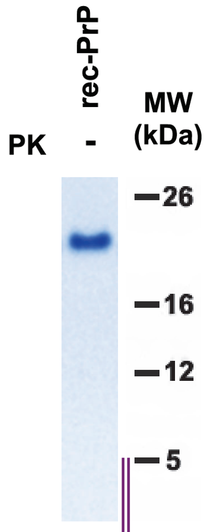
```
WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPPMHFGNEYEDRYYRENMNRFPNQVYYKPVDQYNNQNNFVRDCVNITVKQHMVTTITKGENITETDVKIMERVVEEMCTTQYQKEYQASYQRGAS-
    S     I                            MI    DW           Y      R            H      I   T   T     F      M      Q  V      S   Y EGRS
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

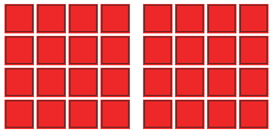
ΔΔG: -17.57



216 AA

NO MISFOLDING

0
Conformers



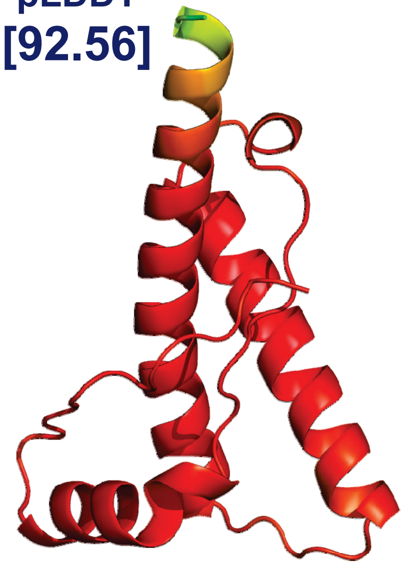
***In vitro* studies**

NOT APPLICABLE

***In vivo* studies**

NOT APPLICABLE

pLDDT
[92.56]



Protein code: 4819

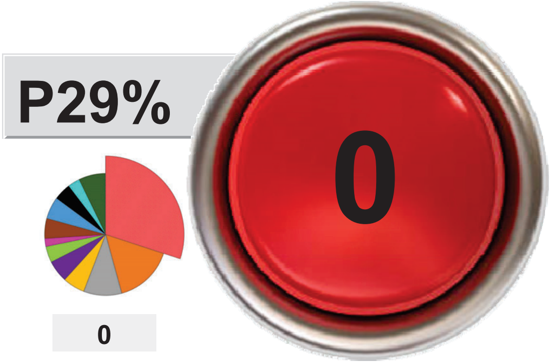
Greater bulldog bat

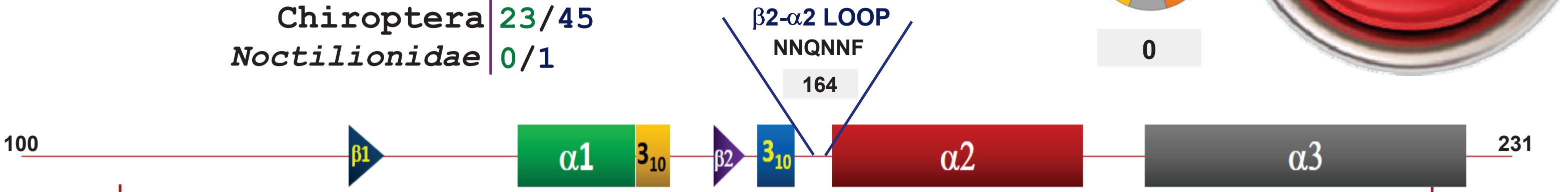
GenBank: BK064113

Noctilio leporinus

Chiroptera	23/45
Noctilionidae	0/1

P29%





```
GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRFPNQVYYRPVDQYNNQNNFVRDCVNITVKEHTVTTTTKGDNFTETDVKIMERVVEEMCTIQYQKEYAAFQRGAS-
WN        I                            M      W           Y                H     I Q            E          M        Q  VT      SQ YYE R S
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

No deletions

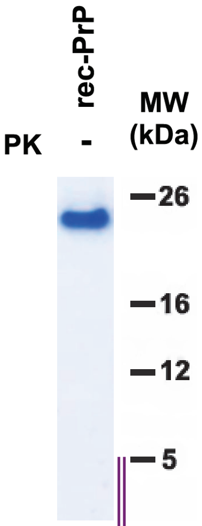
No insertions

No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

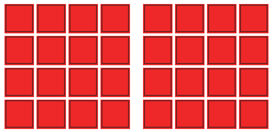
ΔΔG: ND



222 AA

NO MISFOLDING

0
Conformers



In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.94]

Protein code: 3293

Evening bat

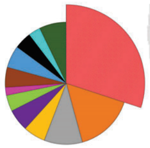
GenBank: BK064115

Nycticeius humeralis

Chiroptera 23/45
Vespertilionidae 7/16

Distinct primary sequence across species

P29%



0

0

β2-α2 LOOP
NNQNNF
164

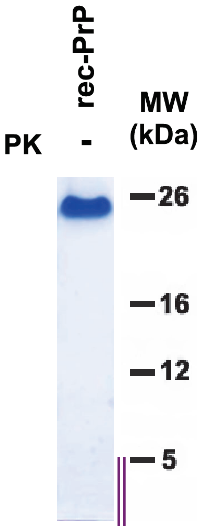
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPTMHFGNEYEDRYYRENMNRFPEQVYYKPVDQYNNQNNFVRDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEEMCTTQYQKEYRASYQRGAS-
          I                            MI    DW           Y N    R            H      I                  V M      Q  V      SQ Y EGRS
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -7.38



227 AA

NO MISFOLDING

0
Conformers

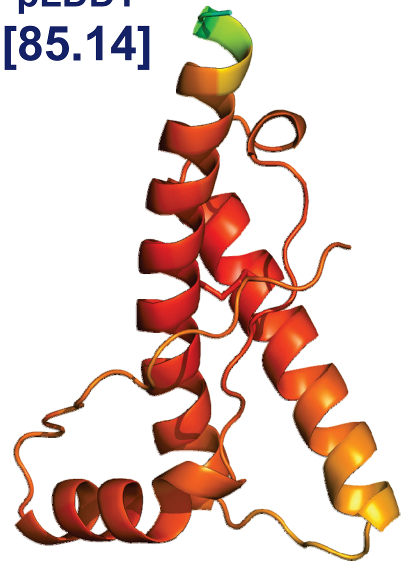
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[85.14]



Protein code: 3295

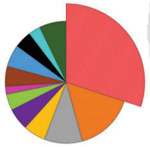
Pale spear-nosed bat

GenBank: XP_035865486

Phyllostomus discolor

`Chiroptera` 23/45
`Phyllostomidae` 2/10

P29%



0

0

β2-α2 LOOP
SNQNNF
273

```
GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMNRFPNQVYYKPVDQYSNQNNFVRDCVNITVKEHTVTTTTKGENFTETDVKIMERVVEEMCTIQYQKEYQAYQRGAS-
WN        I                            M    N W           Y      R     N      H      I Q                  M      Q  VT     S   YE R S
```

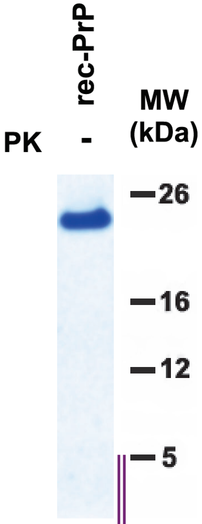
PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
It shows polymorphic variants

Distinct primary sequence across species

Tm^{Exp}: ND

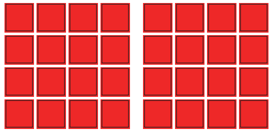
ΔΔG: ND



225 AA

NO MISFOLDING

0
Conformers



***In vitro* studies**

NOT APPLICABLE

***In vivo* studies**

NOT APPLICABLE

pLDDT
[87.53]

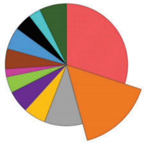
Protein code: 3765

Kuhl's pipistrelle

GenBank: XM_036417932

P39%

5



0-10

Pipistrellus kuhlii

Chiroptera 23/45
Vespertilionidae 7/16

1 species sharing the same primary sequence

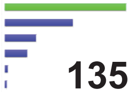
Common pipistrelle
Pipistrellus pipistrellus

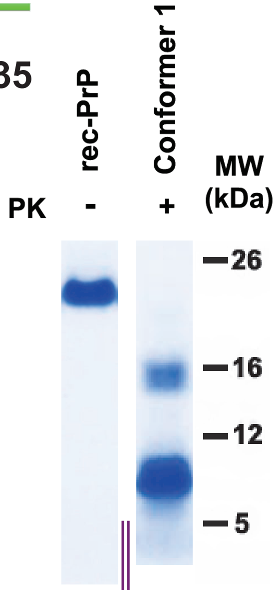
β2-α2 LOOP
SNQNNF
273

```
WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPAMHFGNEYEDRYYRENMNRFPEQVYYYKPVNQYSNQNNFVRDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEEMCTTQYQKEYQAAYQRGSS-
    S    I                               MI    DW               Y N    R  D  N     H      I                              M       Q   V        S  Y EGR
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

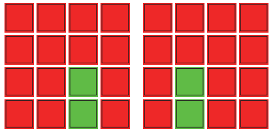
No deletions
No insertions
No polymorphic variants found





218 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -3.52

In vitro studies

TgVole (1x) Not tested

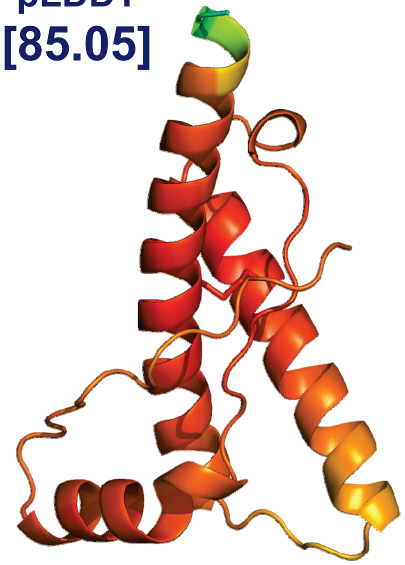
Kuhl's pipistrelle Not tested

In vivo studies

TgVole (1x) Not tested

Kuhl's pipistrelle Not tested

pLDDT
[85.05]



Protein code: 2535

Lump-nosed bat

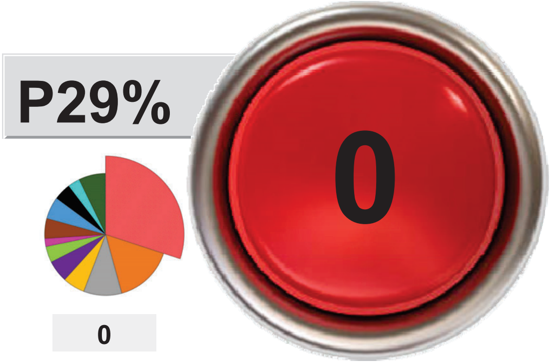
GenBank: OR472453

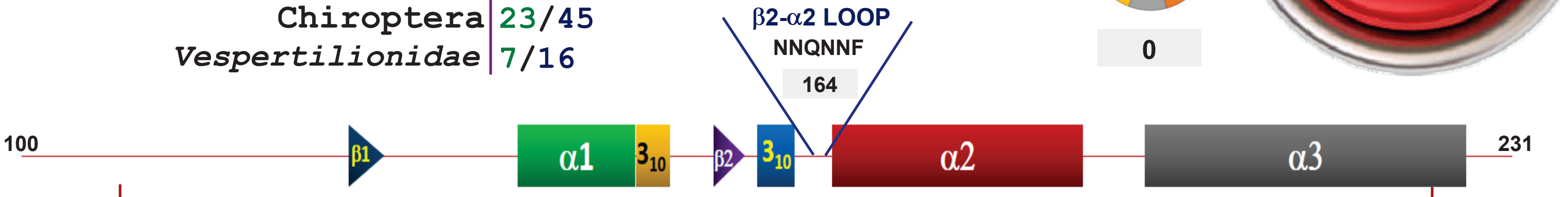
Plecotus auritus

Chiroptera 23/45
Vespertilionidae 7/16

Distinct primary sequence across species

P29%





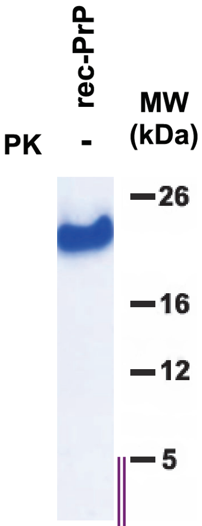
```
WNKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPAMHFGNEYEDRYYRENMNRFPEQVYYKPVDQYNNQNNFVRDCVNITVKQHTVTTTTKGDNFTETDIKIMERVVEEMCTTQYQKEYQASYQRGAS-
    S    I  V                             MI    DW            Y N    R           H      I          E      V M      Q  V      S  Y EGRS
```

PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

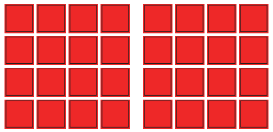
Tm^{Exp}: ND

ΔΔG: -3.01



218 AA

NO MISFOLDING



0 Conformers

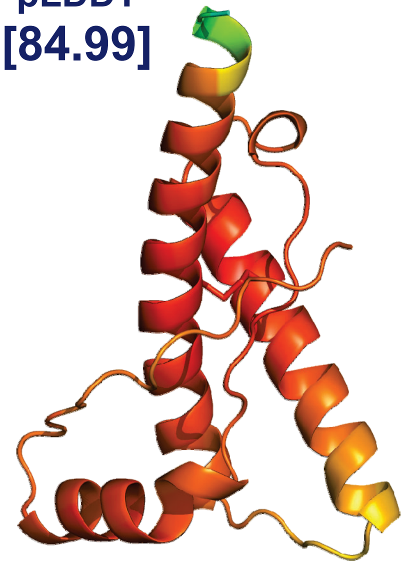
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [84.99]



Protein code: 0114

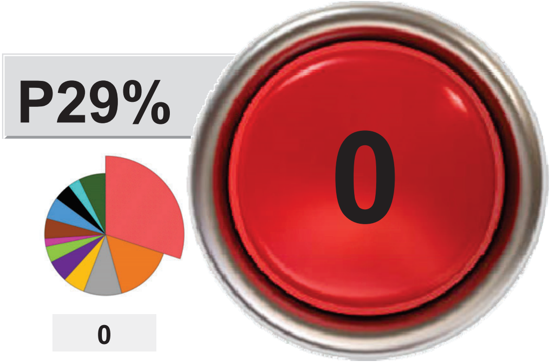
Parnell's mustached bat

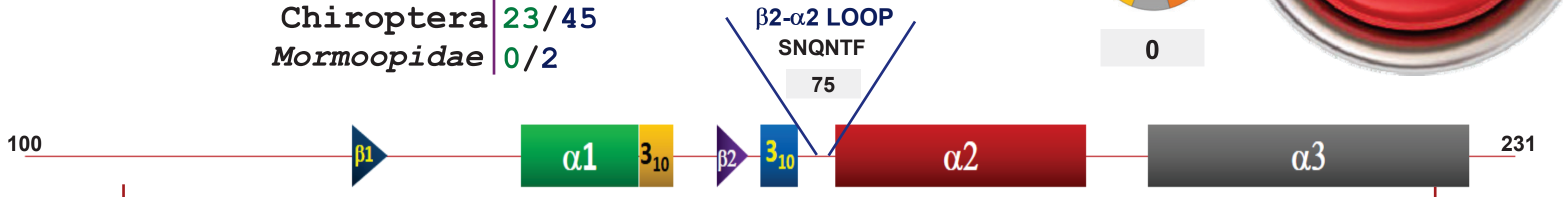
GenBank: BK063967

Pteronotus parnellii

Chiroptera 23/45
Mormoopidae 0/2

P29%



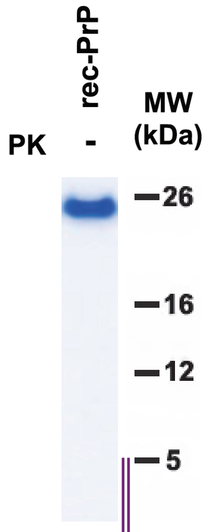


```
GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMHRFPDQVYYRPVDQYSNQNTFVRDCVNITVKEHTVTTTTKGENFTETDVKIMQRVVEEMCTIQYQKEYQAYQRGAS-
WN       I                           M      W          N Y N          N   N H    I Q                     M E   Q  VT    S   YE R S
```

PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

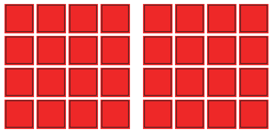
Distinct primary sequence across species



223 AA

NO MISFOLDING

0 Conformers



In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

Tm^{Exp}: ND

ΔΔG: ND

pLDDT [87.17]

Protein code: 3097

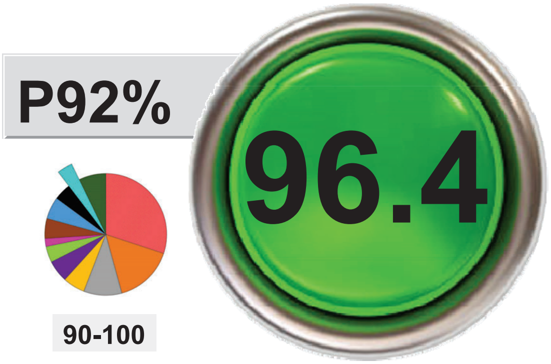
Black flying fox

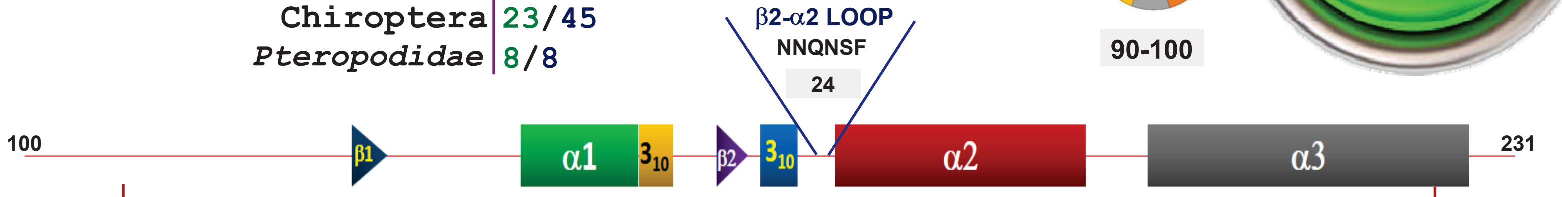
GenBank: XM_015597302

Pteropus alecto

Chiroptera 23/45
Pteropodidae 8/8

P92%





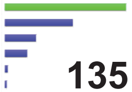
```
WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMNRPLLHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVHDCVNITVKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQQESRAAYHRGAS-
          I                    S  MI     W        N                  N         I                                             V    K  Q Y EGRS
```

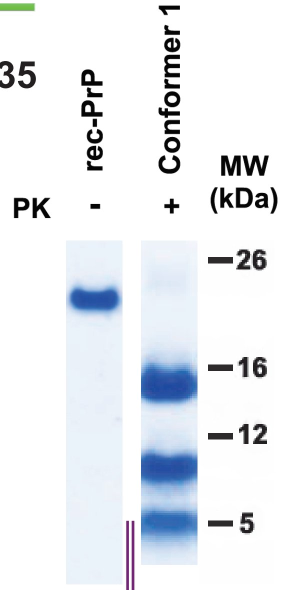
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

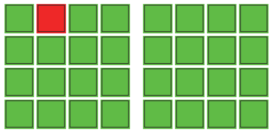
5 species sharing the same primary sequence

- **Indian flying fox** *Pteropus medius*
- **Bonin flying fox** *Pteropus pselaphon*
- **Rodrigues flying fox** *Pteropus rodricensis*
- **Madagascan flying fox** *Pteropus rufus*
- **Large flying fox** *Pteropus vampyrus*





220 AA


1 Conformers

Tm^{Exp}: ND

ΔΔG: -6.57

In vitro studies

TgVole (1x) Not tested

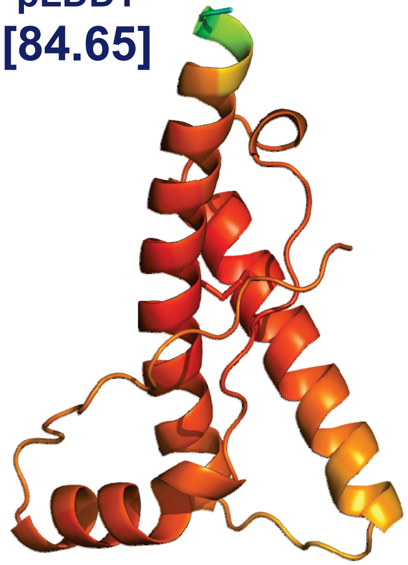
Black flying fox Not tested

In vivo studies

TgVole (1x) Not tested

Black flying fox Not tested

pLDDT [84.65]



Protein code: 1101

Greater horseshoe bat

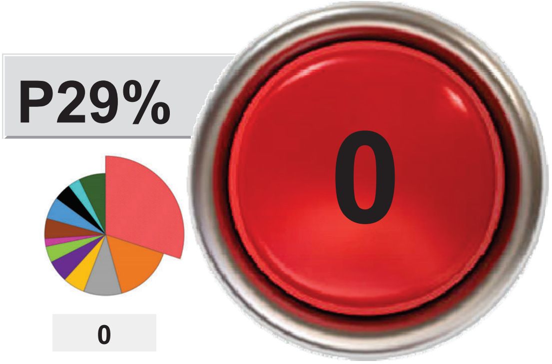
GenBank: BK063922

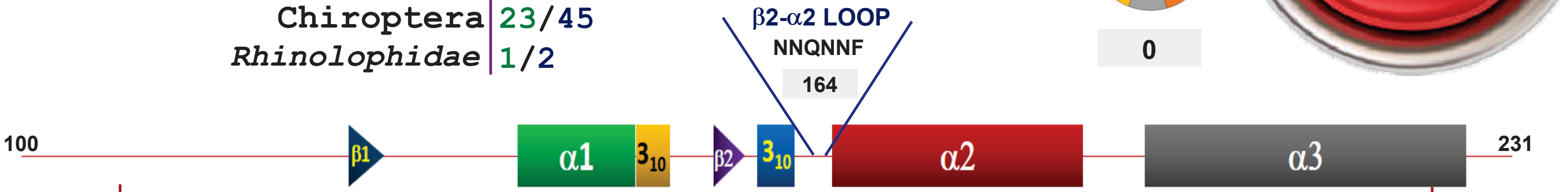
Rhinolophus ferrumequinum

Chiroptera 23/45
Rhinolophidae 1/2

Distinct primary sequence across species

P29%





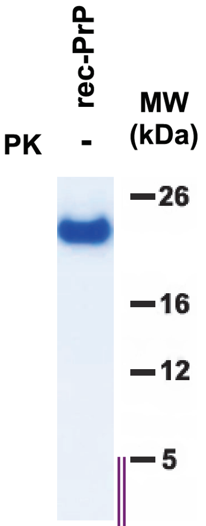
```
WNKPSKPKTSMKHMAGAAAAGAVAGGLGGYMLGSAMSRPLMHFGNDYEDRYYRENMYRYPNQVYYKPVEQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQKESHAAFRRDAS-
         NI  V         V                 MI     W         N         R  D                                           M         V       Q YYEGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -6.69



212 AA

NO MISFOLDING

0
Conformers

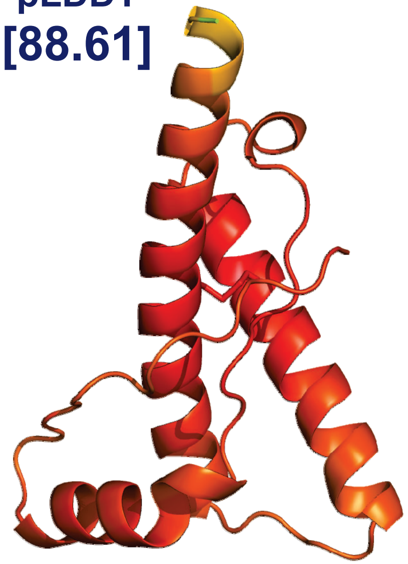
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[88.61]



Protein code: 2030

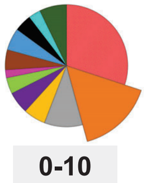
Chinese rufous horseshoe bat

GenBank: BK063992

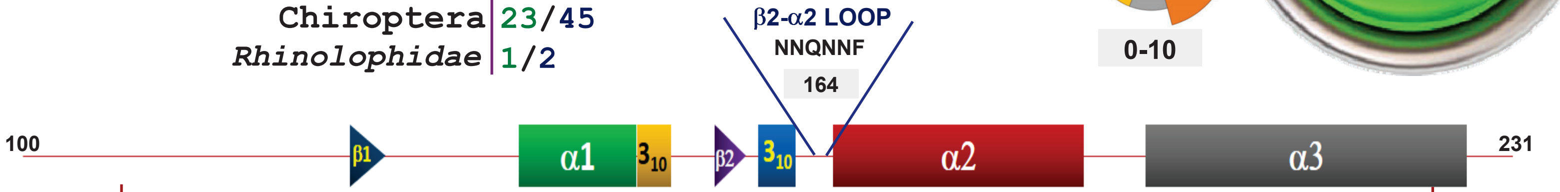
Rhinolophus sinicus

Chiroptera	23/45
Rhinolophidae	1/2

P34%



0.9



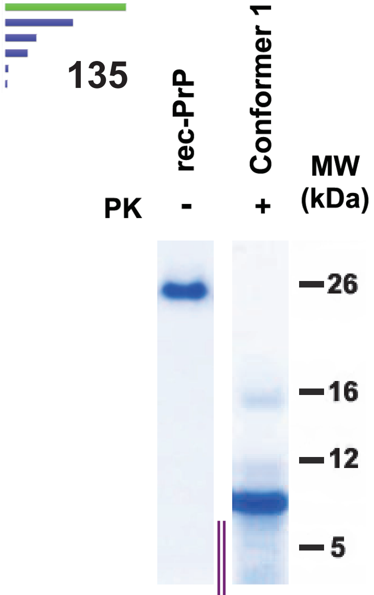
```
WNKPSKPKTSMKHMAGAAAAGAVAGGLGGYMLGSAMSRPPMHFGNDYEDRYYRENMYRYPNQVYYYKPVEQYNNQNNFVHDCVNITIKQHTVTTTSKGENFTETDVKIMERVVEQMCITQYQKEYYASPHRDAS-
          NI  V           V                  MI       W          N          R   D                                  T             M           V          SQ YYEGRS
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

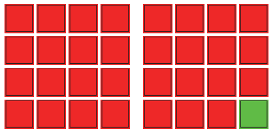
No deletions

No insertions

No polymorphic variants found



212 AA



1
Conformers

Tm^{Exp}: ND

ΔΔG: -3.92

***In vitro* studies**

Not tested
TgVole (1x)

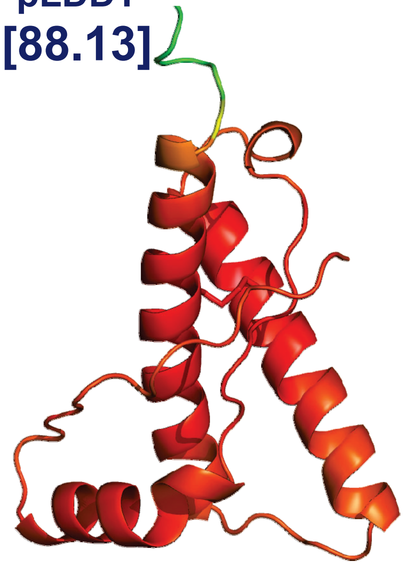
Not tested
Chinese rufous horseshoe bat

***In vivo* studies**

Not tested
TgVole (1x)

Not tested
Chinese rufous horseshoe bat

pLDDT [88.13]



Distinct primary sequence across species

Protein code: 3151

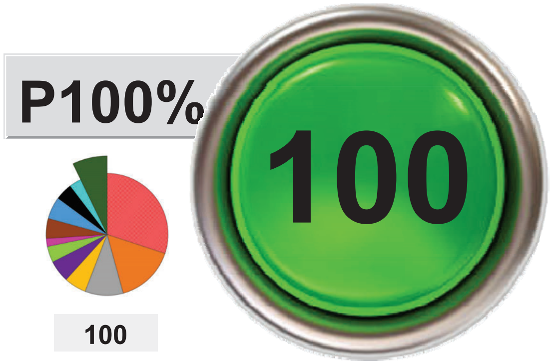
Egyptian fruit bat

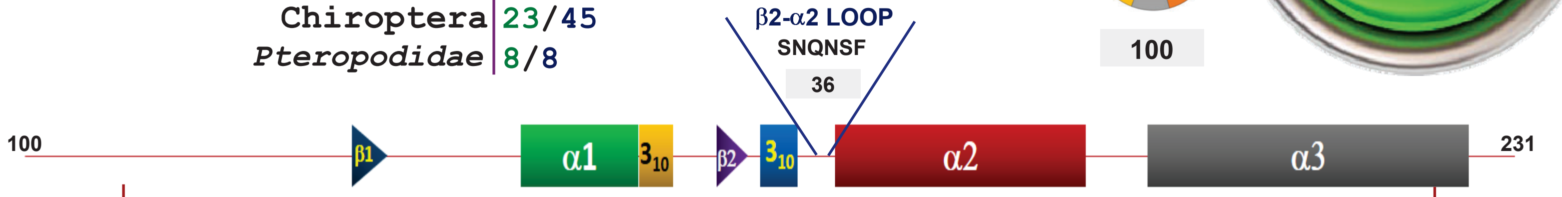
GenBank: XM_016135122

Rousettus aegyptiacus

Chiroptera 23/45
Pteropodidae 8/8

Distinct primary sequence across species





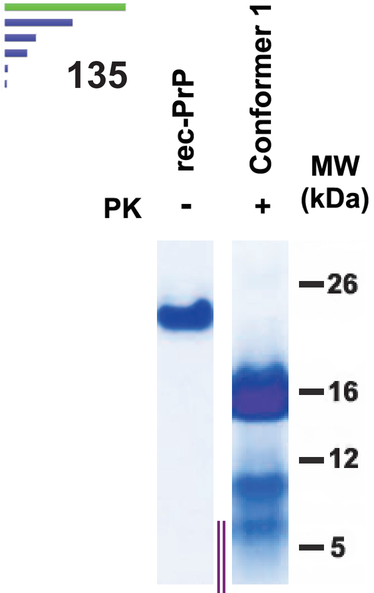
```
WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDYEDRYYRENMYRYPNQVYYRPMEQYSNQNSFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQQESRAAYHRGAS-
             I                                     I     W           N          VD  N   N                                         V    K   Q Y EGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

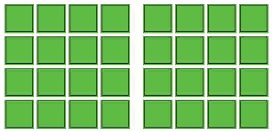
It shows polymorphic variants



203 AA

1

Conformers



Tm^{Exp}: 67.2 ºC

ΔΔG: -20.62

***In vitro* studies**

TgVole (1x) **Propagate**

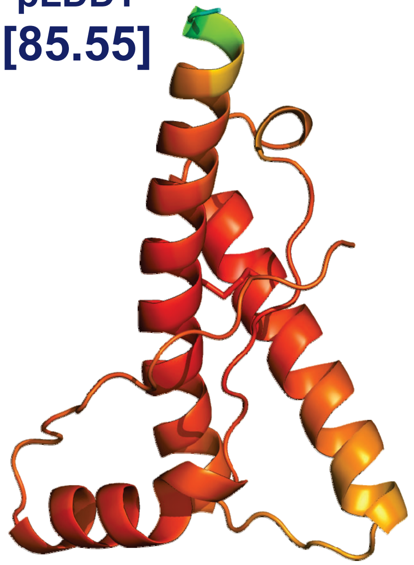
Egyptian fruit bat **Ongoing**

***In vivo* studies**

TgVole (1x) **Infectious**

Egyptian fruit bat **Not tested**

pLDDT
[85.55]



Protein code: 1107

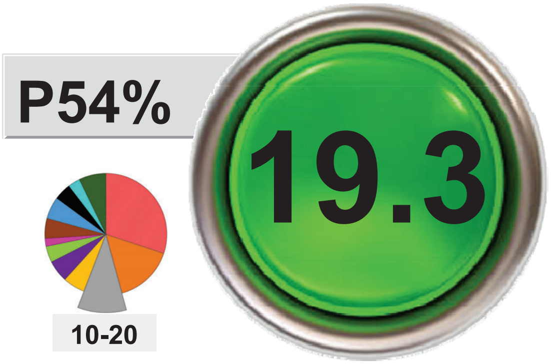
Leschenault's rousette

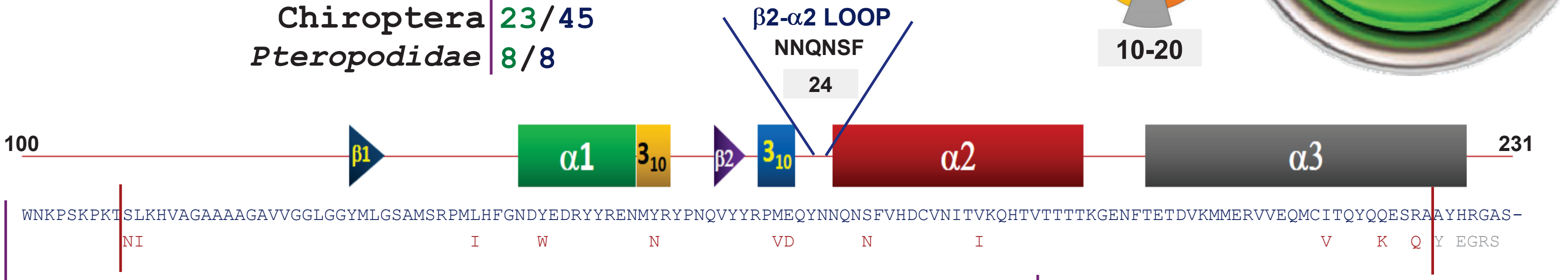
GenBank: BK063997

Rousettus leschenaultii

Chiroptera	23/45
Pteropodidae	8/8

Distinct primary sequence across species

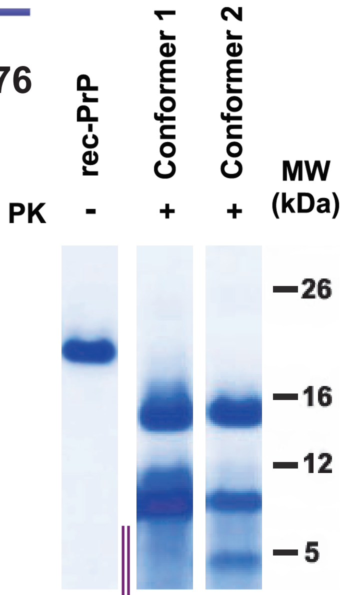




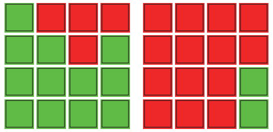
```
WNKPSKPKTSLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDYEDRYYRENMYRYPNQVYYRPMEQYNNQNSFVHDCVNITVKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQQESRAAYHRGAS-
          NI                              I     W         N         VD     N        I                                  V    K  Q Y EGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



195 AA



2
Conformers

Tm^{Exp}: ND

ΔΔG: -20.82

In vitro studies

Not tested
TgVole (1x)

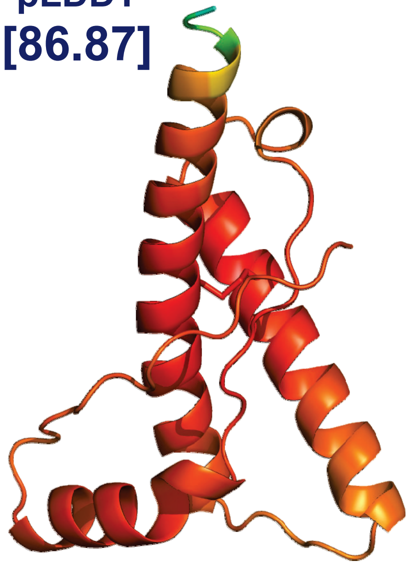
Not tested
Leschenault's rousette

In vivo studies

Not tested
TgVole (1x)

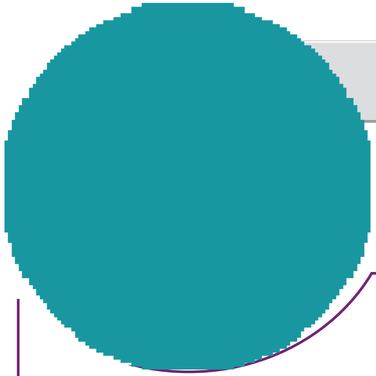
Not tested
Leschenault's rousette

pLDDT
[86.87]



Protein code: 3157

Distinct primary sequence across species



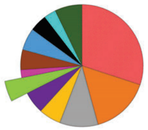
Madagascan rousette

GenBank: BK064805

Rousettus madagascariensis

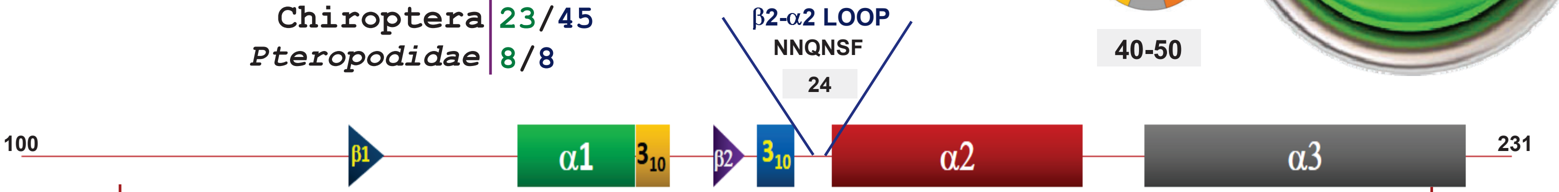
Chiroptera 23/45
Pteropodidae 8/8

P71%



40-50

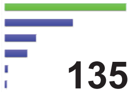
48.2



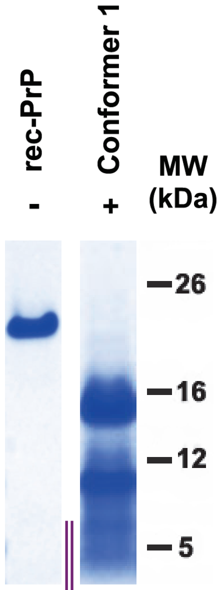
```
WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDYEDRYYRENMYRYPNQVYYRPMEQYNNQNSFVHDCVNITVKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQQESRAAYHRGAS-
          I                                I     W          N          VD      N          I                                       V     K   Q Y EGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

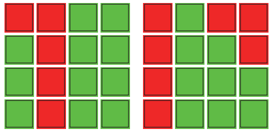


135



203 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -18.77

***In vitro* studies**

TgVole (1x) Not tested

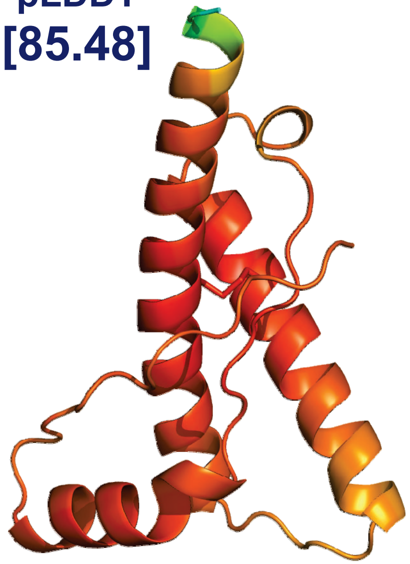
Madagascan rousette Not tested

***In vivo* studies**

TgVole (1x) Not tested

Madagascan rousette Not tested

pLDDT
[85.48]



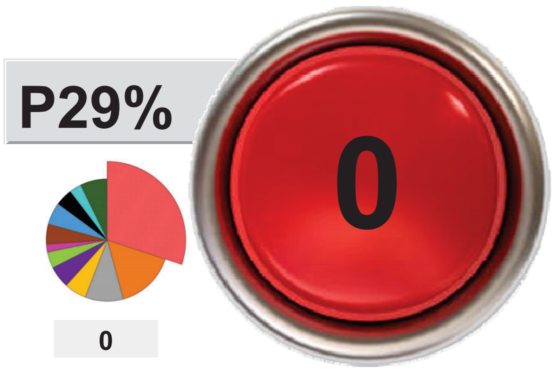
Protein code: 3973

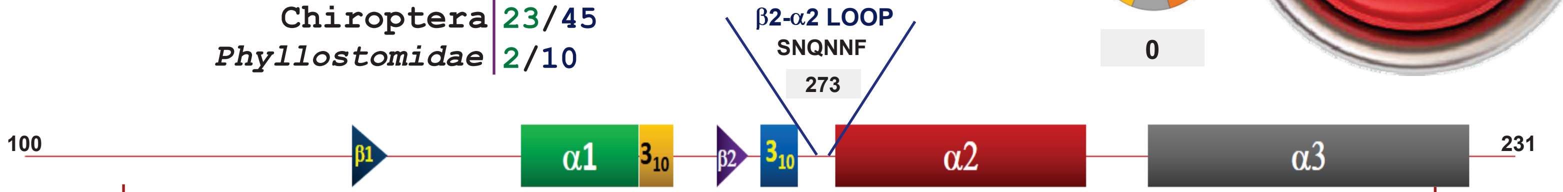
Honduran yellow-shouldered bat

GenBank: BK063970

Sturnira ludovici hondurensis

Chiroptera	23/45
Phyllostomidae	2/10





```
GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLVHFGNDYEDRYYRENMNRFPNQVYYRPVDQYSNQNNFVRDCVNITVKEHTVTTTTKGENFTSTDVKIMERVVEEMCTIQYQKEYQAYQRGAS-
WN       I                                 MI     W           Y           N     H      I Q              E    M      Q  VT     S  YE R S
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions

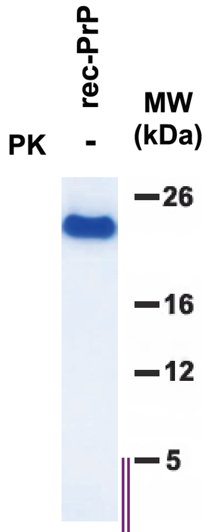
No insertions

No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

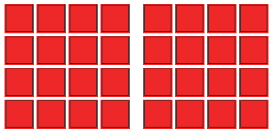
ΔΔG: ND



216 AA

NO MISFOLDING

0 Conformers



In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [84.95]

Protein code: 3126

Distinct primary sequence across species

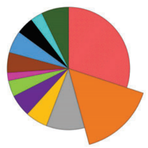
Mexican free-tailed bat

GenBank: BK064001

Tadarida brasiliensis

Chiroptera	23/45
Molossidae	2/2

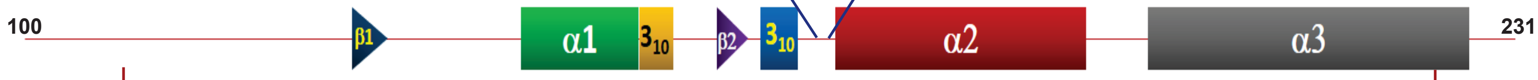
P41%



0-10

7.1

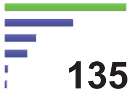
β2-α2 LOOP
SNQNNF
273



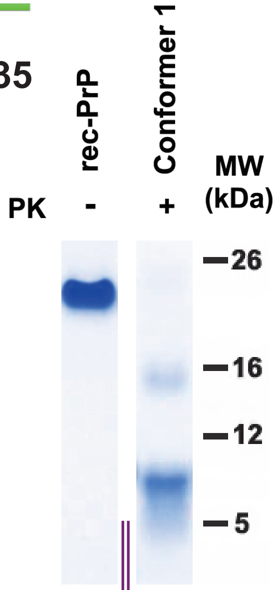
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPPIHFGSDYEDRYYRENMNRFPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTITTTTKGDNFTETDIKIMERVVEEMCTTQYQKEYQAYQRGAS-
I M N W Y R N I V E V M Q V S YE R S

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

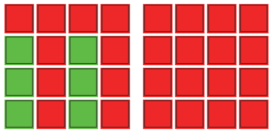


135



224 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) — Not tested

Mexican free-tailed bat — Not tested

In vivo studies

TgVole (1x) — Not tested

Mexican free-tailed bat — Not tested

pLDDT
[86.35]

Protein code: 3162

Stripe-headed round-eared bat

GenBank: BK064003

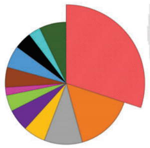
Tonatia saurophila

Chiroptera 23/45
Phyllostomidae 2/10

1 species sharing the same primary sequence

Greater spear-nosed bat
Phyllostomus hastatus

P29%



0

0

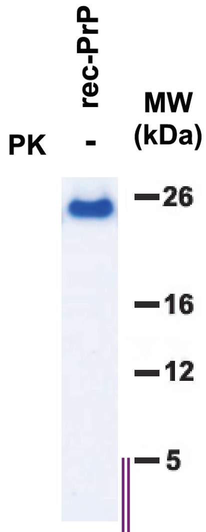
β2-α2 LOOP
SNQNNF
273

```
GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRFPNQVYYKPVDQYSNQNNFVRDCVNITVKEHTVTTTTKGENFTETDVKIMERVVEEMCTIQYQREYQAYQRGAS-
WN        I                            M      W           Y      R     N      H      I Q                  M      Q  VT   K S   YE R S
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND
ΔΔG: ND



225 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.72]

Protein code: 3164

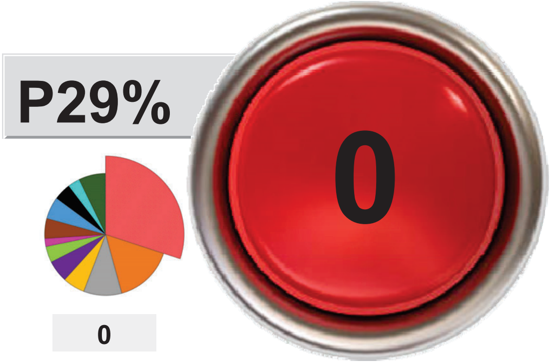
Fringe-lipped bat

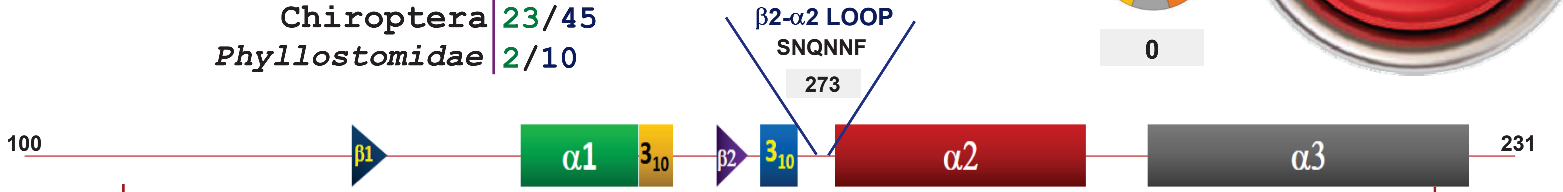
GenBank: BK064958

Trachops cirrhosus

Chiroptera	23/45
Phyllostomidae	2/10

P29%





GGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRFPNQVYYRPVDQYSNQNNFVRDCVNITVKEHTVTTTTKGENFTETDVKIMERVVEEMCTIQYQRESQAYYQRGAS-

WN I M W Y N H I Q M Q VT K EGRS

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions

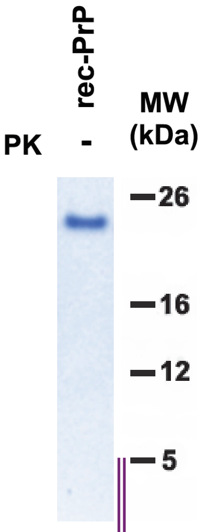
No insertions

No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

ΔΔG: -13.99

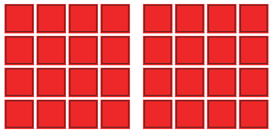


226 AA

NO MISFOLDING

0

Conformers



In vitro studies

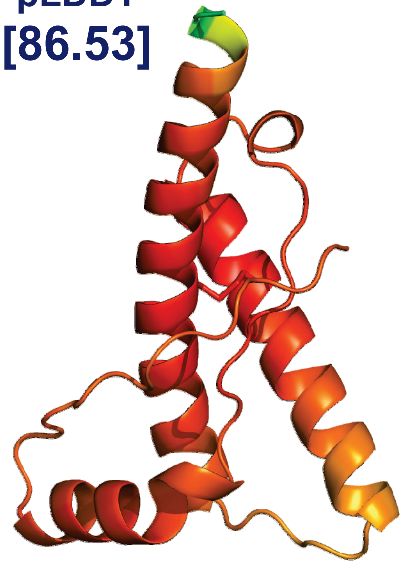
NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT

[86.53]



Protein code: 4512

Distinct primary sequence across species

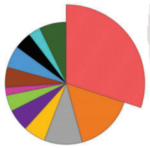
Southern naked-tailed armadillo

GenBank: BK064228

Cabassous unicinctus

Cingulata 1/4
Dasypodidae 1/4

P29%



0

0

β2-α2 LOOP
GSEQSF
2

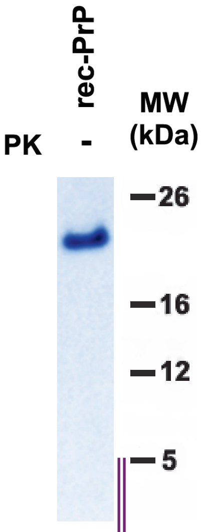
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYLVGSAMSRPLIHFSNDYDDRYYRENMYRYPNQVYYRPLEQYGSEQSFVRDCVNVTIKEHTATTTTKGENFTETDVRVMERVVEQMCVTQYQRESQAAYQRGAG-
          I                   ML       M   G  W         N          VD  NNQNN  H    I   Q  V              KM              K    Y EGRSS
```

PrP sequence differs by 22 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

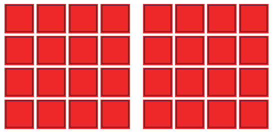
ΔΔG: -14.75



213 AA

NO MISFOLDING

0
Conformers



In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[91.82]

Protein code: 4842

Screaming hairy armadillo

GenBank: BK064063

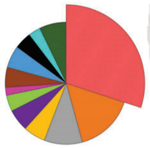
Chaetophractus vellerosus

Cingulata 1/4
Dasypodidae 1/4

1 species sharing the same primary sequence

Six-banded armadillo
Euphractus sexcinctus

P29%



0

0

β2-α2 LOOP
SSERNF
1

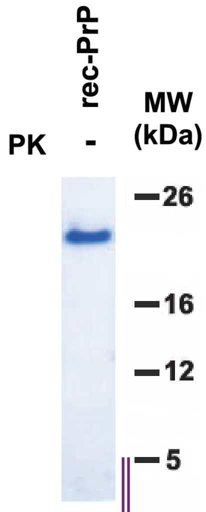
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYLVGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVEQYSSERNFVQDCVNITVKEHTVTTTTKGENFTETDVRMMERVVEQMCITQYQRESQAAFQRGSG-
          I                   ML       M      W         N           D  NNQN   H      I Q                 K          V    K    YYEGR S
```

PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -17.17



211 AA

NO MISFOLDING

0
Conformers

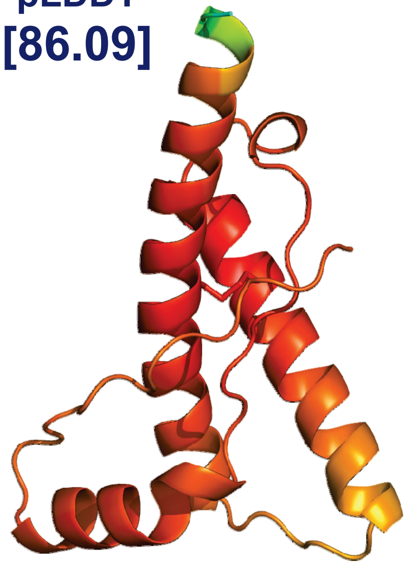
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.09]



Protein code: 3238

Nine-banded armadillo

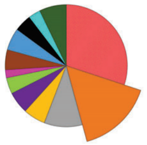
GenBank: EU559337

Dasypus novemcinctus

Cingulata 1/4
Dasypodidae 1/4

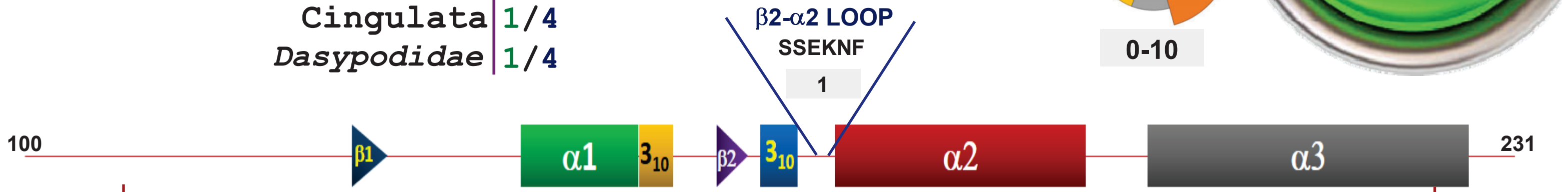
Distinct primary sequence across species

P31%



0-10

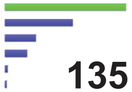
0.4



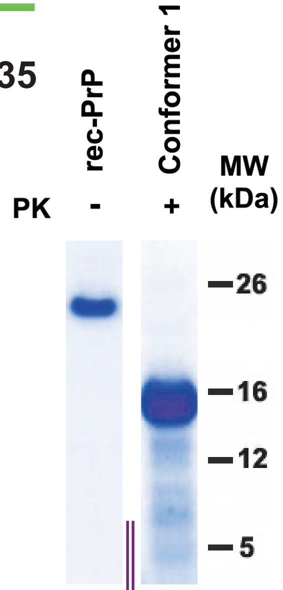
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYLVGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVEQYSSEKNFVHDCVNITIKEHTVTTTTKGENFTETDVRMMERVVEQMCITQYQREAQAAYQRGAG-
           I                ML       M      W         N           D  NNQN          Q                K          V     K S  Y EGRSS
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

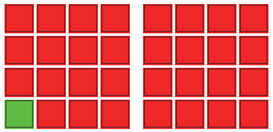


135



210 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -20.08

In vitro studies

Not tested
TgVole (1x)

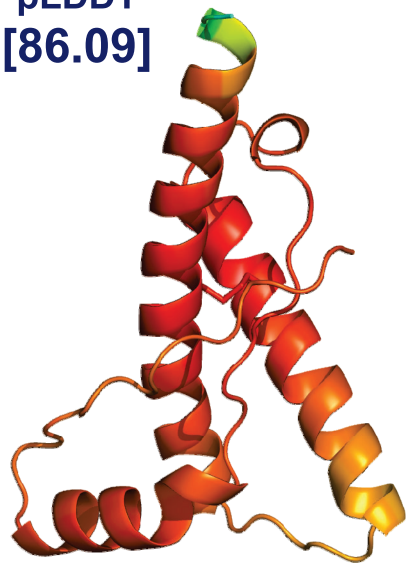
Not tested
Nine-banded armadillo

In vivo studies

Not tested
TgVole (1x)

Not tested
Nine-banded armadillo

pLDDT
[86.09]

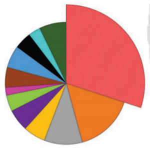


Protein code: 0968

Southern three-banded armadillo

GenBank: BK064002

P29%



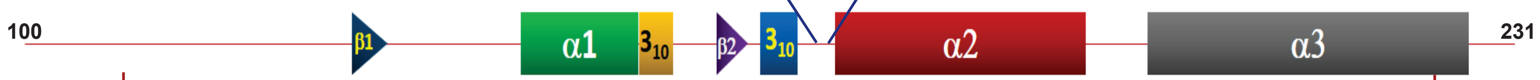
0

0

Tolypeutes matacus

Cingulata 1/4
Dasypodidae 1/4

β2-α2 LOOP
GSEQSF
2



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYLVGSAMNRPLIHFGNDYDDRYYRENMYRYPNQVYYRPLEQYGSEQSFVRDCVNITIKEHTATTTTRGENFTETDVRVMERVVEQMCVTQYQRESQAAYQRGAG-

I ML S M W N VD NNQNN H Q V KM K Y EGRSS

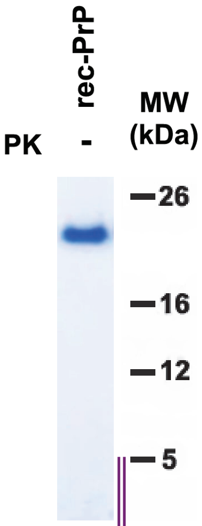
PrP sequence differs by 21 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

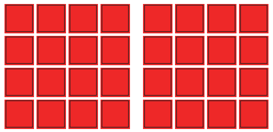
ΔΔG: -8.09



211 AA

NO MISFOLDING

0 Conformers



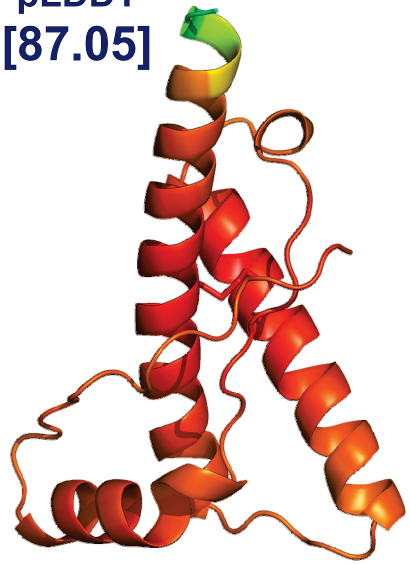
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [87.05]

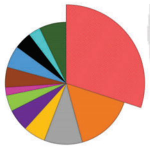


Protein code: 3163

Yellow-footed antechinus

GenBank: BK063971

P29%



0

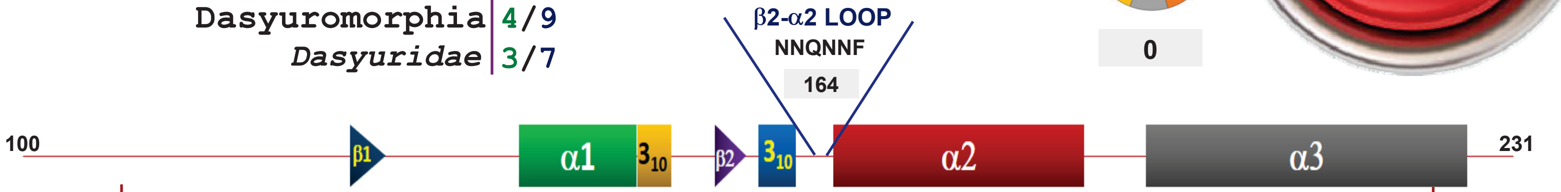
0

Antechinus flavipes

Dasyuromorphia 4/9

Dasyuridae 3/7

Distinct primary sequence across species



```
KWKPDKPKTNMKHVAGAAAAGAVLGGVGGYMLGSAMSRPVMHFGNEWEDRYYRENQYRYPNQVMYRPIDQYNNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYRAAQYSYNLA-
WN  S     I            V  L            MI    D         MN      Y   V                 I    V             V M         V    K SQ YYEGRSS
```

PrP sequence differs by 18 amino acids from the bank vole PrP (see in red)

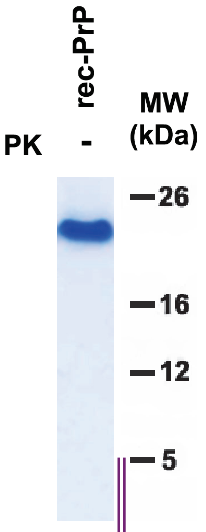
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



218 AA

NO MISFOLDING

In vitro studies

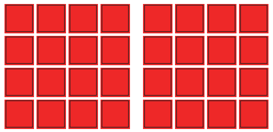
NOT APPLICABLE

In vivo studies

NOT APPLICABLE

0

Conformers



pLDDT [92.27]

Protein code: 3128

Distinct primary sequence across species

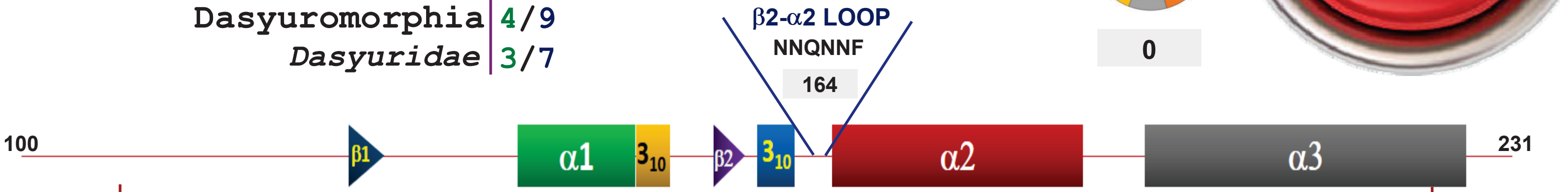
Brown antechinus

GenBank: BK063930

P29%

Antechinus stuartii

Dasyuromorphia 4/9
Dasyuridae 3/7



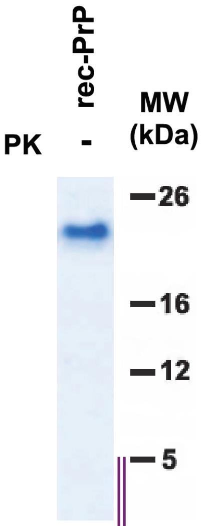
```
KWKPDKPKTNMKHVAGAAAAGAVLGGVGGYMLGSAMSRPVMHFGSDWEDRYYRENQYRYPNQVMYRPIDQYNNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIRIMERVVEQMCITQYQNEYRAAQYSYNLA-
WN  S     I            V  L            MI   N          MN      Y   V               I      V             VKM         V    K SQ YYEGRSS
```

PrP sequence differs by 19 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



218 AA

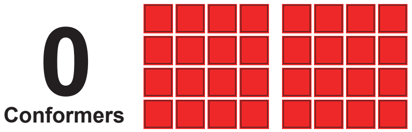
NO MISFOLDING

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE



pLDDT [92.82]

Protein code: 3048

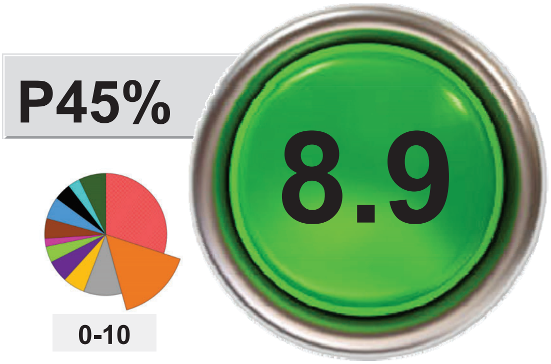
Northern quoll

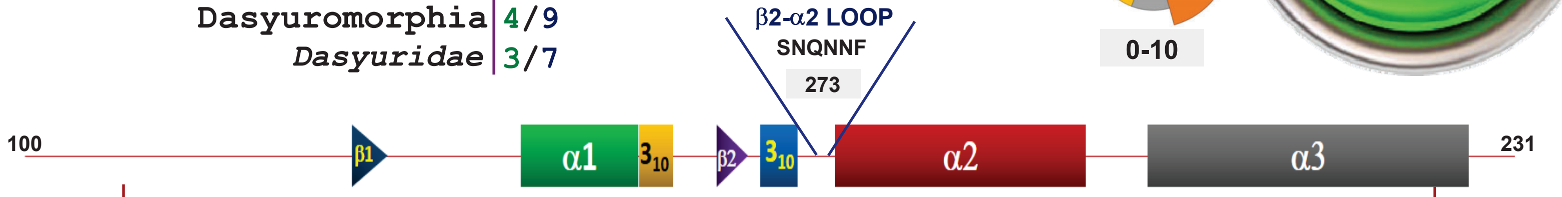
GenBank: BK064760

Dasyurus hallucatus

Dasyuromorphia 4/9
Dasyuridae 3/7

Distinct primary sequence across species

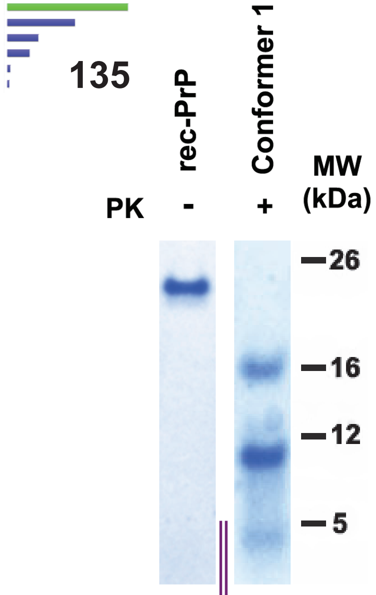




```
KWKPDKPKTNMKQMAGAAAAGAVLGGVSGYVLGSAMSRPIMHFGNDYEDRYYRENQYRYPNQVMYRPIDQYSNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYRAAQYSYNMA-
WN  S     I HV          V  LG  M        MI      W        MN    Y   V   N             I    V             V  M         V    K SQ YYEGRSS
```

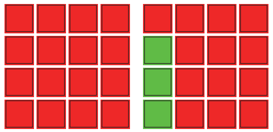
PrP sequence differs by 23 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



228 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

***In vitro* studies**

TgVole (1x) Not tested

Northern quoll Not tested

***In vivo* studies**

TgVole (1x) Not tested

Northern quoll Not tested

pLDDT
[91.53]

Protein code: 3849

Eastern quoll

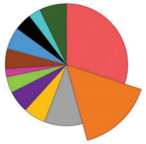
GenBank: BK064810

Dasyurus viverrinus

Dasyuromorphia 4/9
Dasyuridae 3/7

Distinct primary sequence across species

P35%



0-10

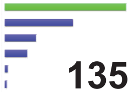
1.4

β2-α2 LOOP
SNQNNF
273

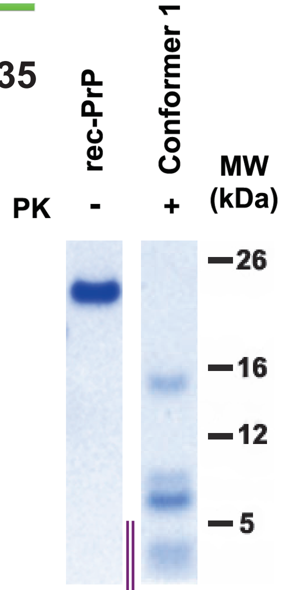
```
KWKPDKPKTNMKQMAGAAAAGAVLGGVGGYVLGSAMSRPVMHFGNDYEDRYYRENQYRYPNQVMYRPIDQYSNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYRAAQYSYNMA-
WN  S     I HV         V  L   M        MI     W        MN      Y   V   N             I    V             V M         V    K SQ YYEGRSS
```

PrP sequence differs by 22 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



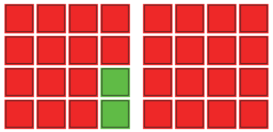
135



218 AA

1

Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

Eastern quoll Not tested

In vivo studies

TgVole (1x) Not tested

Eastern quoll Not tested

pLDDT
[91.97]

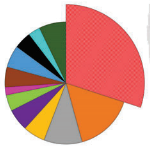
Protein code: 4008

Distinct primary sequence across species

Numbat

GenBank: BK064811

P29%

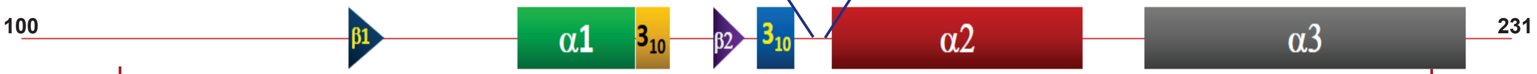


0

Myrmecobius fasciatus

Dasyuromorphia	4/9
Myrmecobiidae	0/1

β2-α2 LOOP
SNQNNF
273



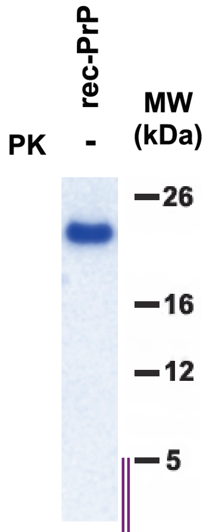
```
KWKPDKPKTNMKHVAGAAAAGAVVGGLGGYVLGSAMSRPIMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYRAAQYSYNMA-
WN   S     I                    M        MI     DW         MN       Y   V   N              I    V              V M          V    K SQ YYEGRSS
```

PrP sequence differs by 19 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



213 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

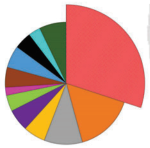
pLDDT
[92.19]

Protein code: 4079

Brush-tailed phascogale

GenBank: BK064816

P29%



0

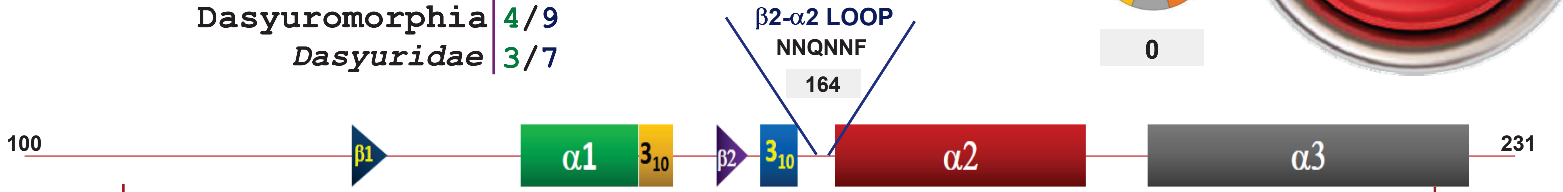
0

Phascogale tapoatafa

Dasyuromorphia 4/9
Dasyuridae 3/7

1 species sharing the same primary sequence

Red-tailed phascogale
Phascogale calura



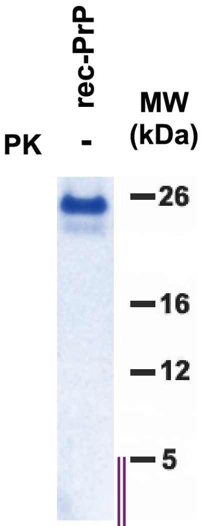
```
KWKPDKPKTNMKQMAGAAAAGAVLGGVGGYMLGSAMSRPVMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYNNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYRAAQYSYNLA-
WN  S     I HV         V  L            MI    DW         MN     Y   V                 I    V             V M         V    K SQ YYEGRSS
```

PrP sequence differs by 21 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



228 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [92.71]

Protein code: 4470

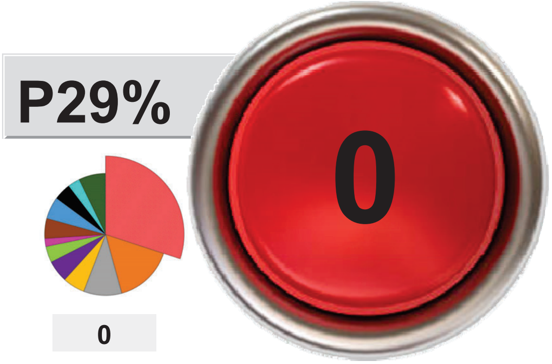
Tasmanian devil

GenBank: XM_003757949

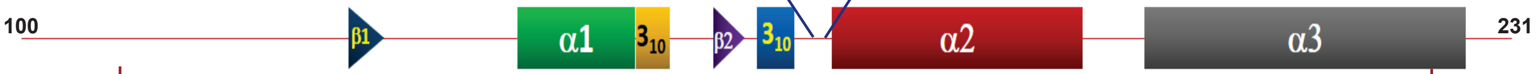
Sarcophilus harrisii

Dasyuromorphia 4/9
Dasyuridae 3/7

P29%



β2-α2 LOOP
SSQNNF
42



KWKPDKPKTNMKHMAGAAAAGAVLGGVGGYVLGSAMSRPIMHFGNDYEDRYYRENQYRYPNQVMYRPIDQYSSQNNFVHDCVNITVKQHTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYRAAQYSYNMA-

WN S I V V L M MI W MN Y V NN I V V M V K SQ YYEGRSS

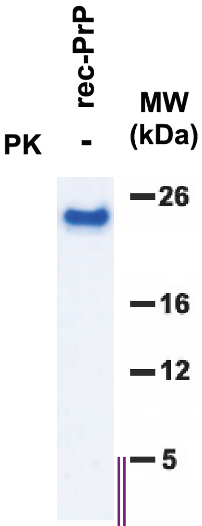
PrP sequence differs by 22 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

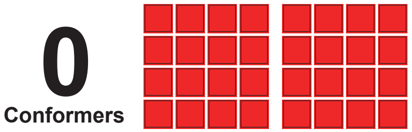
ΔΔG: ND

Distinct primary sequence across species



218 AA

NO MISFOLDING



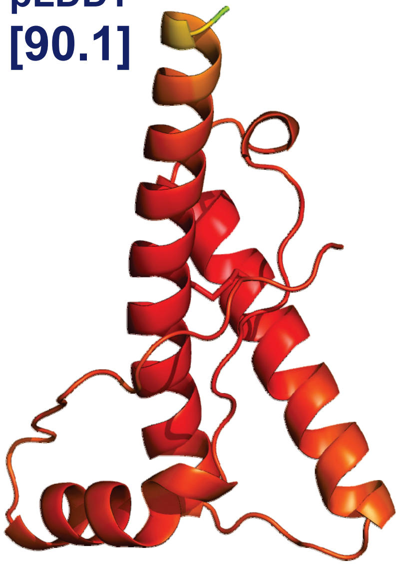
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [90.1]



Protein code: 0970

Fat-tailed dunnart

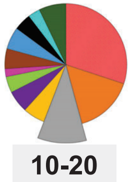
GenBank: BK064171

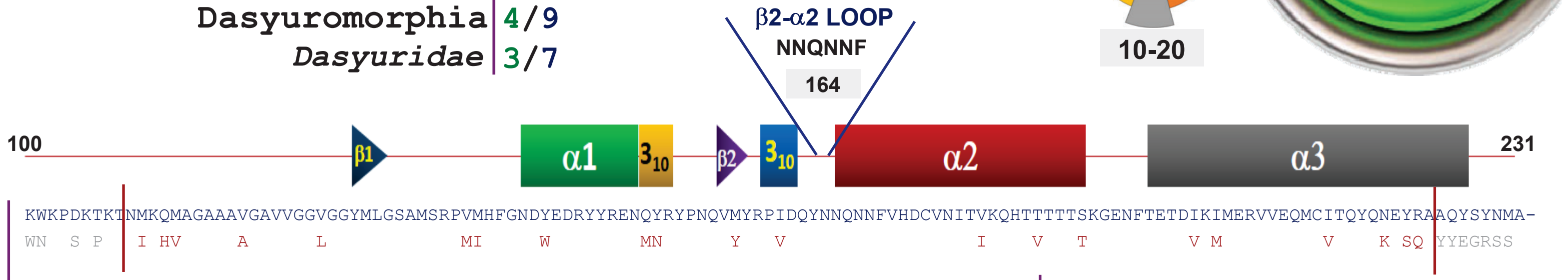
Sminthopsis crassicaudata

Dasyuromorphia 4/9
Dasyuridae 3/7

P55%

19.6



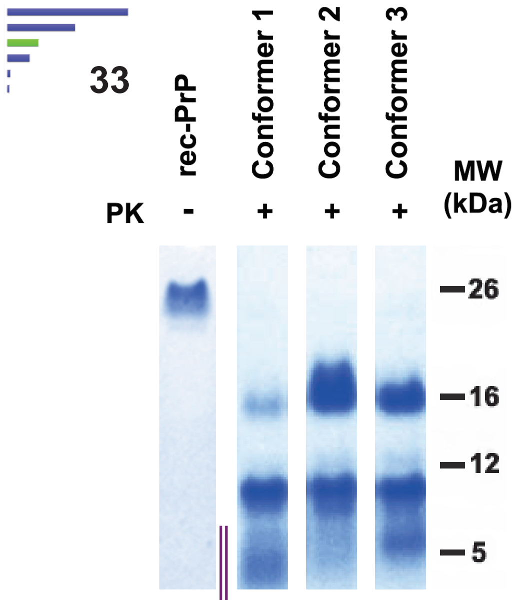


```
KWKPDKTKTNMKQMAGAAAVGAVVGGVGGYMLGSAMSRPVMHFGNDYEDRYYRENQYRYPNQVMYRPIDQYNNQNNFVHDCVNITVKQHTTTTTSKGENFTETDIKIMERVVEQMCITQYQNEYRAAQYSYNMA-
WN  S P  I HV    A    L       MI   W     MN    Y  V                   I   V  T         V M       V    K SQ YYEGRSS
```

PrP sequence differs by 21 amino acids from the bank vole PrP (see in red)

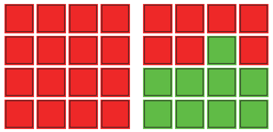
No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species



228 AA

3 Conformers



Tm^{Exp}: ND

ΔΔG: ND

***In vitro* studies**

TgVole (1x) Not tested

Fat-tailed dunnart Not tested

***In vivo* studies**

TgVole (1x) Not tested

Fat-tailed dunnart Not tested

pLDDT [92.93]

Protein code: 3850

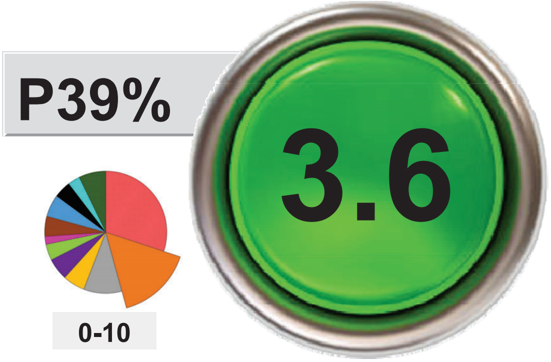
Distinct primary sequence across species

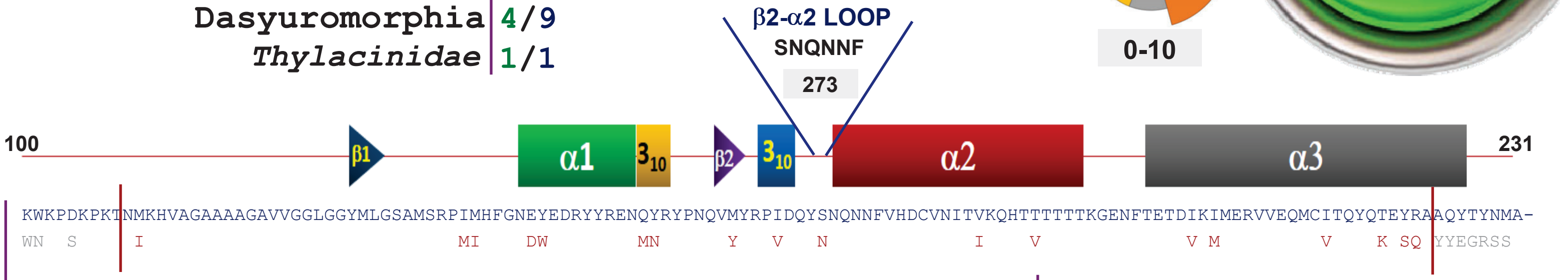
Thylacine

GenBank: BK064189

Thylacinus cynocephalus

Dasyuromorphia	4/9
Thylacinidae	1/1





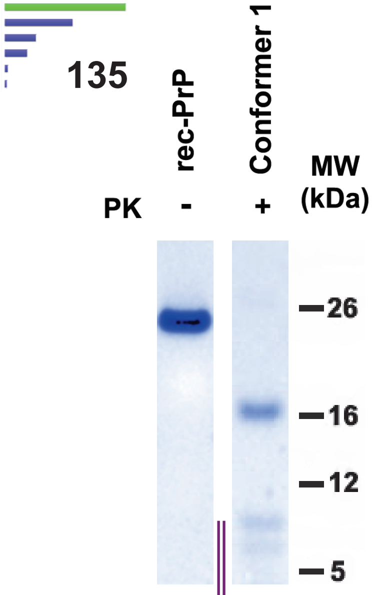
```
KWKPDKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPIMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQTEYRAAQYTYNMA-
WN  S    I                            MI    DW         MN     Y   V   N              I    V                  V M         V    K SQ YYEGRSS
```

PrP sequence differs by 18 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found



208 AA

Tm^{Exp}: ND

ΔΔG: ND

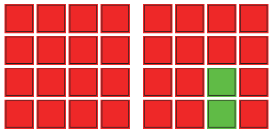
In vitro studies

TgVole (1x)	Ongoing
Thylacine	Not tested

In vivo studies

TgVole (1x)	Ongoing
Thylacine	Not tested

pLDDT [91.45]



1 Conformers

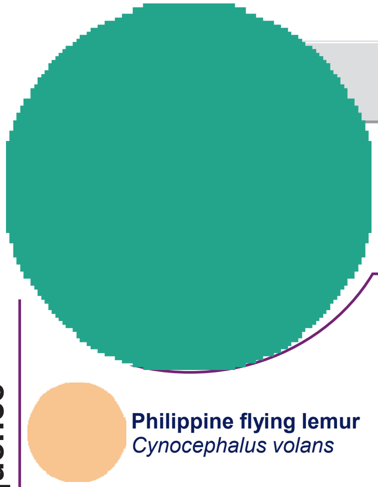
Protein code: 4339

Sunda flying lemur

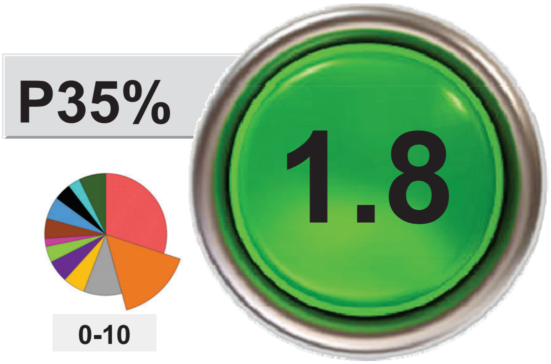
GenBank: AY133034

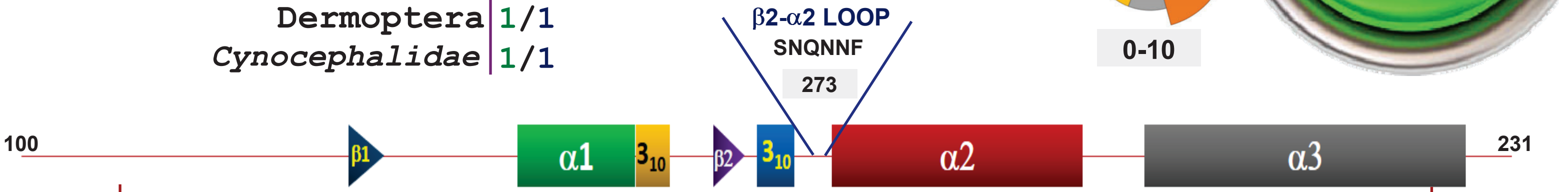
Galeopterus variegatus

Dermoptera 1/1
Cynocephalidae 1/1



1 species sharing the same primary sequence



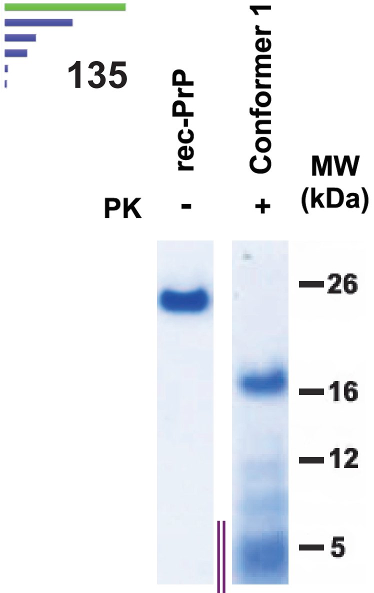


`WGKPSKPKTNLKQMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQKEQQAYYQRGSS-`

`N I HV M W N N I V M V S EGR`

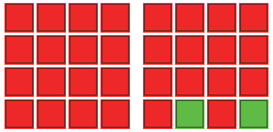
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



212 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -8.07

In vitro studies

No propagation
TgVole (1x)

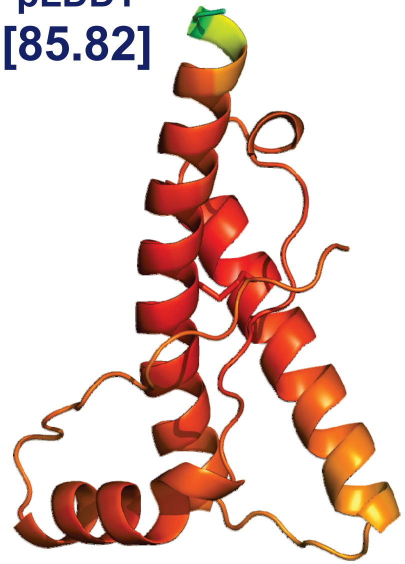
Not tested
Sunda flying lemur

In vivo studies

Ongoing
TgVole (1x)

Not tested
Sunda flying lemur

pLDDT
[85.82]



Protein code: 0957

Virginia opossum

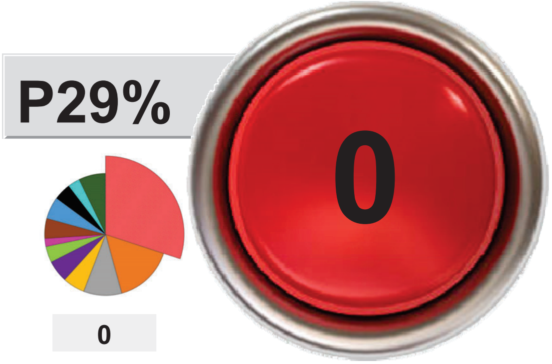
GenBank: BK064768

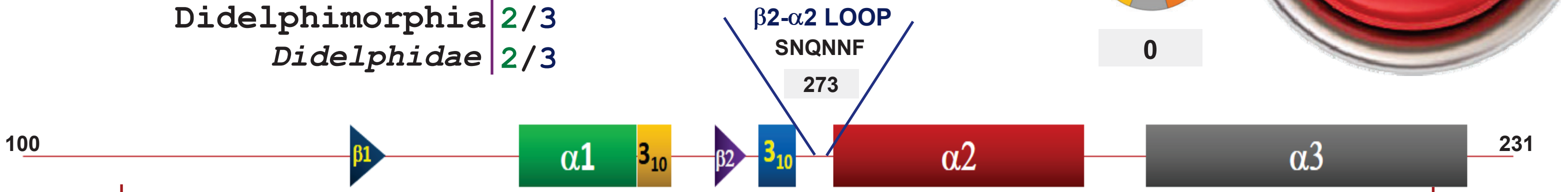
Didelphis virginiana

Didelphimorphia 2/3

Didelphidae 2/3

P29%





```
KWKPDKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPIMHFGNDYEDRYYRENQYRYPNQVMYRPIDQYSNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYRSAYN-
WN  S     I                                MI     W         MN       Y   V   N             I    V                  V M         V     K SQAY EG
```

PrP sequence differs by 18 amino acids from the bank vole PrP (see in red)

No deletions

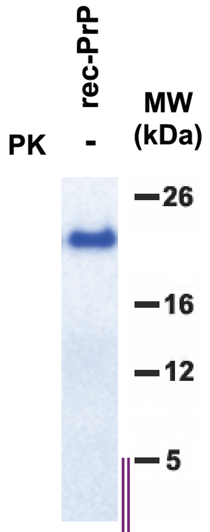
No insertions

No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

ΔΔG: ND

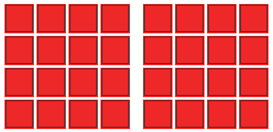


215 AA

NO MISFOLDING

0

Conformers



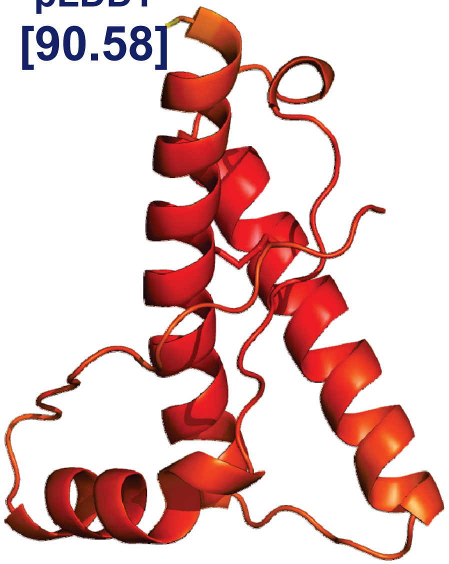
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [90.58]



Protein code: 3918

Distinct primary sequence across species

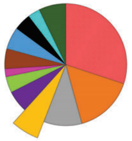
Agile gracile opossum

GenBank: BK063958

Gracilinanus agilis

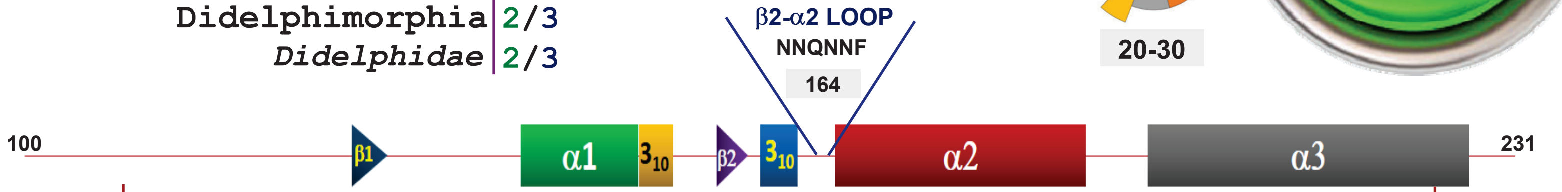
`Didelphimorphia` 2/3
`Didelphidae` 2/3

P57%



20-30

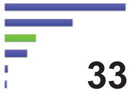
22.9



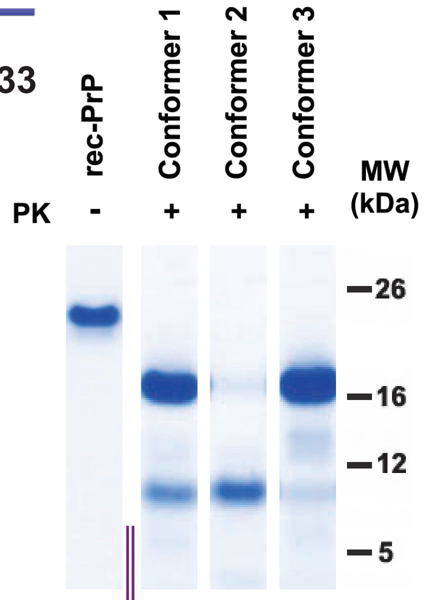
```
KWKPDKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPIMHFGNDYEDRYYRENQYRYPNQVMYRPIEQYNNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEQRAAYS-
WN  S      I                             MI     W          MN        Y   VD                        I     V                 V M          V     K SQ Y EG
```

PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

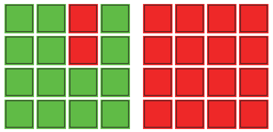


33



214 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Ongoing

Agile gracile opossum Not tested

In vivo studies

TgVole (1x) Ongoing

Agile gracile opossum Not tested

pLDDT
[87.25]

Protein code: 3086

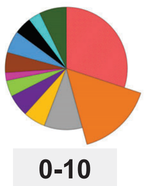
Opossum

GenBank: NM_001040028

Monodelphis domestica

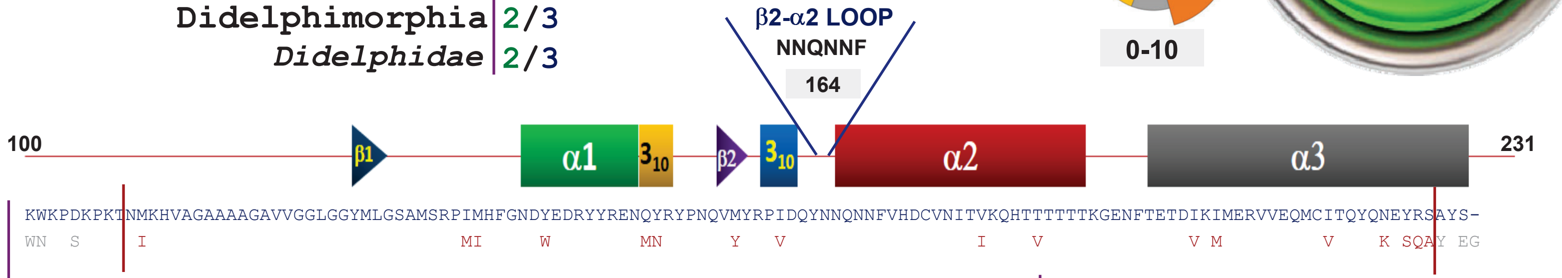
Didelphimorphia 2/3
Didelphidae 2/3

P39%



3.6

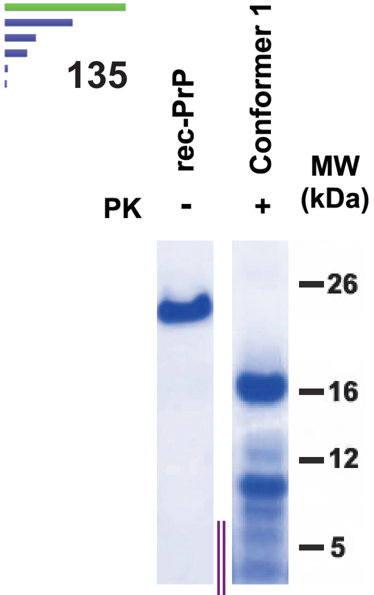
Distinct primary sequence across species



KWKPDKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPIMHFGNDYEDRYYRENQYRYPNQVMYRPIDQYNNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYRSAYS-
WN S I MI W MN Y V I V V M V K SQAY EG

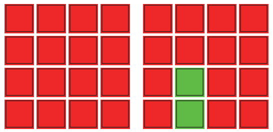
PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
It shows polymorphic variants



215 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

No propagation
TgVole (1x)

Not tested
Opossum

In vivo studies

Non infectious
TgVole (1x)

Not tested
Opossum

pLDDT
[93.24]

Protein code: 0398

Woylie

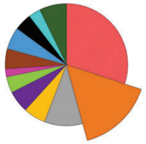
GenBank: **BK064808**

Bettongia penicillata ogilbyi

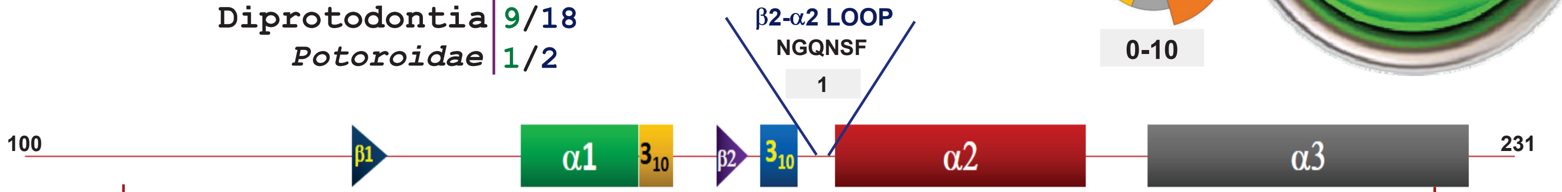
Diprotodontia 9/18
Potoroidae 1/2

Distinct primary sequence across species

P45%


0-10

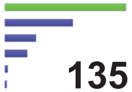
9.8

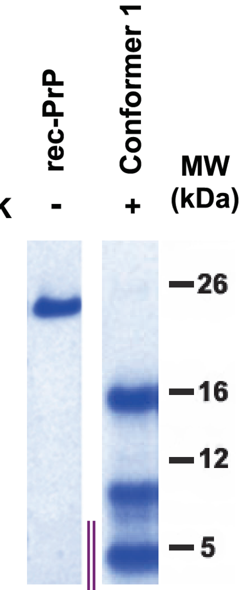


```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVIHFGNEYEDRYYRENQYRYPNQVMYRPIDQYNGQNSFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAQRYYNM-
WN  S     I                             M     DW        MN      Y   V    N  N         I    V             V M         V    K S  YYEGRSS
```

PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

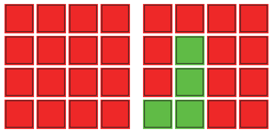
No deletions
No insertions
No polymorphic variants found


135



216 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x)	Not tested
Woylie	Not tested

In vivo studies

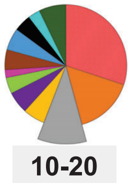
TgVole (1x)	Not tested
Woylie	Not tested

pLDDT
[92.82]

Protein code: 3976

Western pygmy possum

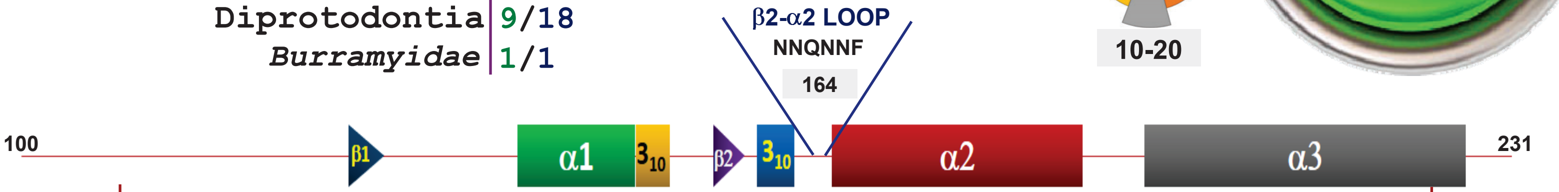
GenBank: **BK064813**



P46%

Cercartetus concinnus

`Diprotodontia` 9/18
`Burramyidae` 1/1



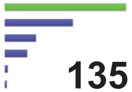
`KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGNAMSRPPIHFGNEYEDRYYRENQNRYPNQVMYRPIDQYNNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQAEYQAAQRGYN-`

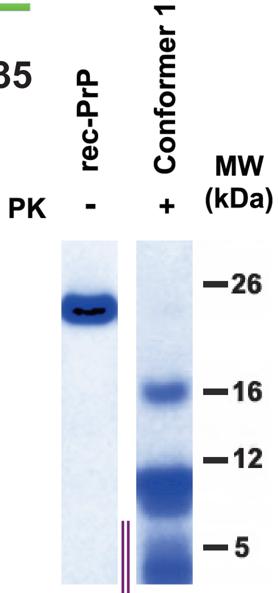
`WN S I S M DW M Y V I V V M V K S YYE RSS`

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

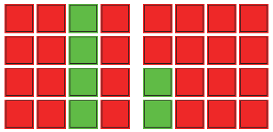
Distinct primary sequence across species





212 AA

1
Conformers



Tm^{Exp}: ND
ΔΔG: ND

***In vitro* studies**

TgVole (1x) **Propagate**

Western pygmy possum **Not tested**

***In vivo* studies**

TgVole (1x) **Infectious**

Western pygmy possum **Not tested**

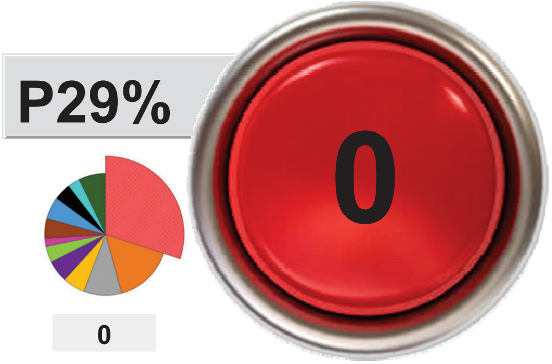
pLDDT
[86.86]

Protein code: 4104

Matschie's tree-kangaroo

GenBank: BK064823

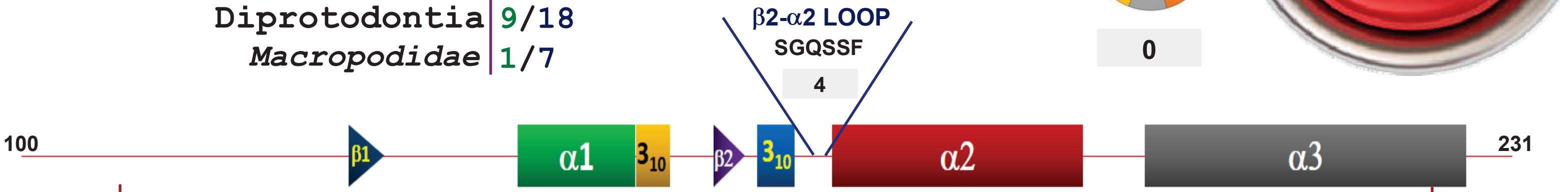
P29%



Dendrolagus matschiei

Diprotodontia 9/18
Macropodidae 1/7

Distinct primary sequence across species



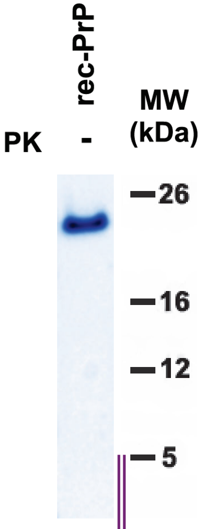
```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVIHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSGQSSFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAQRYYNM-
WN  S     I                                M      DW        MN      Y   V    NN NN          I    V                V M          V    K S  YYEGRSS
```

PrP sequence differs by 19 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -23.84



216 AA

NO MISFOLDING

0 Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [94.09]

Protein code: 4627

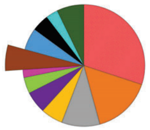
Leadbeater's possum

GenBank: BK064074

Gymnobelideus leadbeateri

Diprotodontia 9/18
Petauridae 1/2

P74%



60-70

60.2

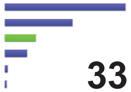
β2-α2 LOOP
SSQSNF
1

```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSSQSNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAAQRGYN-
WN  S     I                            MI    DW        MN      Y   V   NN N          I    V             V M         V    K S   YYEGRSS
```

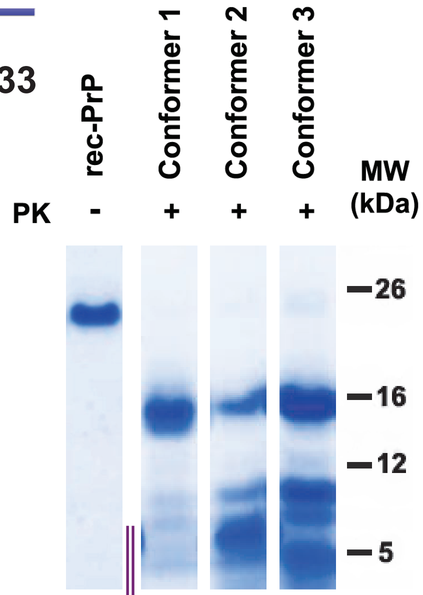
PrP sequence differs by 19 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

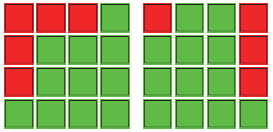


33



215 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: ND

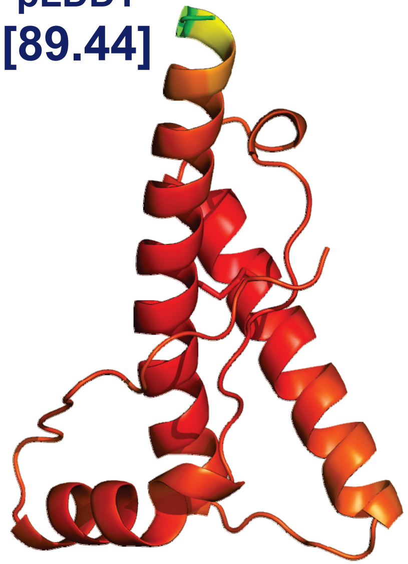
In vitro studies

TgVole (1x)	Not tested
Leadbeater's possum	Not tested

In vivo studies

TgVole (1x)	Not tested
Leadbeater's possum	Not tested

pLDDT
[89.44]



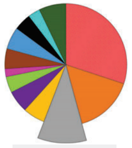
Protein code: 3252

Rufous hare-wallaby

GenBank: BK064777

P48%

12.5



10-20

Lagorchestes hirsutus

Diprotodontia 9/18
Macropodidae 1/7

Distinct primary sequence across species

β2-α2 LOOP
SGQNSF
3

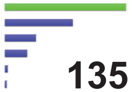
```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSGQNSFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAQRYYNM-
WN  S     I                            MI    DW        MN      Y   V   NN  N         I    V             V M         V    K S  YYEGRSS
```

PrP sequence differs by 19 amino acids from the bank vole PrP (see in red)

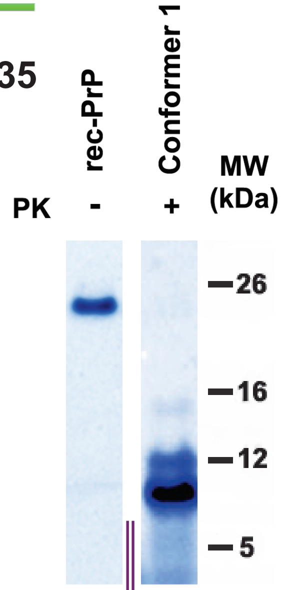
No deletions

No insertions

No polymorphic variants found

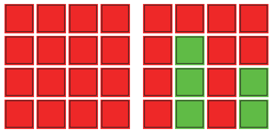


135



216 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

Not tested
TgVole (1x)

Not tested
Rufous hare-wallaby

In vivo studies

Not tested
TgVole (1x)

Not tested
Rufous hare-wallaby

pLDDT
[92.38]

Protein code: 3934

Wallaby

GenBank: AY659988

Macropus eugenii

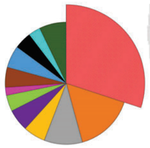
Diprotodontia 9/18
Macropodidae 1/7

2 species sharing the same primary sequence

Western Brush Wallaby
Macropus irma

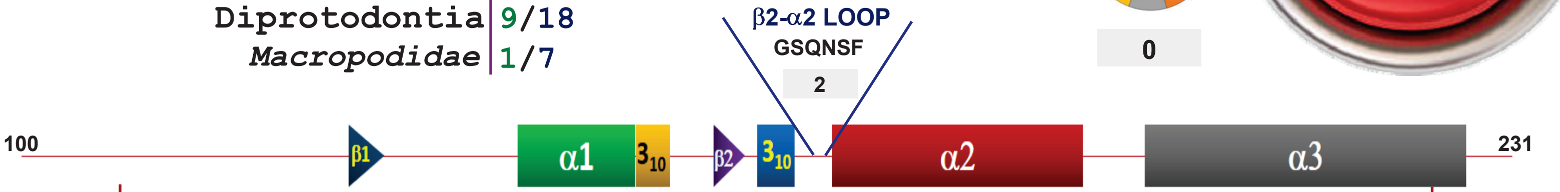
Red-necked wallaby
Macropus rufogriseus

P29%



0

0



```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYGSQNSFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAQRYYNM-
WN  S    I                              MI    DW        MN     Y   V   NN  N          I    V                V M         V    K S YYEGRSS
```

PrP sequence differs by 19 amino acids from the bank vole PrP (see in red)

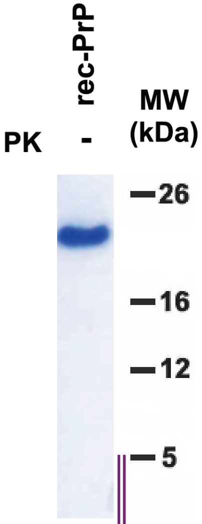
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



216 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[92.2]

Protein code: 3333

Eastern grey kangaroo

GenBank: BK064781

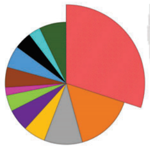
Macropus giganteus

Diprotodontia 9/18
Macropodidae 1/7

1 species sharing the same primary sequence

Western grey kangaroo
Macropus fuliginosus

P29%



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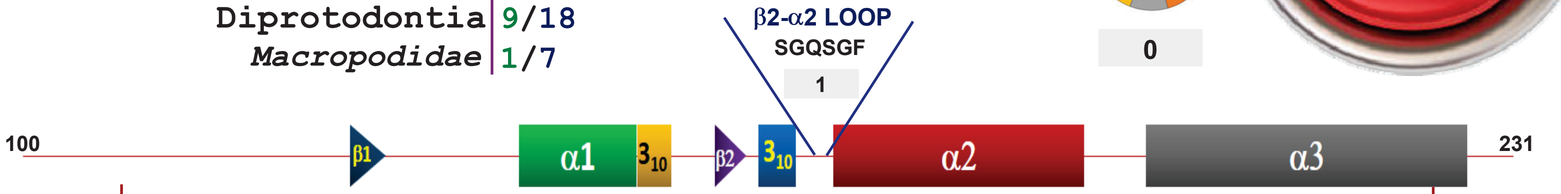
0



KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSGQSGFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAQRYYNM-

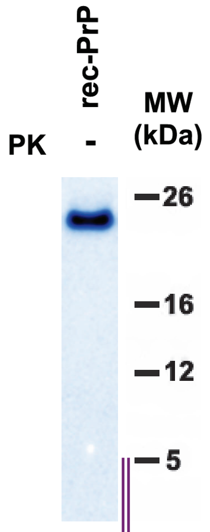
WN S I MI DW MN Y V NN NN I V V M V K S YYEGRSS

PrP sequence differs by 20 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



216 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[92.16]

Protein code: 3938

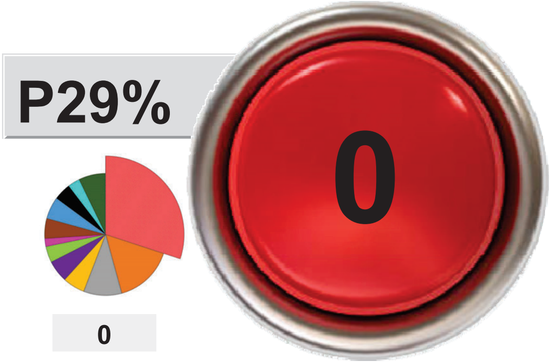
Red kangaroo

GenBank: OR47271

Macropus rufus

Diprotodontia 9/18
Macropodidae 1/7

P29%



β2-α2 LOOP
SGQSSF
4

```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYVLGSAMSRPVMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSGQSSFVHDCVNITVKEHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAQRYYNM-
WN  S     I                   M        MI    DW        MN      Y   V   NN NN         I Q  V             V M         V    K S  YYEGRSS
```

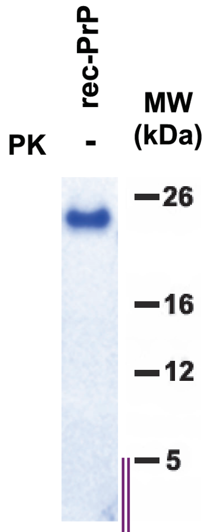
PrP sequence differs by 22 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

ΔΔG: ND



216 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[91.7]

Protein code: 3775

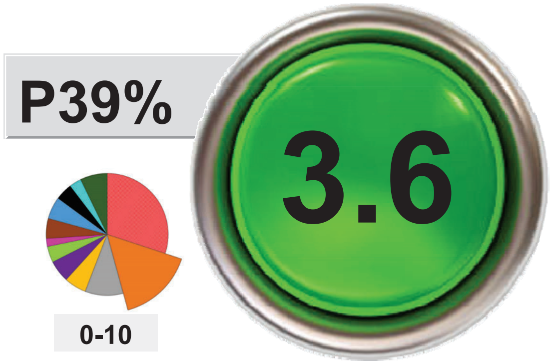
Distinct primary sequence across species

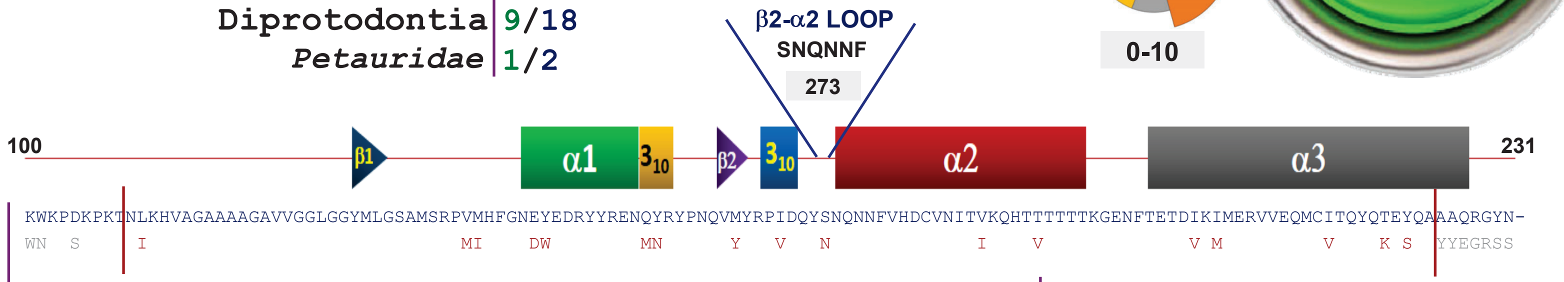
Sugar glider

GenBank: BK064219

Petaurus breviceps

Diprotodontia	9/18
Petauridae	1/2





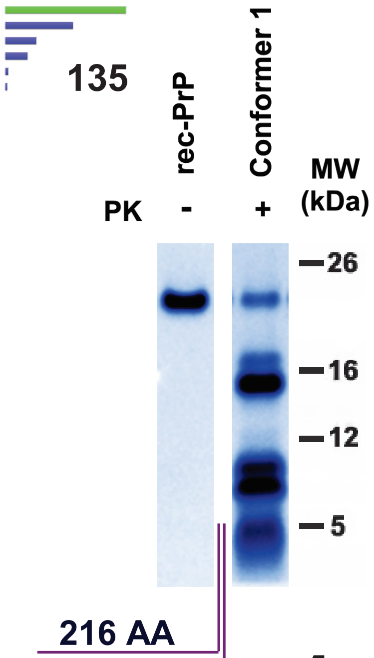
```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQTEYQAAAQRGYN-
WN  S   I                             MI    DW       MN     Y  V  N             I   V           V M         V   K S  YYEGRSS
```

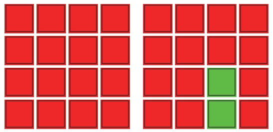
PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found





Tm^{Exp}: ND

ΔΔG: -22.28

In vitro studies

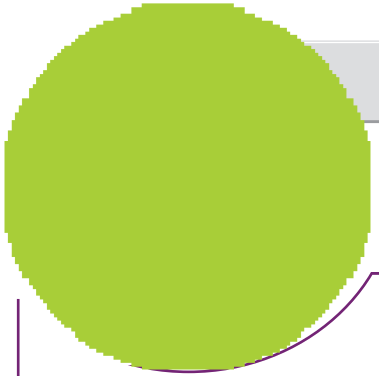
TgVole (1x)	Not tested
Sugar glider	Not tested

In vivo studies

TgVole (1x)	Not tested
Sugar glider	Not tested

pLDDT
[93.64]

Protein code: 4816



Yellow-footed rock-wallaby

GenBank: OR47266

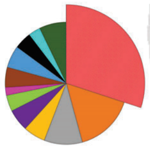
Petrogale xanthopus

Diprotodontia 9/18
Macropodidae 1/7

Swamp wallaby
Wallabia bicolor

1 species sharing the same primary sequence

P29%



0

β2-α2 LOOP
SGQSSF
4

```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSGQSSFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAQRYYNM-
WN  S   I                               MI   DW        MN     Y   V   NN NN           I    V                 V M         V    K S YYEGRSS
```

PrP sequence differs by 20 amino acids from the bank vole PrP (see in red)

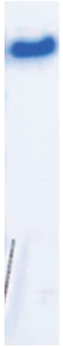
No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND

PK **rec-PrP** **-**

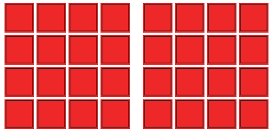
MW (kDa)



216 AA

NO MISFOLDING

0
Conformers



In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [92.57]

Protein code: 3762

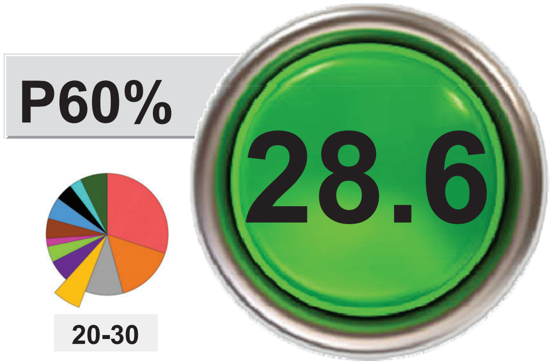
Ground cuscus

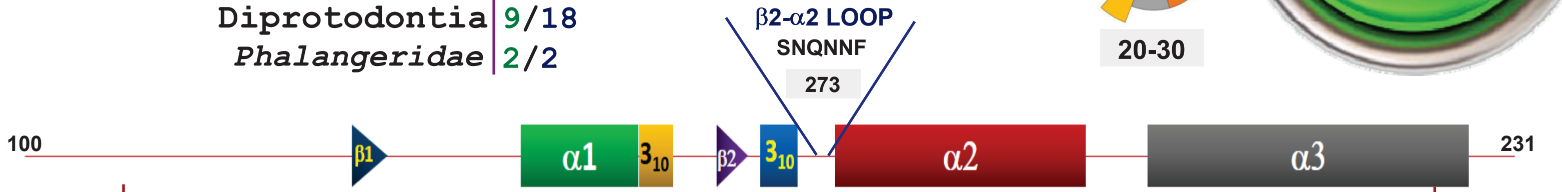
GenBank: BK064791

Phalanger gymnotis

Diprotodontia 9/18

Phalangeridae 2/2





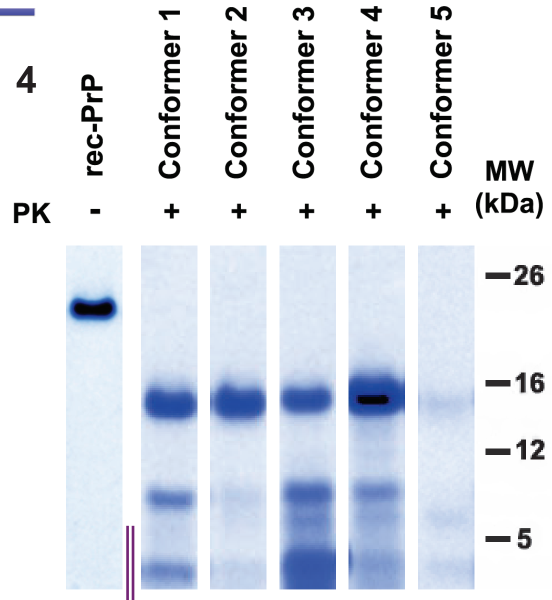
```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVIHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQAEYQAAQRGYN-
WN  S     I                            M    DW         MN      Y   V   N            I    V             V M         V    K S  YYE RSS
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

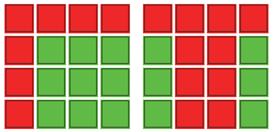
No deletions

No insertions

No polymorphic variants found



213 AA



5 Conformers

Tm^{Exp}: ND

ΔΔG: ND

***In vitro* studies**

TgVole (1x) Not tested

Ground cuscus Not tested

***In vivo* studies**

TgVole (1x) Not tested

Ground cuscus Not tested

pLDDT [89.54]

Distinct primary sequence across species

Protein code: 3956

Koala

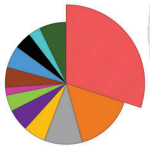
GenBank: XM_020985342

Phascolarctos cinereus

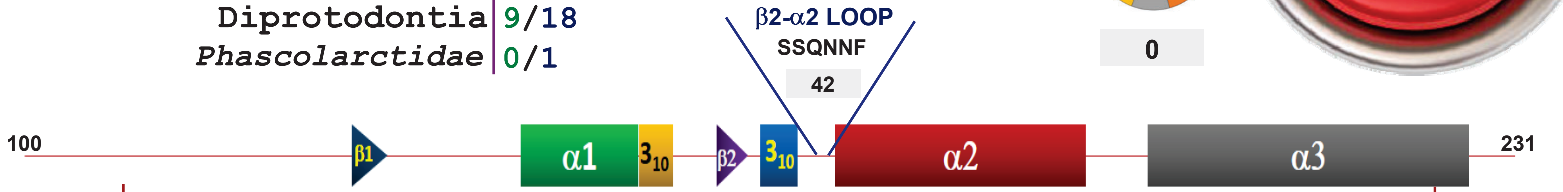
Diprotodontia 9/18
Phascolarctidae 0/1

Distinct primary sequence across species

P29%



0



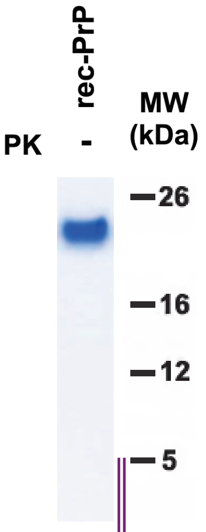
```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPIMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSSQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYRAAQQGYGY-
WN  S     I                            MI    DW        MN      Y   V   NN            I    V             V M         V    K SQ  YYE RSS
```

PrP sequence differs by 19 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

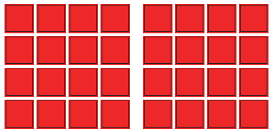
ΔΔG: ND



217 AA

NO MISFOLDING

0
Conformers



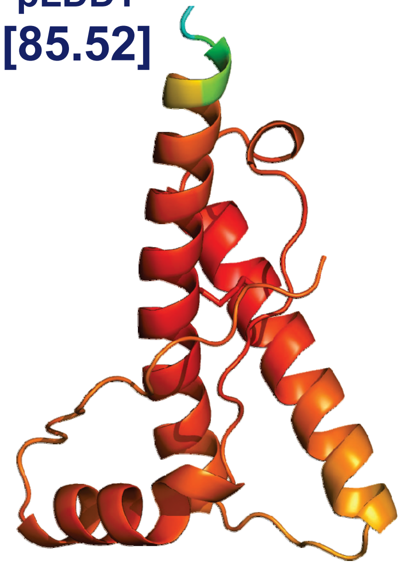
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [85.52]



Protein code: 0935

Gilbert's potoroo

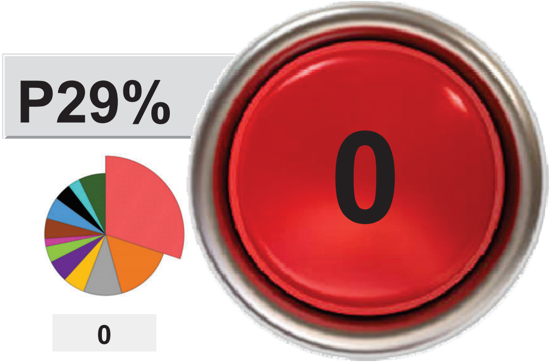
GenBank: BK064793

Potorous gilbertii

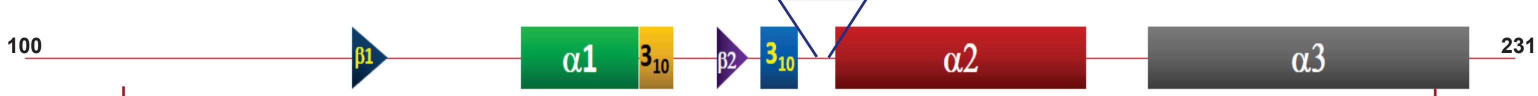
Diprotodontia 9/18
Potoroidae 1/2

Distinct primary sequence across species

P29%



β2-α2 LOOP
SGQNSF
3



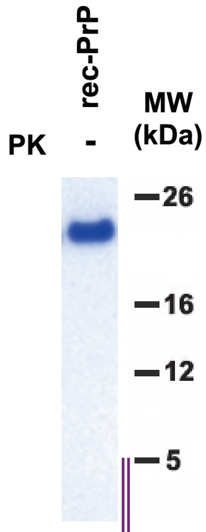
```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVIHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSGQNSFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAQRYYNM-
WN  S     I                            M    DW        MN       Y   V    NN N         I    V             V M          V    K S YYEGRSS
```

PrP sequence differs by 18 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



216 AA

NO MISFOLDING

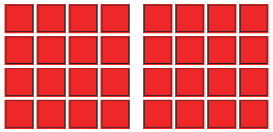
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

0
Conformers



pLDDT [92.95]

Protein code: 3958

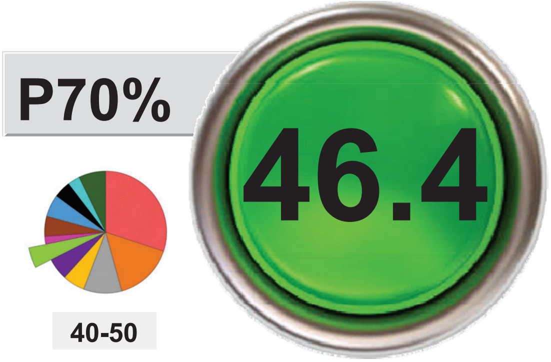
Western ringtail

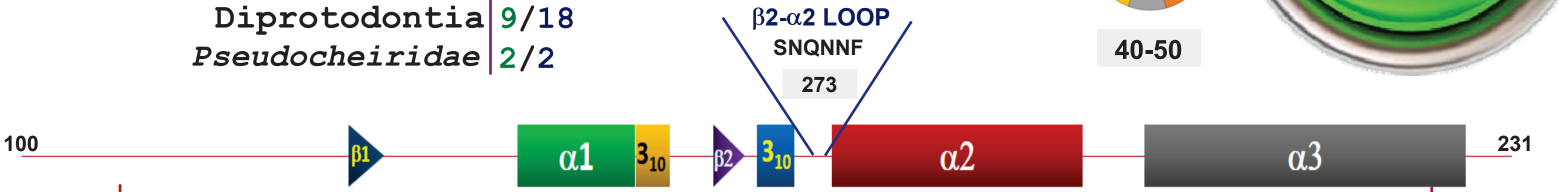
GenBank: BK064794

Pseudocheirus peregrinus

Diprotodontia 9/18
Pseudocheiridae 2/2

P70%



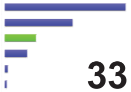


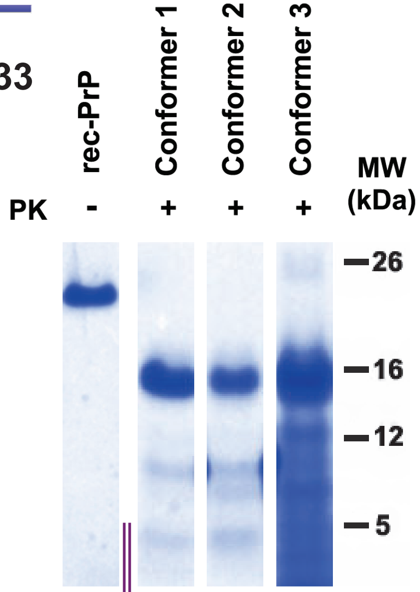
```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAAQRGYN-
WN  S    I                            MI   DW        MN    Y  V  N          I    V                V M         V   K S  YYEGRSS
```

PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

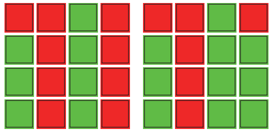
Distinct primary sequence across species





216 AA

3
Conformers



Tm^{Exp}: ND
ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

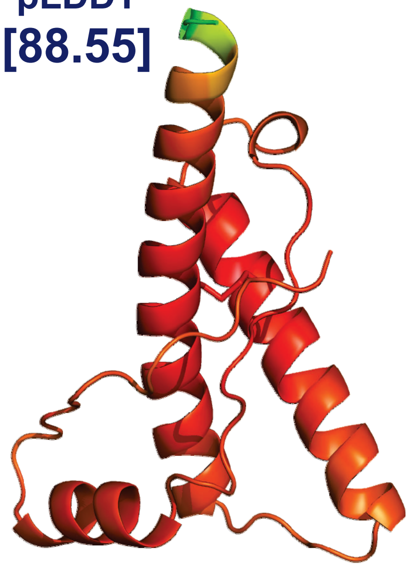
Western ringtail Not tested

In vivo studies

TgVole (1x) Not tested

Western ringtail Not tested

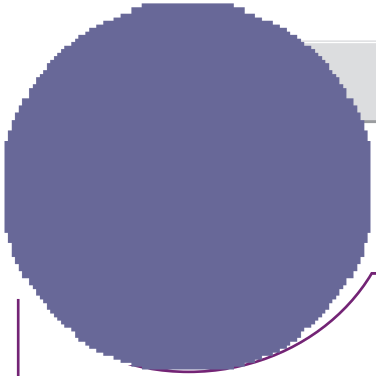
pLDDT
[88.55]



Protein code: 3959

Plush-coated ringtail possum

GenBank: BK064795



Pseudochirops corinnae

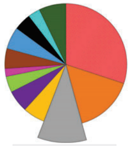
Diprotodontia 9/18
Pseudocheiridae 2/2

Coppery ringtail possum
Pseudochirops cupreus

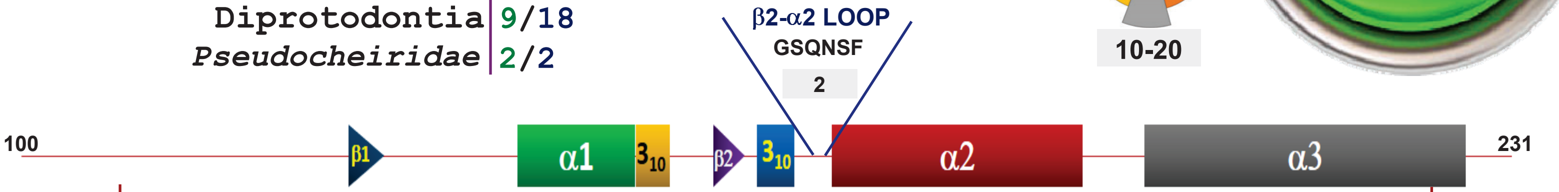
1 species sharing the same primary sequence

P49%

12.9



10-20

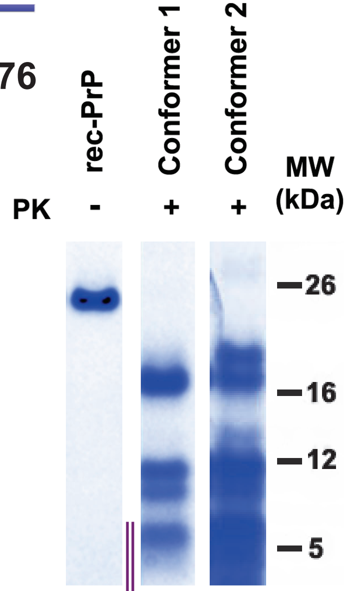


```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYGSQNSFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAAQRGYN-
WN  S    I                               MI    DW         MN      Y   V   NN  N         I    V                   V M         V    K S  YYEGRSS
```

PrP sequence differs by 19 amino acids from the bank vole PrP (see in red)

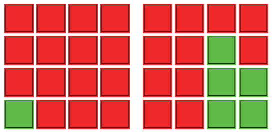
No deletions
No insertions
No polymorphic variants found

76



216 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

Plush-coated ringtail possum Not tested

In vivo studies

TgVole (1x) Not tested

Plush-coated ringtail possum Not tested

pLDDT
[88.63]

Protein code: 3960

Quokka

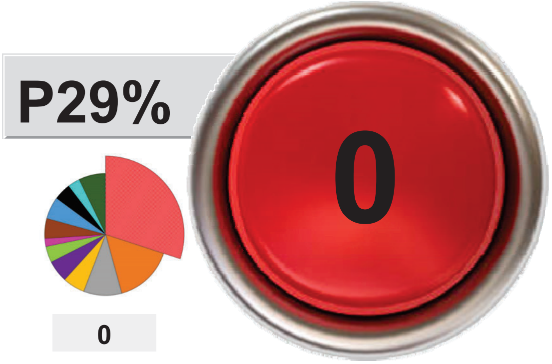
GenBank: BK064765

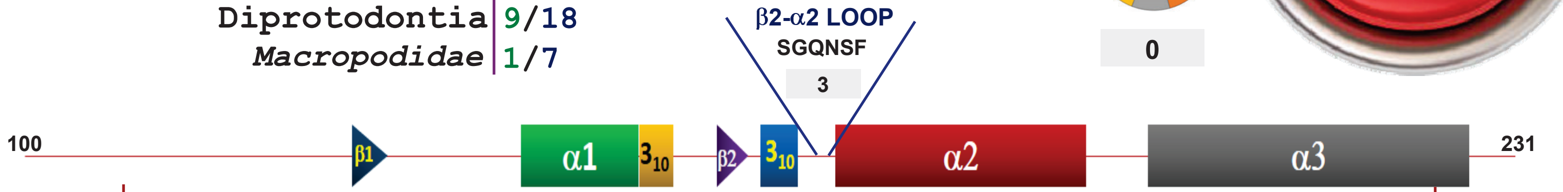
Setonix brachyurus

Diprotodontia 9/18

Macropodidae 1/7

P29%





```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYVLGSAMSRPVMHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSGQNSFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYQAAQRYYNM-
WN  S    I                  M         MI    DW         MN       Y   V   NN N         I    V              V M          V    K S YYEGRSS
```

PrP sequence differs by 20 amino acids from the bank vole PrP (see in red)

No deletions

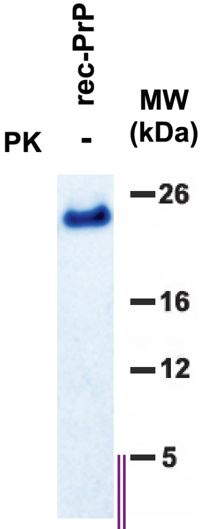
No insertions

No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

ΔΔG: ND



216 AA

NO MISFOLDING

0

Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT

[93.34]

Protein code: 3862

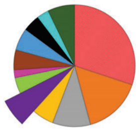
Common brushtail possum

GenBank: L38993

Trichosurus vulpecula

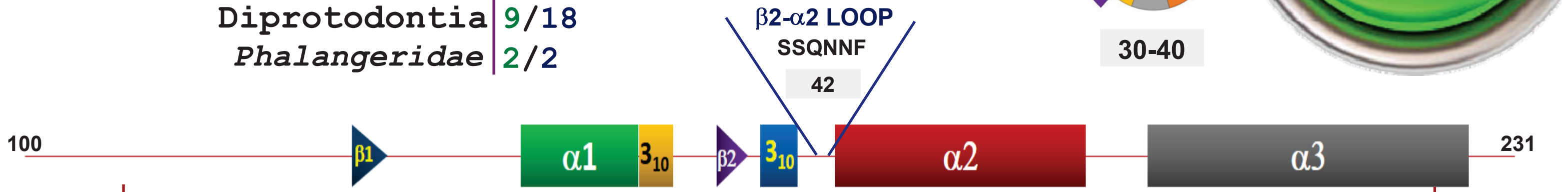
Diprotodontia 9/18
Phalangeridae 2/2

P64%



30-40

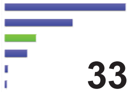
33.9



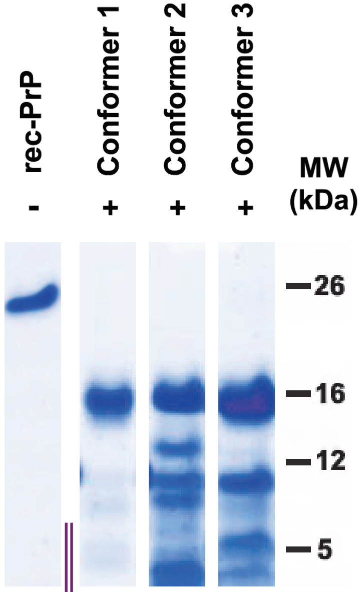
```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVIHFGNEYEDRYYRENQYRYPNQVMYRPIDQYSSQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQAEYEAAAQRAYN-
WN  S     I                           M     DW        MN      Y   V   NN              I   V           V M        V   K SQ YYEGRSS
```

PrP sequence differs by 18 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

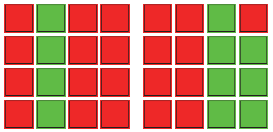


33



214 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

Common brushtail possum Not tested

In vivo studies

TgVole (1x) Not tested

Common brushtail possum Not tested

pLDDT
[92.87]

Distinct primary sequence across species

Protein code: 1335

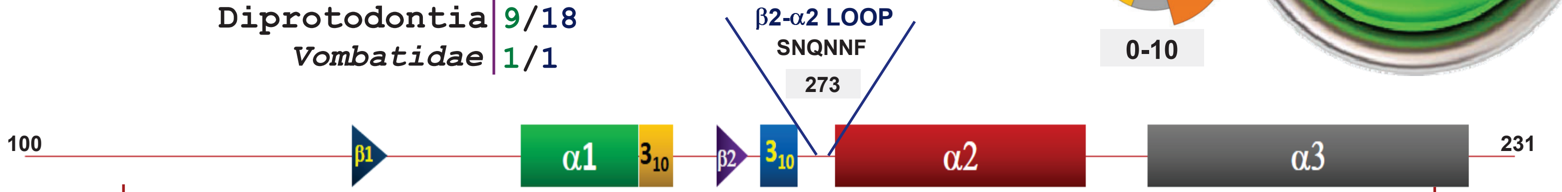
Common wombat

GenBank: XM_027865324

Vombatus ursinus

Diprotodontia 9/18
Vombatidae 1/1

Distinct primary sequence across species

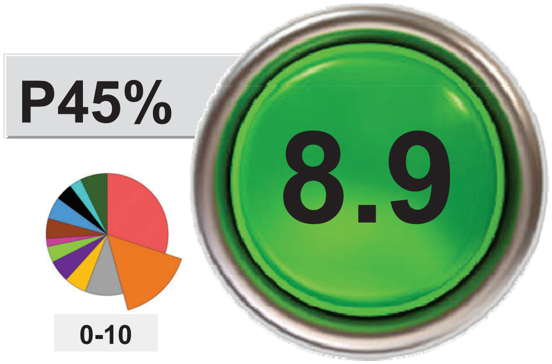


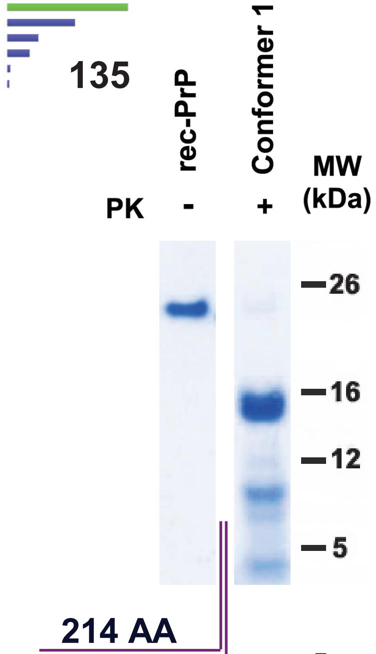
```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPVIHFGNDYEDRYYRENQYRYPNQVMYRPIDQYSNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYRAAQQGYYY-
WN  S     I                             M      W        MN      Y   V   N             I    V             V M         V    K SQ YYE RSS
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

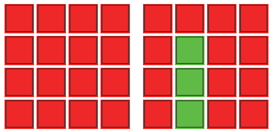
No deletions
No insertions
No polymorphic variants found

P45%





214 AA



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

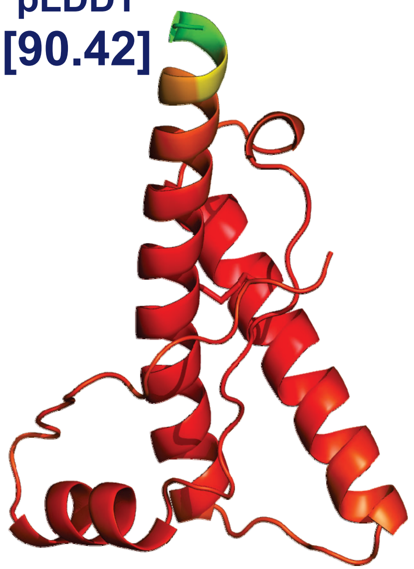
Common wombat Not tested

In vivo studies

TgVole (1x) Not tested

Common wombat Not tested

pLDDT
[90.42]



Protein code: 1100

Four-toed hedgehog

GenBank: OR47273

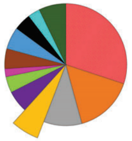
Atelerix albiventris

Erinaceomorpha 3/3
Erinaceidae 3/3

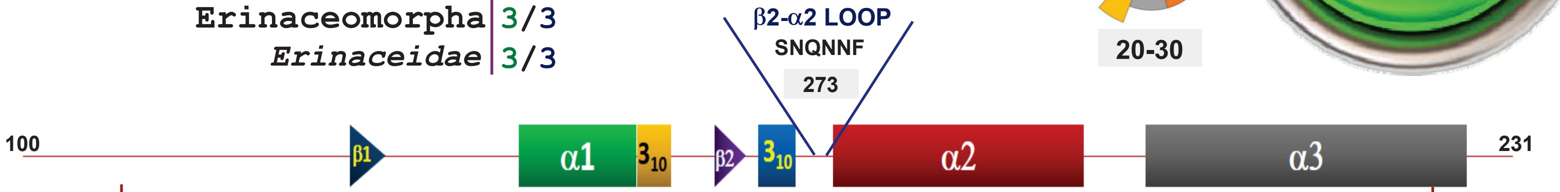
Distinct primary sequence across species

P58%

25.4



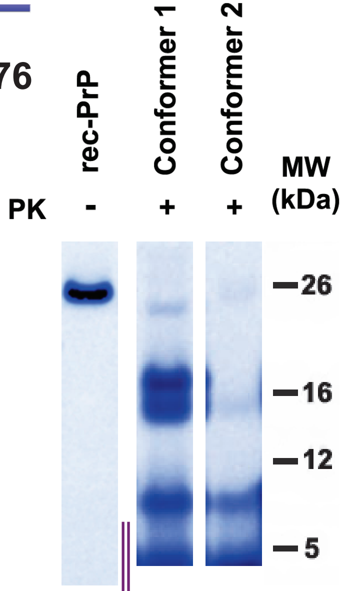
20-30



```
WNKPNKPKTNIKHVAGAAAAGAVVGGLGGYLVGSAMSRPPIHFGNDYEDRYYRENINRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQARAYHNGAS-
    S                         ML       M      W        M         R     N             I                  V M         V    KESQAYYEGRS
```

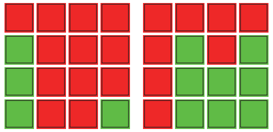
PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



226 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

Four-toed hedgehog Not tested

In vivo studies

TgVole (1x) Not tested

Four-toed hedgehog Not tested

pLDDT
[88.74]

Protein code: 4029

European hedgehog

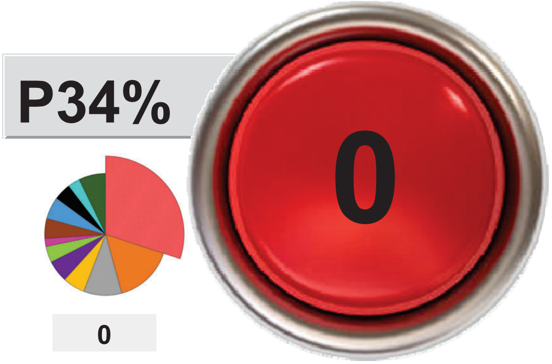
GenBank: EU572708

Erinaceus europaeus

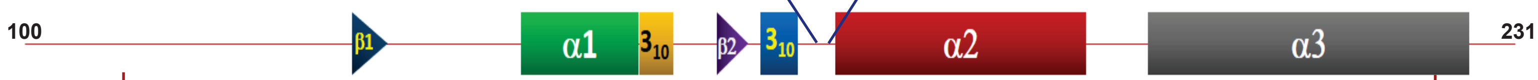
Erinaceomorpha 3/3
Erinaceidae 3/3

Distinct primary sequence across species

P34%



β2-α2 LOOP
SNQNNF
273



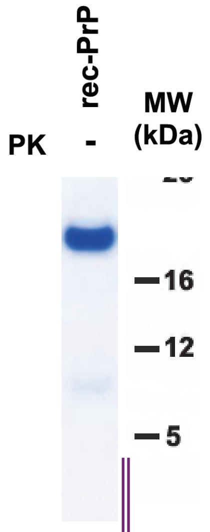
```
WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYLVGSAMSRPPIHFGNDYEDRYYRENINRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQQARAYHDGAS-
     S   I                ML           M       W           M          R      N             I                      M          V    KESQAYYEGRS
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

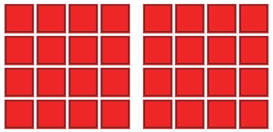
Tm^{Exp}: ND

ΔΔG: ND



216 AA

NO MISFOLDING



0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

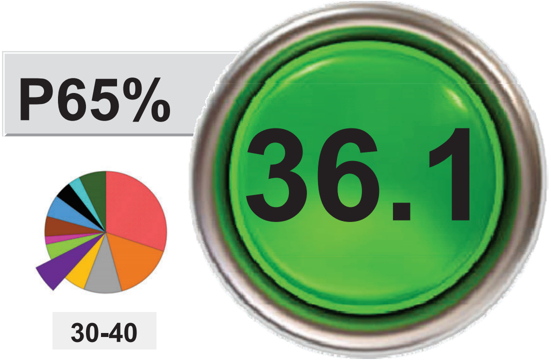
pLDDT
[90.76]

Protein code: 0931

Short-tailed gymnure

GenBank: AY133044

P65%

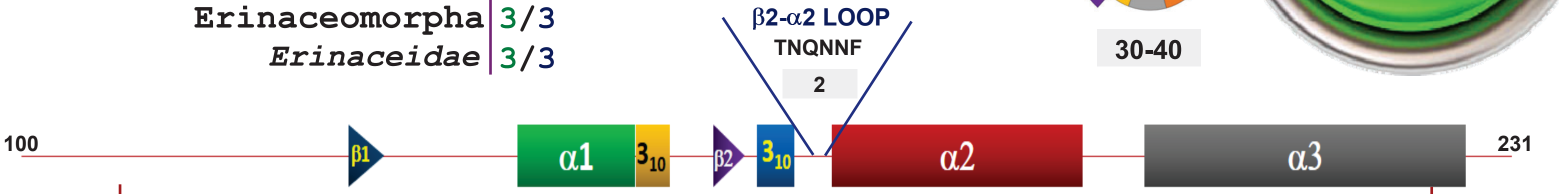


Hylomys suillus

Erinaceomorpha 3/3

Erinaceidae 3/3

Distinct primary sequence across species



WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPIIHFGNDYEDRYYRENMNRYPNQVYYRPVDQYTNQNNFVHDCTNITIKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQEAYRAYQQNHGT-

N I M W N V V M V KESQ YEGRSS

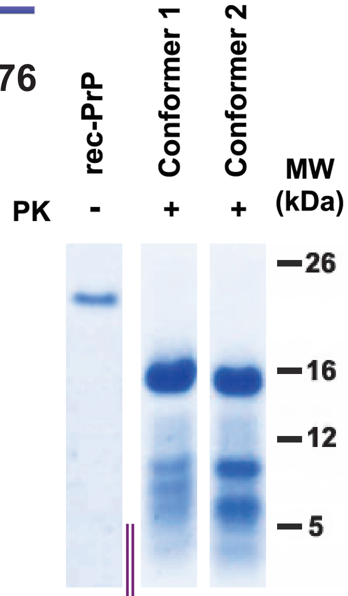
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

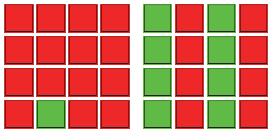
No polymorphic variants found

76



223 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -10.37

In vitro studies

TgVole (1x) Not tested

Short-tailed gymnure Not tested

In vivo studies

TgVole (1x) Not tested

Short-tailed gymnure Not tested

pLDDT
[90.72]

Protein code: 1344

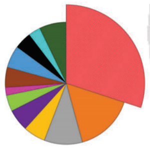
Rock hyrax

GenBank: AY133057

Procavia capensis

Hyracoidea 0/1
Procaviidae 0/1

P29%



0

0

1 species sharing the same primary sequence

Yellow-spotted rock hyrax
Heterohyrax brucei

β2-α2 LOOP
SSENNF
8

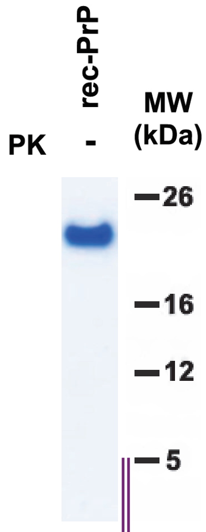
```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVNEYSSENNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCMTQYQKEFQAYQRGSS-
 N        I                             M       W          N            DQ  NNQ         I                        V M          V       S   YE R S
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



211 AA

NO MISFOLDING

0
Conformers

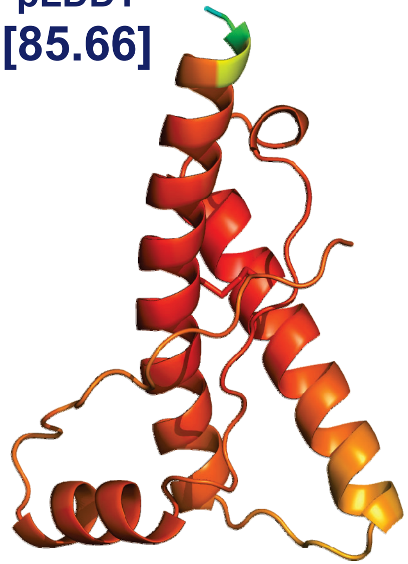
***In vitro* studies**

NOT APPLICABLE

***In vivo* studies**

NOT APPLICABLE

pLDDT
[85.66]



Protein code: 0952

Brown hare

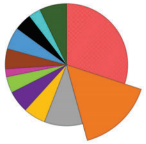
GenBank: OR472454

Lepus europaeus

Lagomorpha 4/5
Leporidae 3/4

P40%

5.9



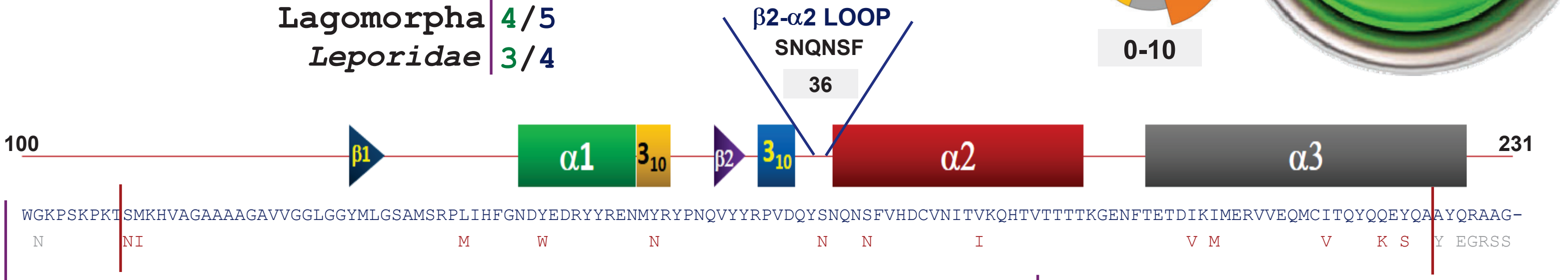
0-10

3 species sharing the same primary sequence

Snowshoe hare
Lepus americanus

Mountain hare
Lepus timidus

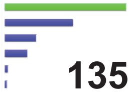
White-tailed jackrabbit
Lepus townsendii



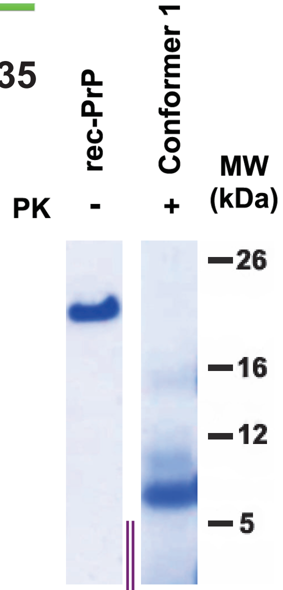
```
WGKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQEYQAAYQRAAG-
 N       NI                             M     W          N                N   N         I                  V M         V    K S  Y EGRSS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

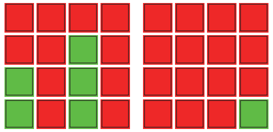
No deletions
No insertions
No polymorphic variants found



135



210 AA



1
Conformers

Tm^{Exp}: ND

ΔΔG: -17.76

In vitro studies

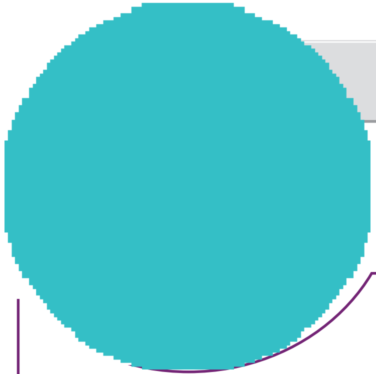
TgVole (1x)	Not tested
Brown hare	Not tested

In vivo studies

TgVole (1x)	Not tested
Brown hare	Not tested

pLDDT
[90.29]

Protein code: 0533



American pika

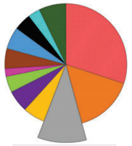
GenBank: EU555402

Ochotona princeps

Lagomorpha 4/5
Ochotonidae 1/1

P53%

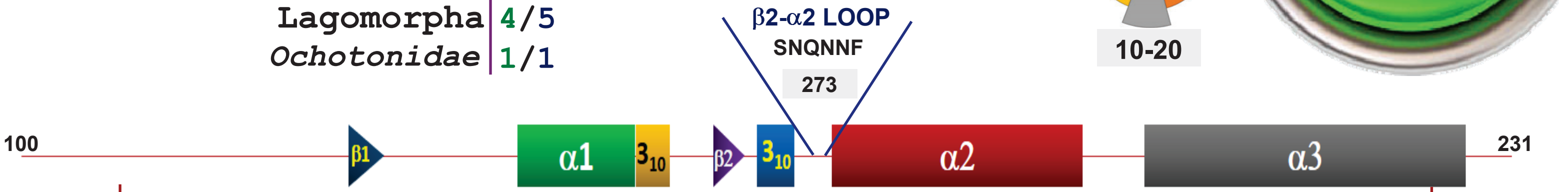
17.9



10-20

Plateau pika
Ochotona curzoniae

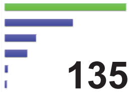
1 species sharing the same primary sequence



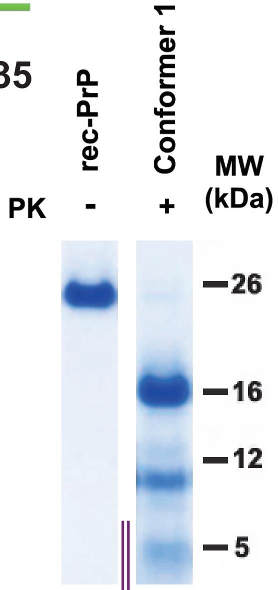
```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPIIHFGNEYEDRYYRDNMYRYPNQVYYKPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDIKMMERVVEQMCVTQYQQEYQASYQRAAS-
 N       I                                M      DW      E  N        R      N                                V                   K S  Y EGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

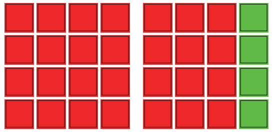


135



210 AA

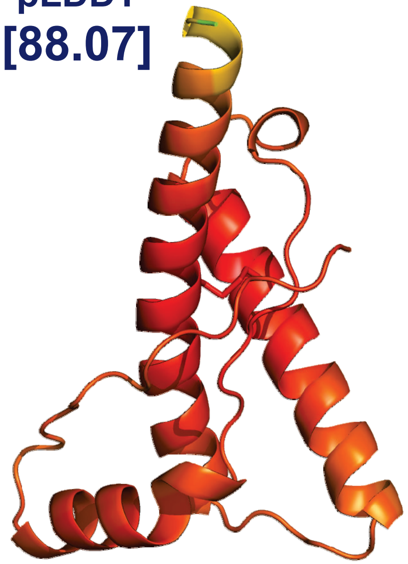
1
Conformers



Tm^{Exp}: ND

ΔΔG: -12.67

pLDDT
[88.07]



In vitro studies

TgVole (1x)	Not tested
American pika	Not tested

In vivo studies

TgVole (1x)	Not tested
American pika	Not tested

Protein code: 1140

Rabbit

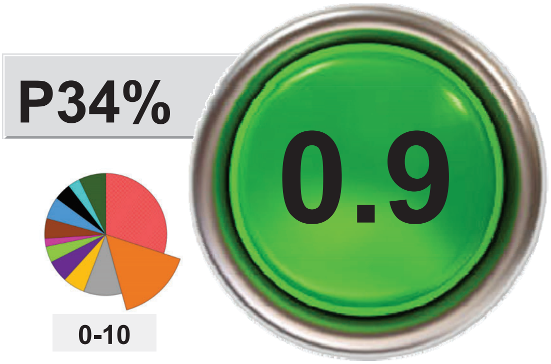
GenBank: NM_001082021

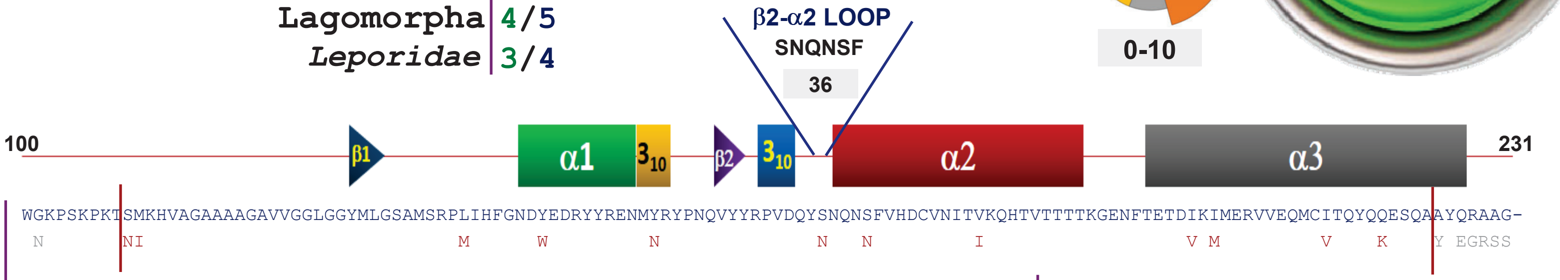
Oryctolagus cuniculus

Lagomorpha 4/5
Leporidae 3/4

Distinct primary sequence across species

P34%





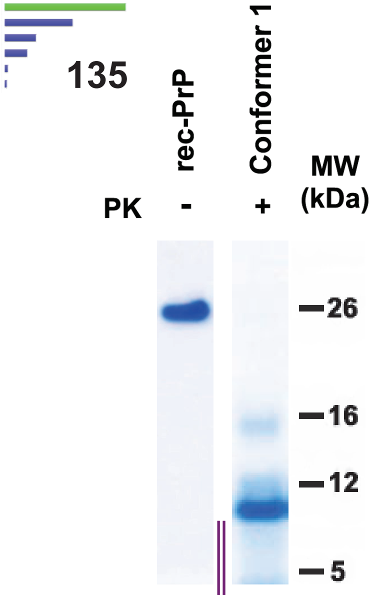
WGKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQESQAAYQRAAG-

N NI M W N N N I V M V K Y EGRSS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

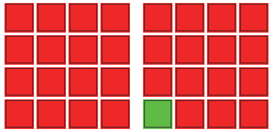
No deletions
No insertions
No polymorphic variants found

135



210 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -13.56

In vitro studies

TgVole (1x)	Propagate
Rabbit	Ongoing

In vivo studies

TgVole (1x)	Infectious
TgRabbit	Ongoing

pLDDT
[89.85]

Protein code: 0135

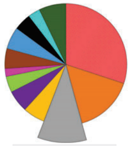
Brush rabbit

GenBank: BK063974

Sylvilagus bachmani

Lagomorpha 4/5
Leporidae 3/4

P49%



10-20

12.5

β2-α2 LOOP
SNQNSF
36

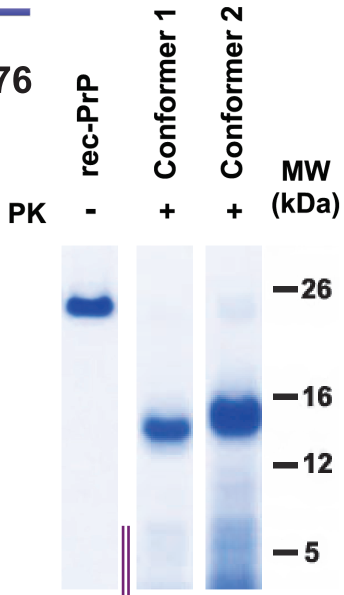
```
WGKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVEQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQEYQAAYQRAAG-
 N        NI                              M      W          N           D  N   N          I                      V M          V     K S   Y EGRSS
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

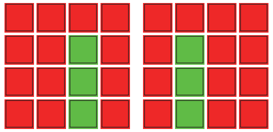
Distinct primary sequence across species

76



210 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -15.86

***In vitro* studies**

TgVole (1x) Not tested

Brush rabbit Not tested

***In vivo* studies**

TgVole (1x) Not tested

Brush rabbit Not tested

pLDDT [89.61]

Protein code: 3131

Distinct primary sequence across species

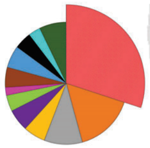
New England cottontail

GenBank: BK064962

Sylvilagus transitionalis

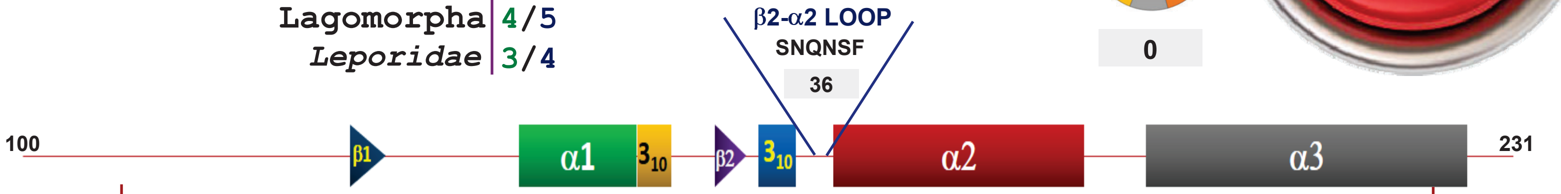
Lagomorpha 4/5
Leporidae 3/4

P29%



0

0



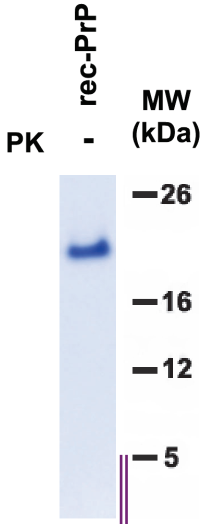
```
WGKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQEYQAAYQRGAS-
 N       NI                          M      W         N                 N   N         I                     V M          V    K S  Y EGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -18.5



210 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[92.35]

Protein code: 4742

Cape elephant shrew

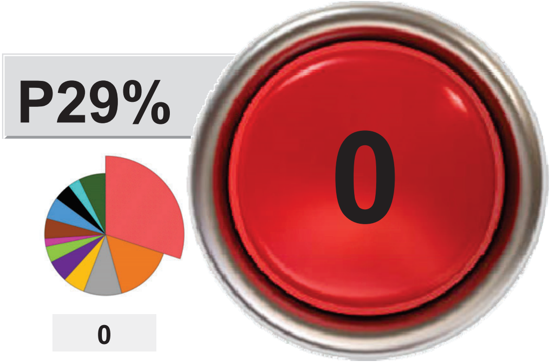
GenBank: XM_006894222

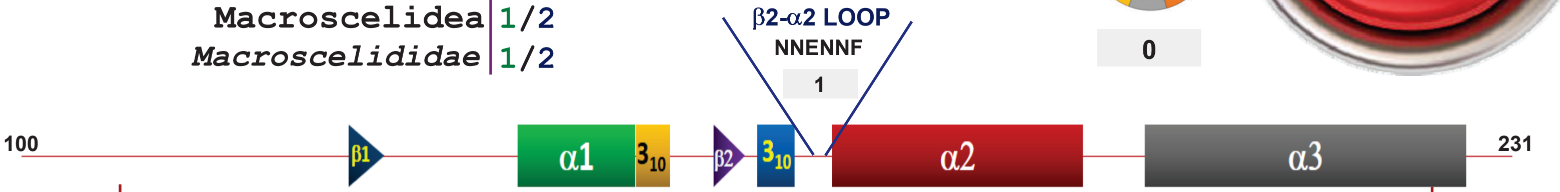
Elephantulus edwardii

`Macroscelidea` 1/2
`Macroscelididae` 1/2

Distinct primary sequence across species

P29%





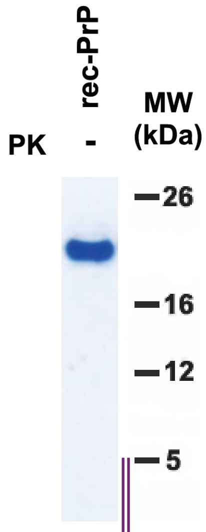
```
WGKPNKPKTNMKNMAGAAAAGAVVGGLGGYMLGSAMSRPPMHFGNDYEDRYYRENMNRYPNQVYYKPVNQYNNENNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQKESMAYQRGSS-
 N  S     I HV                         MI     W                  R  D    Q           I    V             V M         V       Q  YE R S
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



213 AA

NO MISFOLDING

0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[88.74]

Protein code: 0972

Distinct primary sequence across species

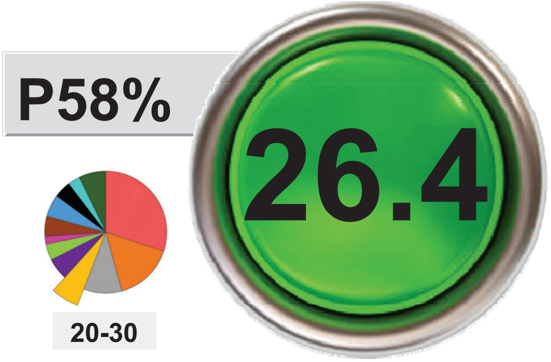
Round-eared elephant shrew

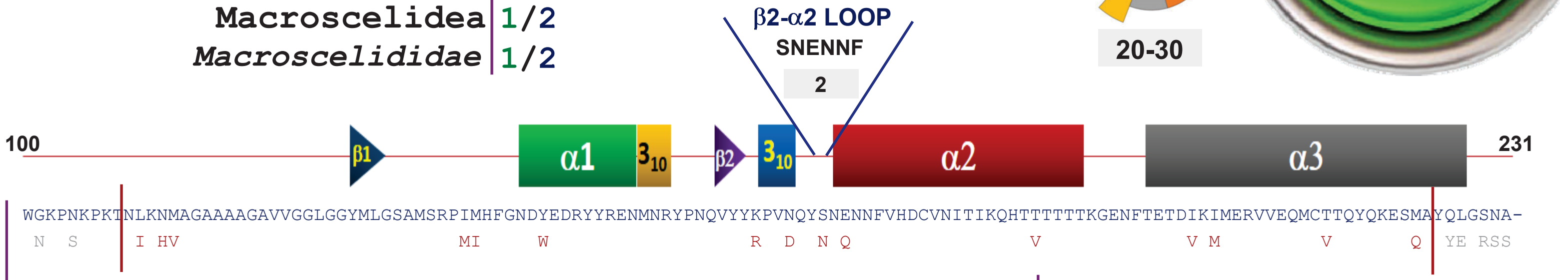
GenBank: AY133059

Macroscelides proboscideus

Macroscelidea 1/2
Macroscelididae 1/2

P58%

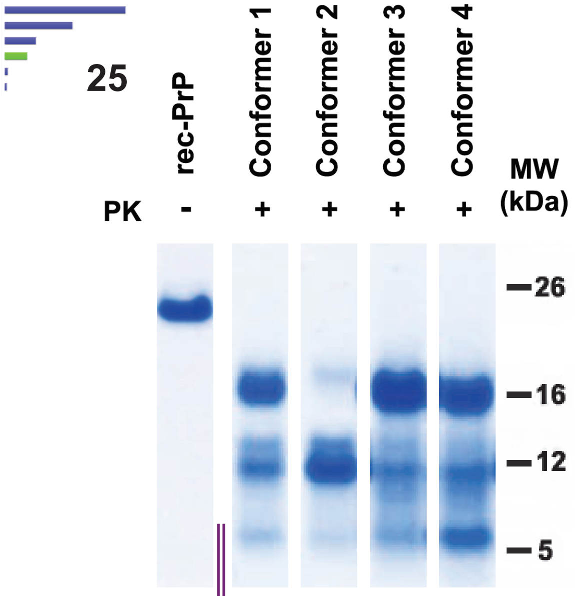




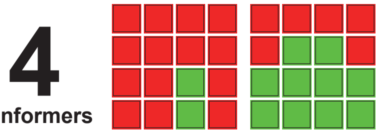
```
WGKPNKPKTNLKNMAGAAAAGAVVGGLGGYMLGSAMSRPIMHFGNDYEDRYYRENMNRYPNQVYYKPVNQYSNENNFVHDCVNITIKQHTTTTTTKGENFTETDIKIMERVVEQMCTTQYQKESMAYQLGSNA-
 N  S    I HV                         MI   W                   R  D  N Q                 V                V M       V       Q  YE RSS
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



215 AA



Tm^{Exp}: ND

ΔΔG: -9.98

***In vitro* studies**

Not tested
TgVole (1x)

Not tested
Round-eared elephant shrew

***In vivo* studies**

Not tested
TgVole (1x)

Not tested
Round-eared elephant shrew

pLDDT
[89.61]

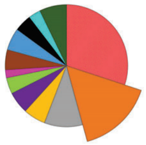
Protein code: 1343

Colocolo opossum

GenBank: BK064161

P39%

3.6



0-10

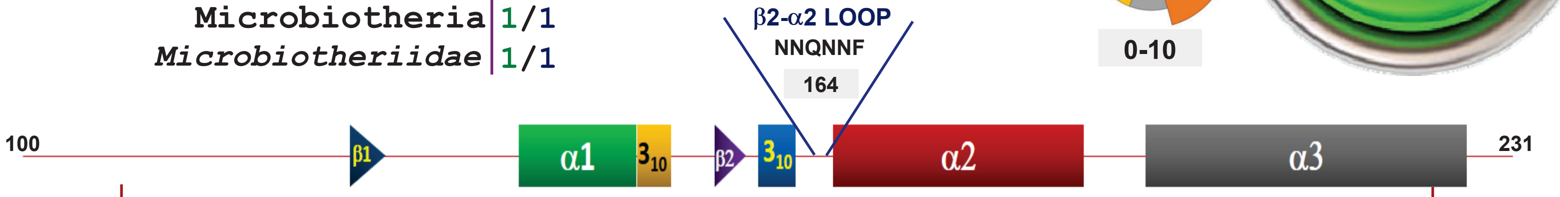
Dromiciops gliroides

Microbiotheria 1/1

Microbiotheriidae 1/1

1 species sharing the same primary sequence

Pancho's colocolo opossum
Dromiciops bozinovici



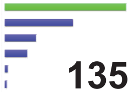
```
KWKPDKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPAMHFGNDYEDRYYRENQNRYPNQVMYRPVDQYNNQNNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEQRAAQYNYNI-
WN  S   I                               MI    W         M       Y                        I    V                   V M          V     K SQ YYEGRSS
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

No deletions

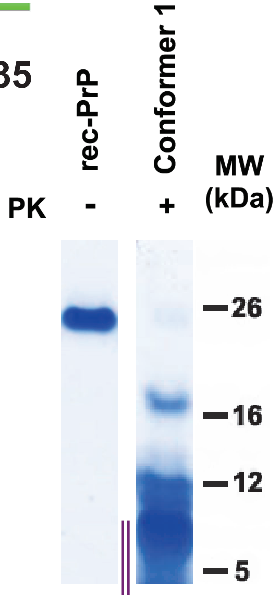
No insertions

No polymorphic variants found



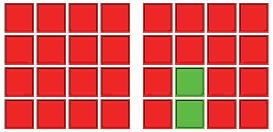
135

202 AA



1

Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

No propagation
TgVole (1x)

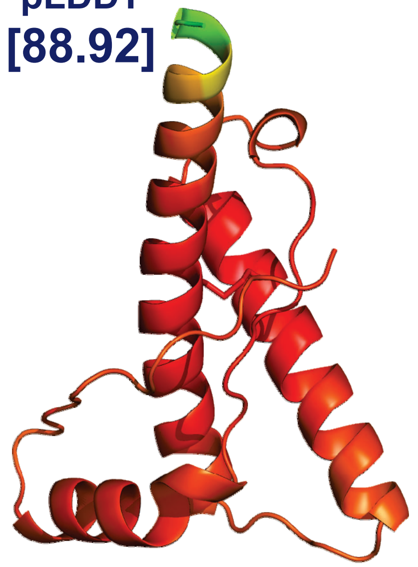
Not tested
Colocolo opossum

In vivo studies

Ongoing
TgVole (1x)

Not tested
Colocolo opossum

pLDDT
[88.92]



Protein code: 3732

Platypus

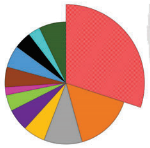
GenBank: XM_029065640

Ornithorhynchus anatinus

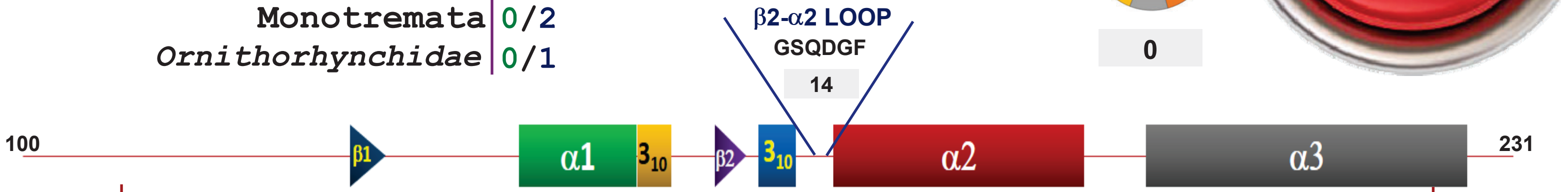
Monotremata 0/2
Ornithorhynchidae 0/1

P29%

0



0



```
KYKPDKPKTGMKHVAGAAAAGAVVGGLGGYMIGSAMSRPPMHFGNEFEDRYYRENQNRYPNQVYYRPVDQYGSQDGFVRDCVNITVTQHTVTTTE GKNLNETDVKIMTRVVEQMCVNQYRAEYQARSS-
WN  S    NI                    L       MI    DW        M               NN NN  H      IK       TK E FT     M E        T  QK S  YYEG
```

PrP sequence differs by 26 amino acids from the bank vole PrP (see in red)

One deletion

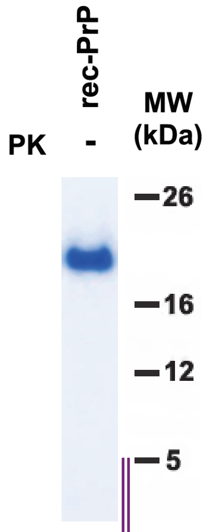
No insertions

No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

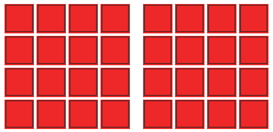
ΔΔG: ND



208 AA

NO MISFOLDING

0
Conformers



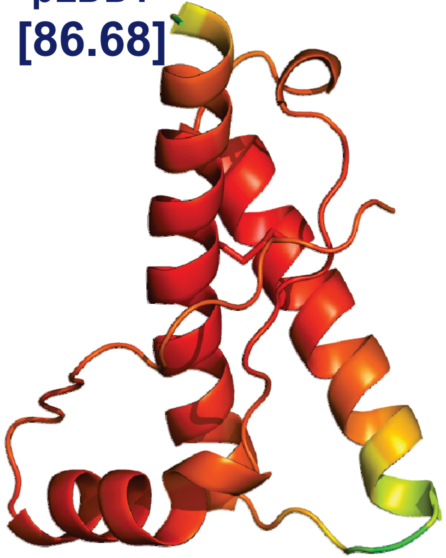
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.68]



Protein code: 0944

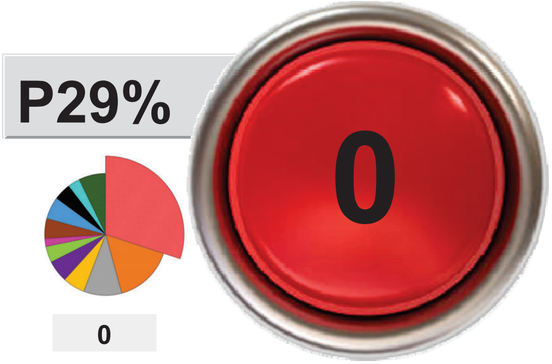
Distinct primary sequence across species

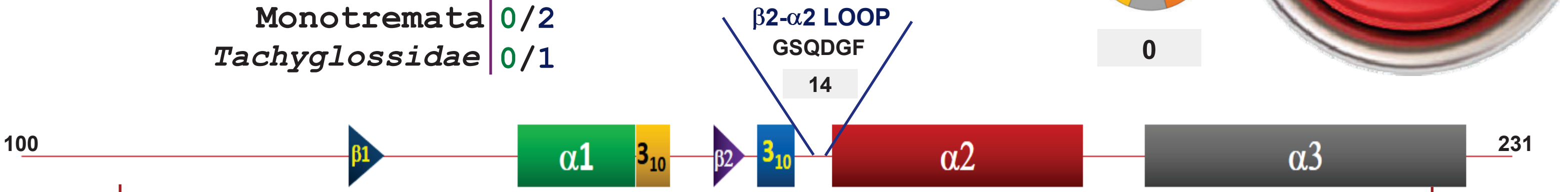
Short-beaked echidna

GenBank: BK063950

Tachyglossus aculeatus

Monotremata 0/2
Tachyglossidae 0/1





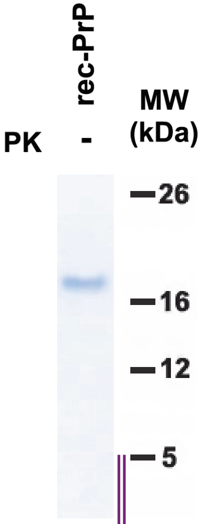
```
KYKPDKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPPMHFGNDYEDRYYRENQYRYPNQVYYYRPVDQYGSQDGFVRDCVNITVTQHTVTTTE GKNFNETDVKIMTRVVEQMCVNQYQAEYRARS-
WN  S    NI                             MI     W        MN             NN NN  H       IK       TK E  T     M E        T   K SQ YYE
```

PrP sequence differs by 24 amino acids from the bank vole PrP (see in red)

One deletion
No insertions
No polymorphic variants found

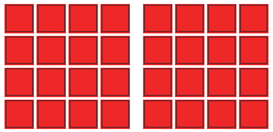
Tm^{Exp}: ND

ΔΔG: ND



197 AA

NO MISFOLDING



0 Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [88.52]

Protein code: 3077

Southern marsupial mole

GenBank: BK064812

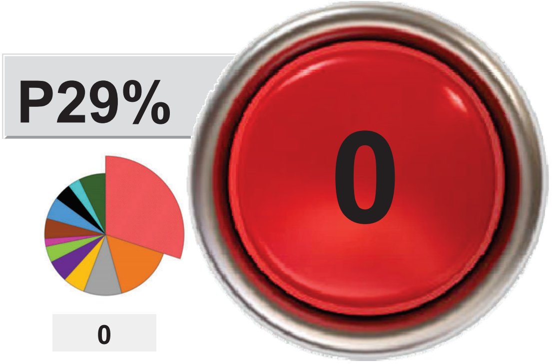
Notoryctes typhlops

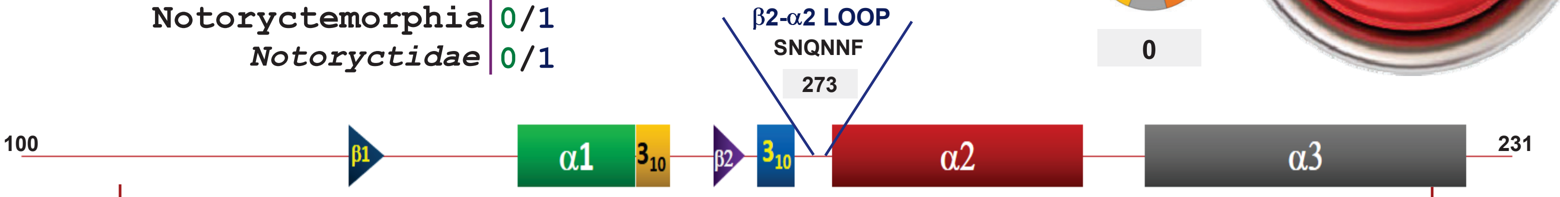
Notoryctemorphia 0/1

Notoryctidae 0/1

Distinct primary sequence across species

P29%





```
KWKPDKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPIMHFGNDYEDRYYRENQYRYPNQVMYRPIDQYSNQNNFVHDCVNITVKEHTTTTTTKGENFTETDIKIMERVVEQMCITQYQNEYAAQYRYNMA-
WN  S     I                            MI     W        MN      Y   V   N             I Q  V             V M         V    K SQ Y EGRSS
```

PrP sequence differs by 18 amino acids from the bank vole PrP (see in red)

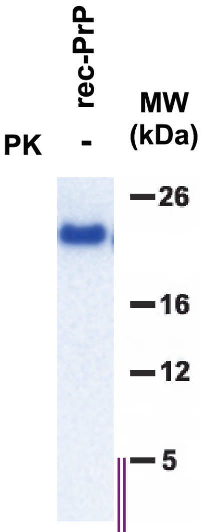
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -15.2



215 AA

NO MISFOLDING

0

Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [93.3]

Protein code: 4081

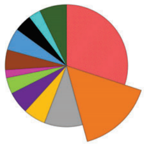
Southern white rhinoceros

GenBank: XM_014790100

Ceratotherium simum simum

Perissodactyla 6/6
Rhinocerotidae 1/1

P36%



0-10

2

3 species sharing the same primary sequence

Bornean rhinoceros
Dicerorhinus sumatrensis harrissoni

Black rhinoceros
Diceros bicornis

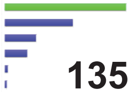
White rhinoceros
Rhinoceros unicornis

β2-α2 LOOP
SNQNNF
273

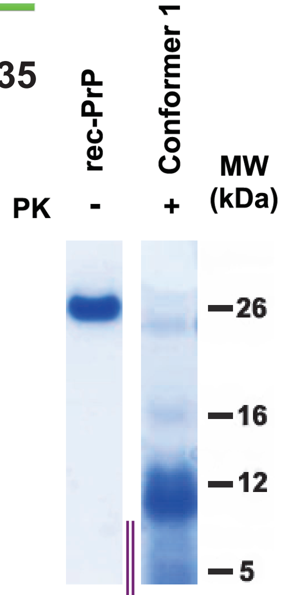
```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVSEYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQREYEAFQQRGAS-
          I  V                         M      W         N           DQ N             I                               V    K SQYYEGRS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

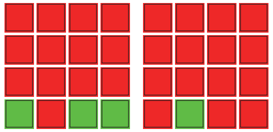


135



212 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -11.01

In vitro studies

TgVole (1x) — Not tested

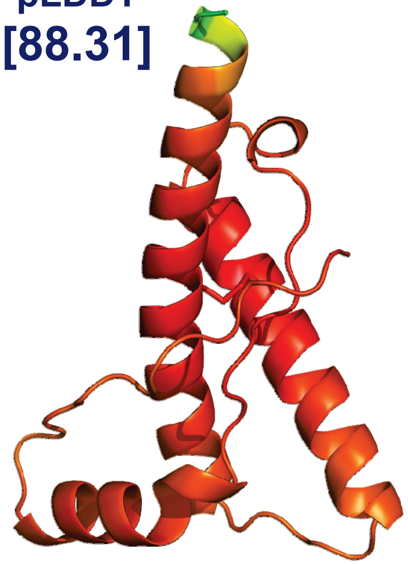
Southern white rhinoceros — Not tested

In vivo studies

TgVole (1x) — Not tested

Southern white rhinoceros — Not tested

pLDDT [88.31]



Protein code: 0955

Asinus

GenBank: BK064942

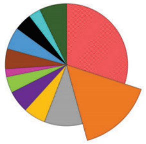
Equus asinus

Perissodactyla 6/6
Equidae 3/3

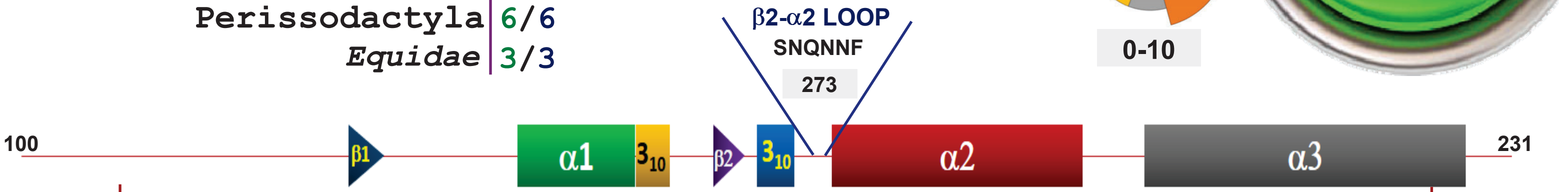
1 species sharing the same primary sequence

African wild ass
Equus africanus

P39%


0-10

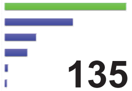
3.6

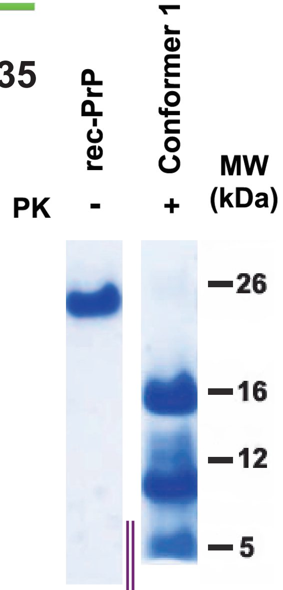


```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVNEYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQKEYEAFQQRGAS-
          I                            M      W         N           DQ N             I                    M         V       SQ YYEGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

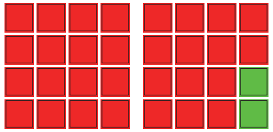
No deletions
No insertions
It shows polymorphic variants


135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -2.76

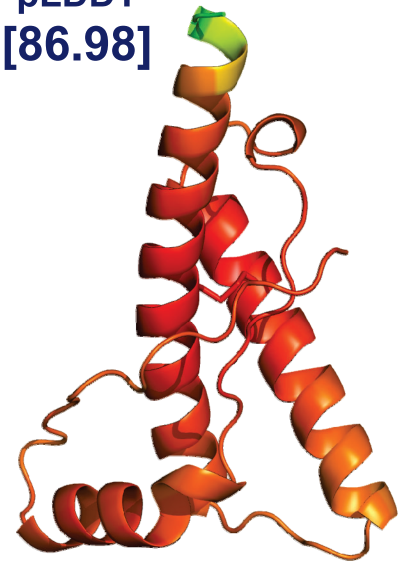
In vitro studies

TgVole (1x)	Not tested
Asinus	Not tested

In vivo studies

TgVole (1x)	Not tested
Asinus	Not tested

pLDDT
[86.98]



Protein code: 1070

Horse

GenBank: EU887260

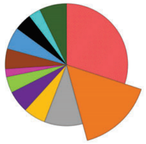
Equus caballus ferus

Perissodactyla 6/6
Equidae 3/3

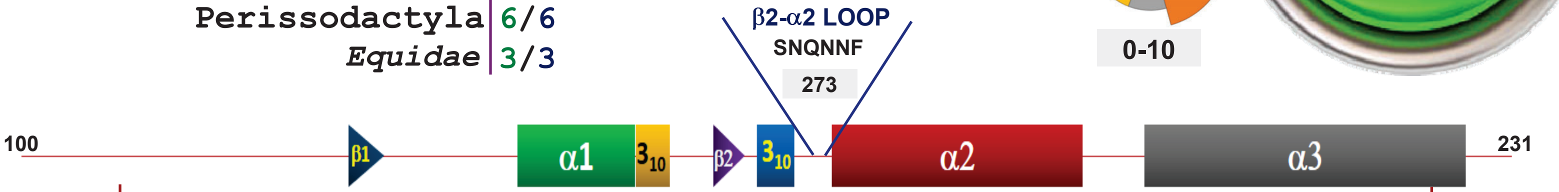
5 species sharing the same primary sequence

- 🟥 **Burchell's zebra** *Equus burchellii*
- ⬜ **Grévy's zebra** *Equus grevyi*
- 🟩 **Kiang** *Equus kiang*
- 🟦 **Grant's zebra** *Equus quagga boehmi*
- 🟦 **Mountain zebra** *Equus zebra hartmannae*

P41%


0-10

7.1



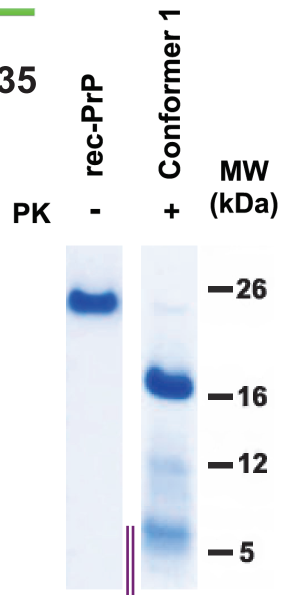
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVSEYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQKEYEAFQQRGAS-
          I                            M      W         N           DQ N             I                    M         V      SQ YYEGRS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

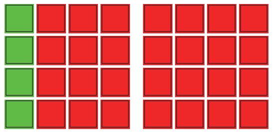
No deletions
No insertions
It shows polymorphic variants

135

211 AA



1 Conformers



Tm^{Exp}: ND

ΔΔG: -4.71

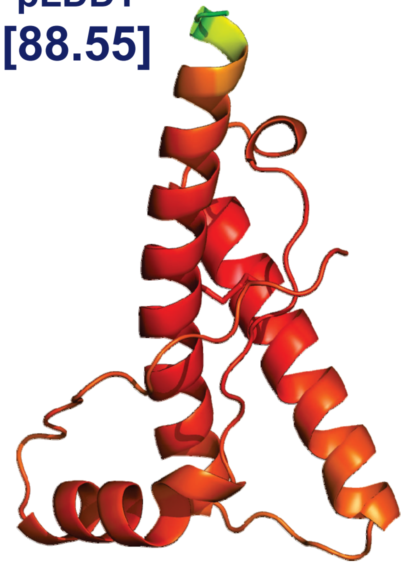
In vitro studies

TgVole (1x)	**Propagate**
Horse	**Ongoing**

In vivo studies

TgVole (1x)	**Ongoing**
Horse	**Not tested**

pLDDT
[88.55]



Protein code: 0115

Przewalski's horse

GenBank: XM_008519788

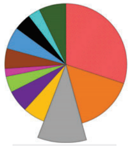
Equus caballus przewalskii

Perissodactyla 6/6
Equidae 3/3

Distinct primary sequence across species

P51%

14.3



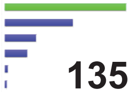
10-20

β2-α2 LOOP
SNQNNF
273

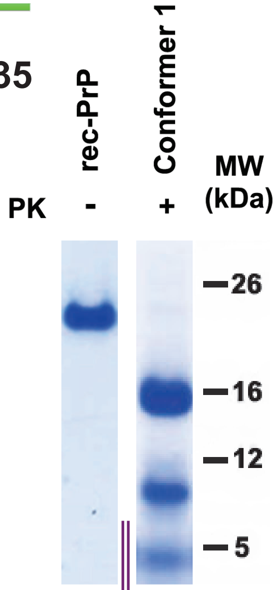
```
WNKPSKPKTNIKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVSEYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQKEYEAFQQRGAS-
                                              M       W          N             DQ N             I                      M          V       SQ YYEGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

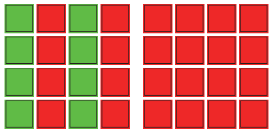


135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -8.75

In vitro studies

TgVole (1x) Not tested

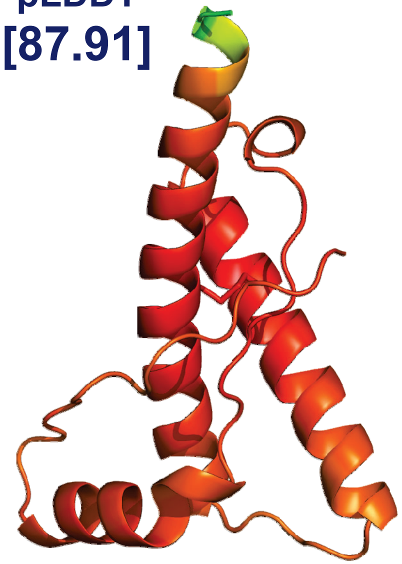
Przewalski's horse Not tested

In vivo studies

TgVole (1x) Not tested

Przewalski's horse Not tested

pLDDT
[87.91]



Malayan tapir

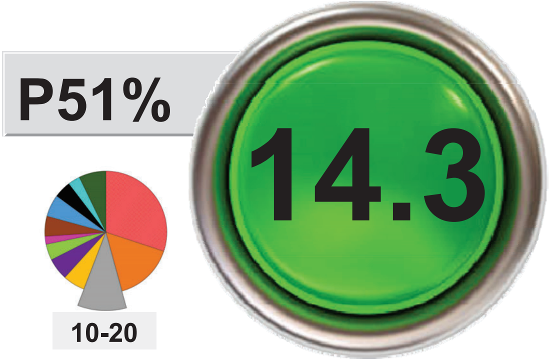
GenBank: BK063977

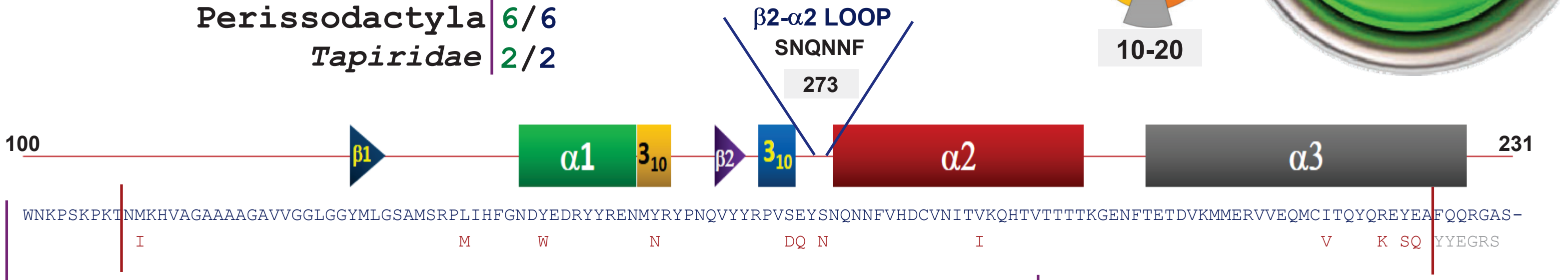
Tapirus indicus

Perissodactyla 6/6
Tapiridae 2/2

Distinct primary sequence across species

P51%

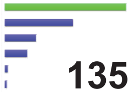


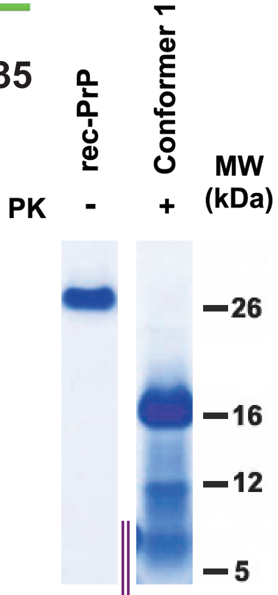


```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYYRPVSEYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQREYEAFQQRGAS-
           I                                M      W          N            DQ N              I                                    V     K SQ YYEGRS
```

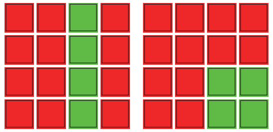
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found





212 AA



Tm^{Exp}: ND

ΔΔG: -9.07

***In vitro* studies**

TgVole (1x) Not tested

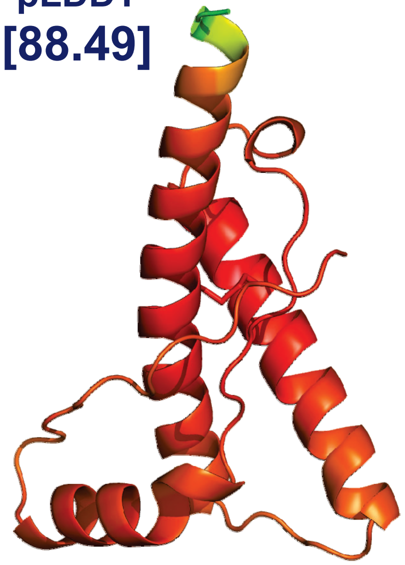
Malayan tapir Not tested

***In vivo* studies**

TgVole (1x) Not tested

Malayan tapir Not tested

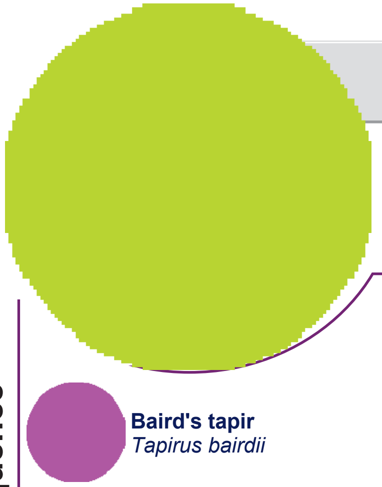
pLDDT
[88.49]



Protein code: 3134

South American tapir

GenBank: BK063978



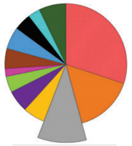
1 species sharing the same primary sequence

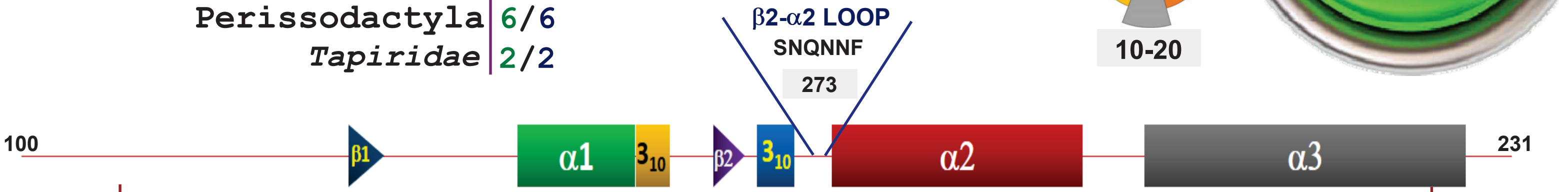
Tapirus terrestris

Perissodactyla	6/6
Tapiridae	2/2

P51%

14.3





```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMHRYPNQVYYYRPVSEYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQREYEAFQQRGAS-
          I  V                          M   N W         N            DQ N             I                    M         V    K SQ YYEGRS
```

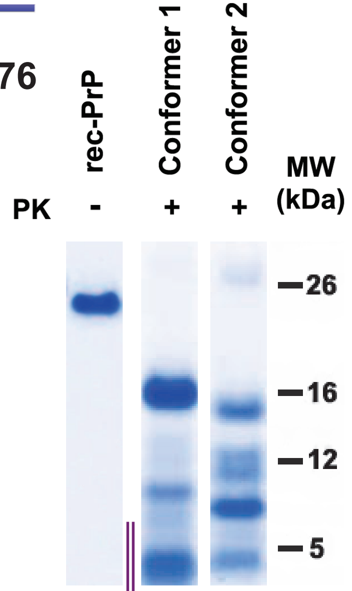
PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

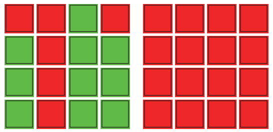
No polymorphic variants found

76



212 AA

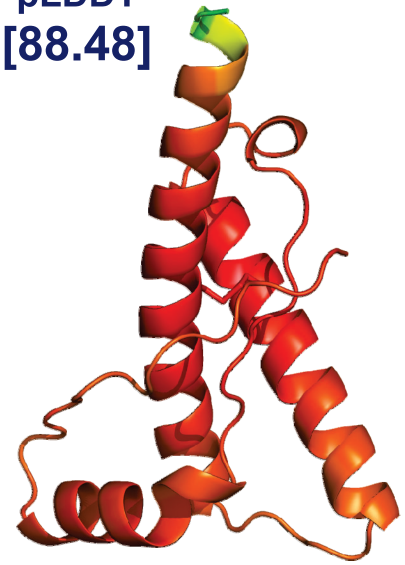
2
Conformers



Tm^{Exp}: ND

ΔΔG: -7.74

pLDDT
[88.48]



***In vitro* studies**

TgVole (1x)	**Not tested**
South American tapir	**Not tested**

***In vivo* studies**

TgVole (1x)	**Not tested**
South American tapir	**Not tested**

Protein code: 3135

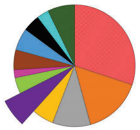
Pangolin

GenBank: XM_017663893

Manis javanica

Pholidota 3/3
Manidae 3/3

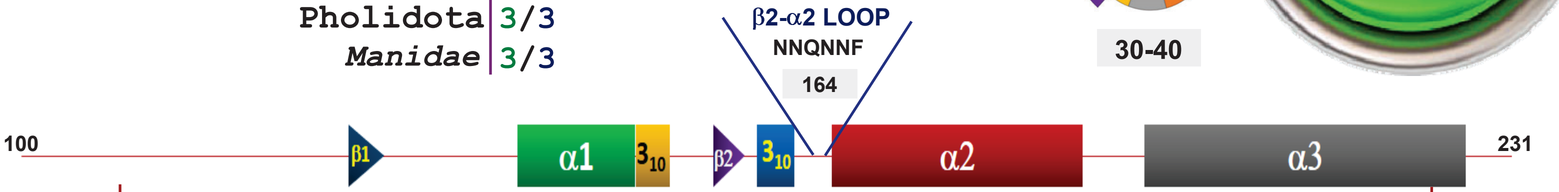
P66%



38.6

1 species sharing the same primary sequence

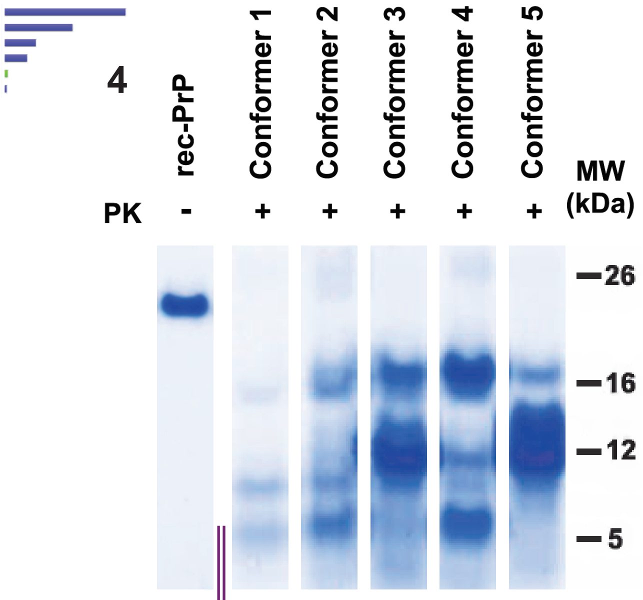
Indian pangolin
Manis crassicaudata



```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQKEYQAASYQRGAS-
 N        I                           M      W          N                                 I                    V            V        S  YYEG SS
```

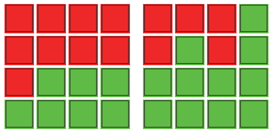
PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



215 AA

5
Conformers



Tm^{Exp}: ND

ΔΔG: ND

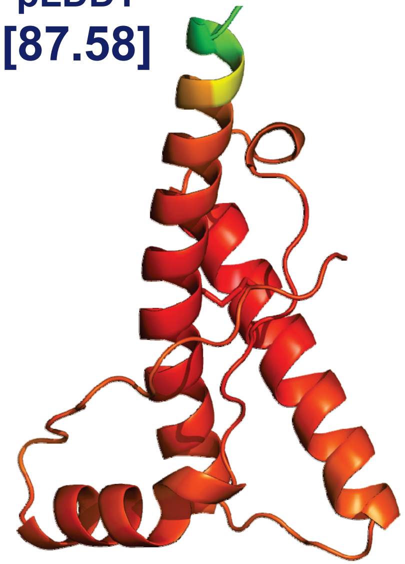
In vitro studies

TgVole (1x)	Ongoing
Pangolin	Not tested

In vivo studies

TgVole (1x)	Ongoing
Pangolin	Not tested

pLDDT
[87.58]



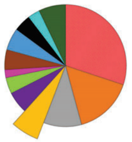
Protein code: 0942

Chinese pangolin

GenBank: BK063962

P56%

22.1



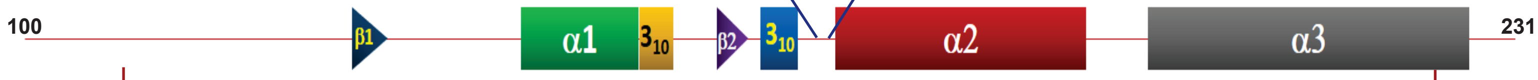
20-30

Manis pentadactyla

Pholidota 3/3
Manidae 3/3

Distinct primary sequence across species

β2-α2 LOOP
NNQNNF
164

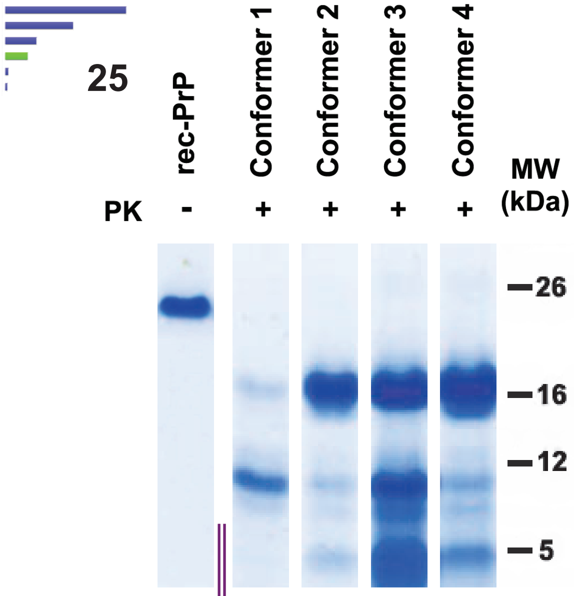


WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQKEYQATSYQRGAS-

N I M W N I V V S YYEG SS

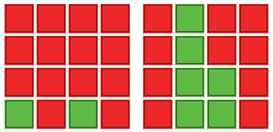
PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



215 AA

4
Conformers



Tm^{Exp}: ND

ΔΔG: ND

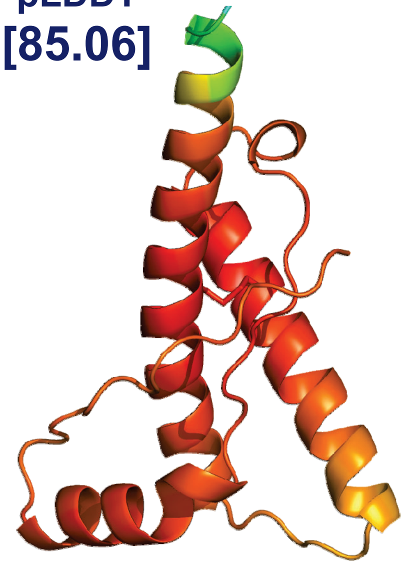
In vitro studies

TgVole (1x)	Not tested
Chinese pangolin	Not tested

In vivo studies

TgVole (1x)	Not tested
Chinese pangolin	Not tested

pLDDT
[85.06]



Protein code: 3092

Tree pangolin

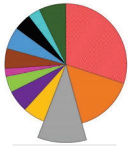
GenBank: BK063960

Manis tricuspis

Pholidota 3/3

Manidae 3/3

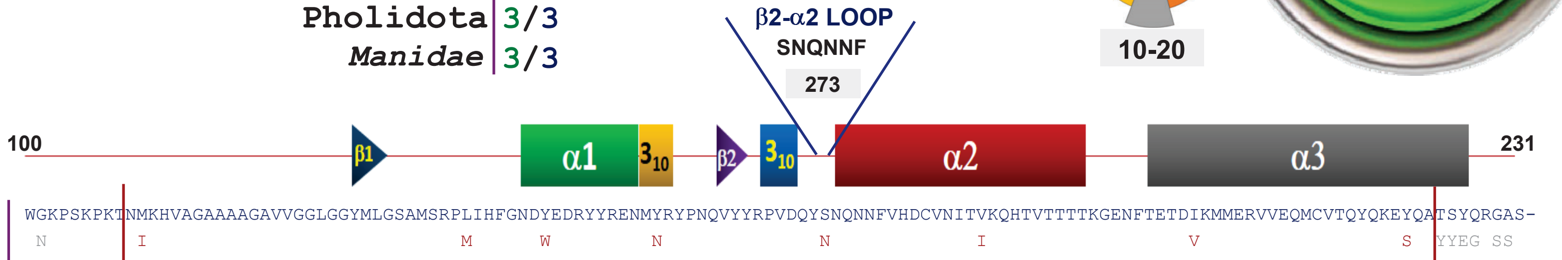
P52%



10-20

17

Distinct primary sequence across species



```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCVTQYQKEYQATSYQRGAS-
 N       I                        M      W         N               N              I                  V                    S  YYEG SS
```

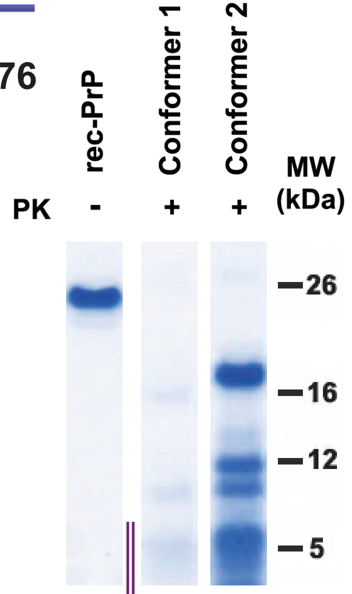
PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

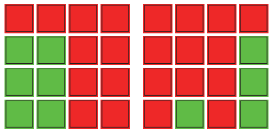
76



215 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

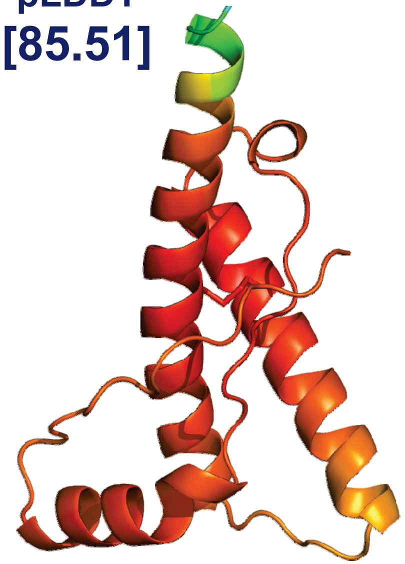
Tree pangolin Not tested

In vivo studies

TgVole (1x) Not tested

Tree pangolin Not tested

pLDDT [85.51]



Protein code: 3089

Brown-throated sloth

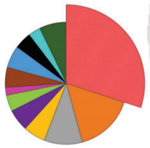
GenBank: BK063934

Bradypus variegatus

Pilosa 1/5
Bradypodidae 0/1

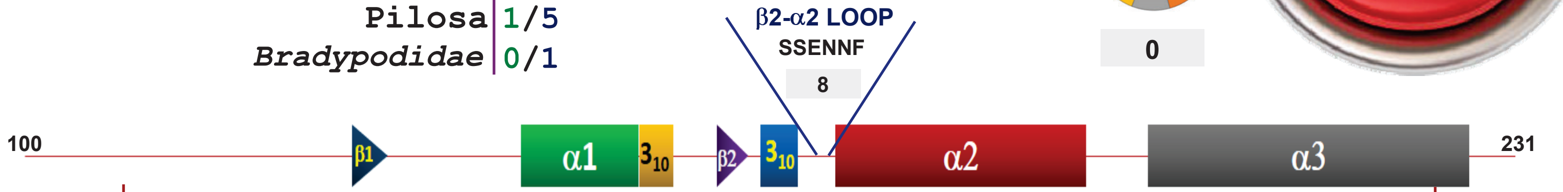
P29%

0



0

Distinct primary sequence across species



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYLVGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSSENNFVRDCVNITIKEHTVTTTTKGENFTETDIKMMERVVEQMCVTQYKTEYQAAYRQGSS-

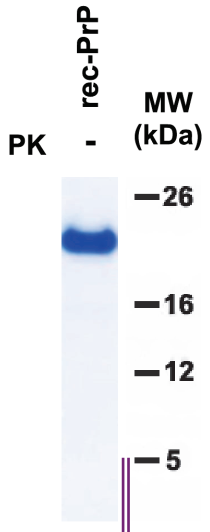
I ML M W N R NNQ H Q V QK S Y EGR

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -11.57



217 AA

NO MISFOLDING

0
Conformers

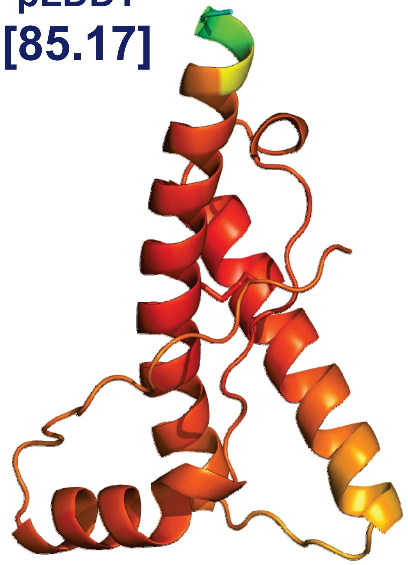
***In vitro* studies**

NOT APPLICABLE

***In vivo* studies**

NOT APPLICABLE

pLDDT
[85.17]



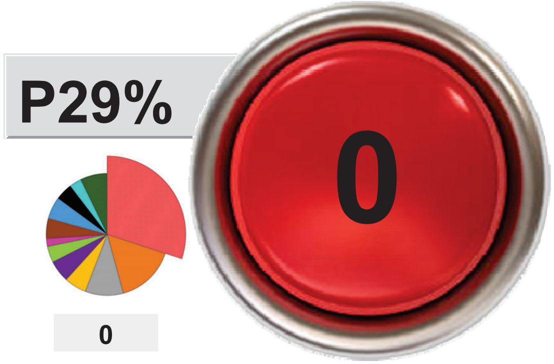
Protein code: 3057

Linnaeus's two-toed sloth

GenBank: BK063945

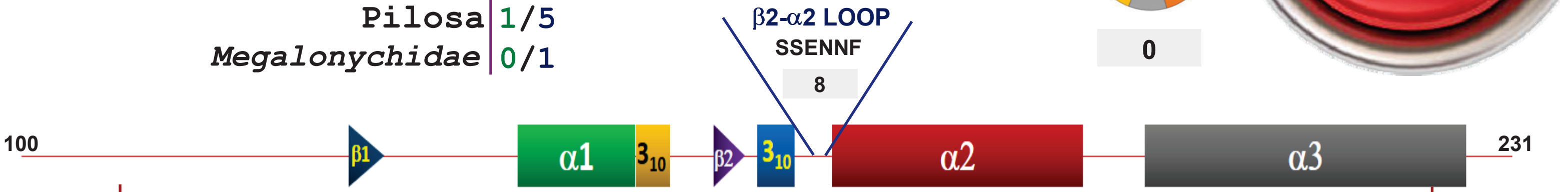
Choloepus didactylus

Pilosa 1/5
Megalonychidae 0/1



1 species sharing the same primary sequence

Hoffmann's two-toed sloth
Choloepus hoffmanni



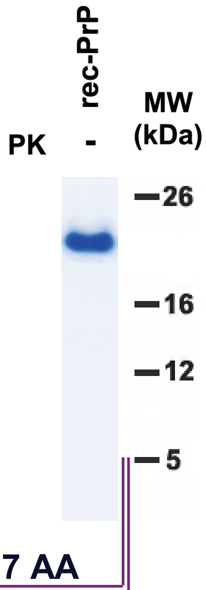
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYLVGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYKPVDQYSSENNFVRDCVNITIKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYKTEYQAAYQRGSS-
          I                  ML        M   N  W         N        R     NNQ    H        Q                V           V   QK S  Y EGR
```

PrP sequence differs by 18 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -14.14



217 AA

NO MISFOLDING

0
Conformers

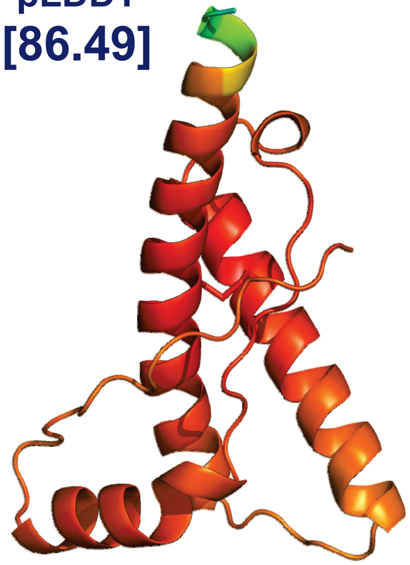
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.49]



Protein code: 3071

Silky anteater

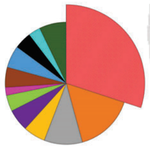
GenBank: AY133063

Cyclopes didactylus

Pilosa 1/5
Cyclopedidae 0/1

Distinct primary sequence across species

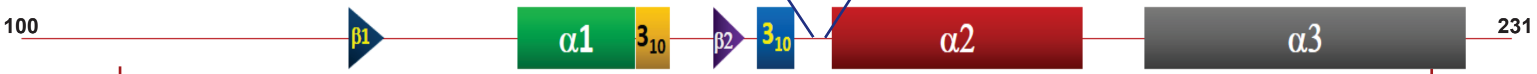
P29%



0

0

β2-α2 LOOP
SSENNF
8



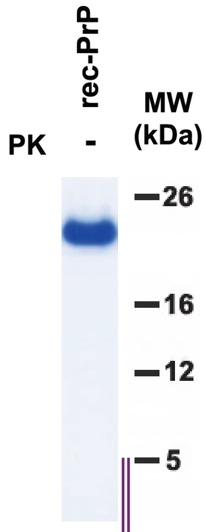
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYLVGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVNQYSSENNFVRDCVNITIKEHTVTTTTKGENFTETDVKMMERVVEQMCITQYKQESQAAYYQRGSS-
           I                     ML       M       W          N         R  D  NNQ    H        Q                                  V    QK    Y EG S
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



216 AA

NO MISFOLDING

0
Conformers

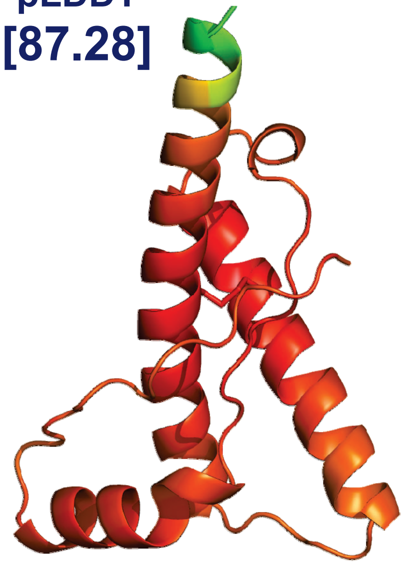
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[87.28]



Protein code: 0923

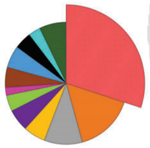
Giant anteater

GenBank: BK063979

Myrmecophaga tridactyla

Pilosa 1/5
Myrmecophagidae 1/2

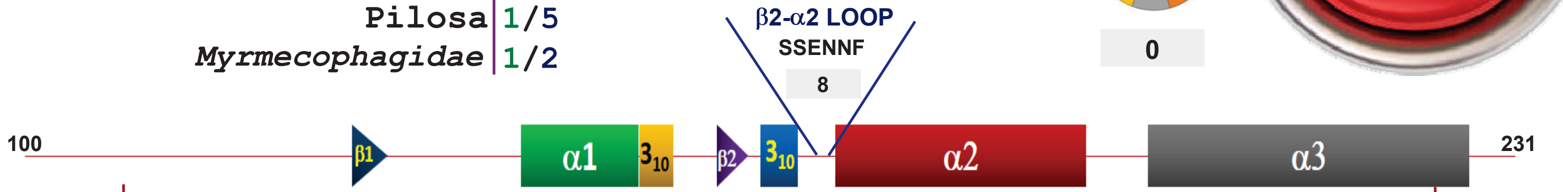
P29%



0

0

Distinct primary sequence across species



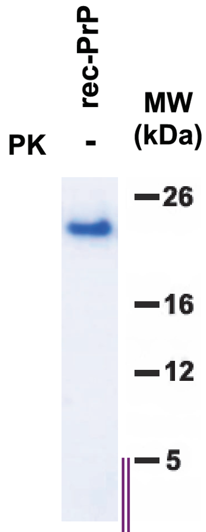
```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYLVGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVNQYSSENNFVHDCVNITIKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAAYFHGGS-
          I  V                ML       M      W         N        R  D  NNQ             Q                V           V    K    Y EGRS
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

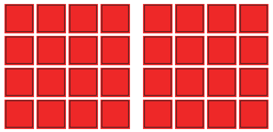
Tm^{Exp}: ND

ΔΔG: -15.61



214 AA

NO MISFOLDING



0
Conformers

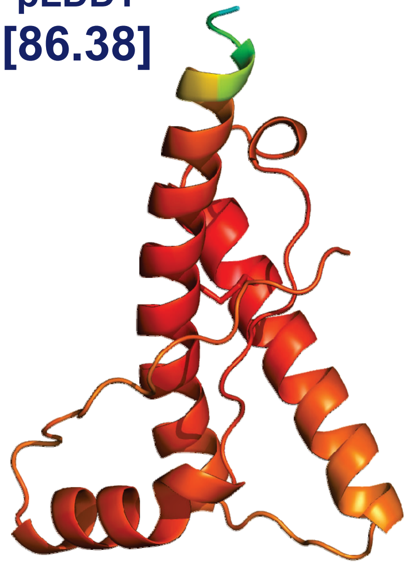
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.38]



Protein code: 3136

Southern tamandua

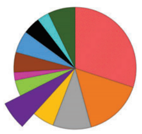
GenBank: BK063980

Tamandua tetradactyla

Pilosa 1/5
Myrmecophagidae 1/2

P65%

36.6



30-40

β2-α2 LOOP
SSENNF
8

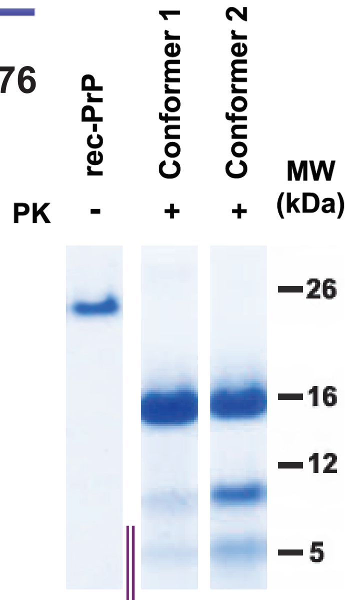
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYLVGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVNQYSSENNFVHDCVNITIKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAAYFHGGS-
           I                       ML       M      W         N         R  D  NNQ           Q              V          V    K    Y EGRS
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

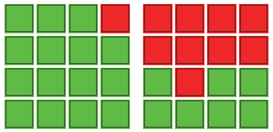
Distinct primary sequence across species

76



214 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -10.89

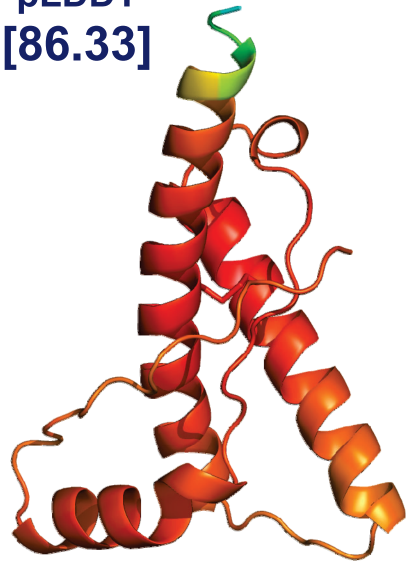
In vitro studies

TgVole (1x)	Not tested
Southern tamandua	Not tested

In vivo studies

TgVole (1x)	Not tested
Southern tamandua	Not tested

pLDDT
[86.33]



Protein code: 3137

Red-handed howler

GenBank: AY765382

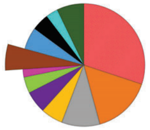
Alouatta belzebul

Primates	35/45
Atelidae	3/5

1 species sharing the same primary sequence

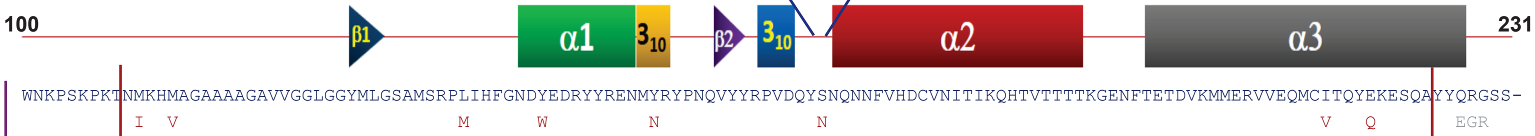
Mantled howler
Alouatta palliata

P75% **63.6**



60-70

β2-α2 LOOP
SNQNNF
273

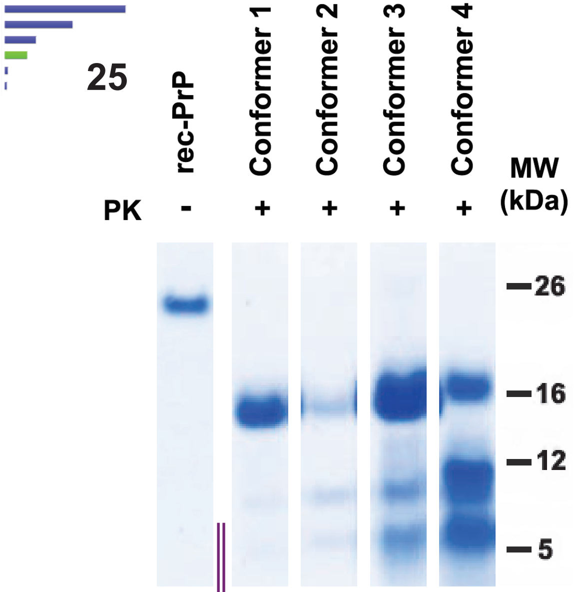


```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-
           I  V                              M      W         N                N                                                V    Q         EGR
```

PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

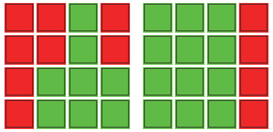
No deletions
No insertions
No polymorphic variants found

25



210 AA

4
Conformers



Tm^{Exp}: ND

ΔΔG: -0.92

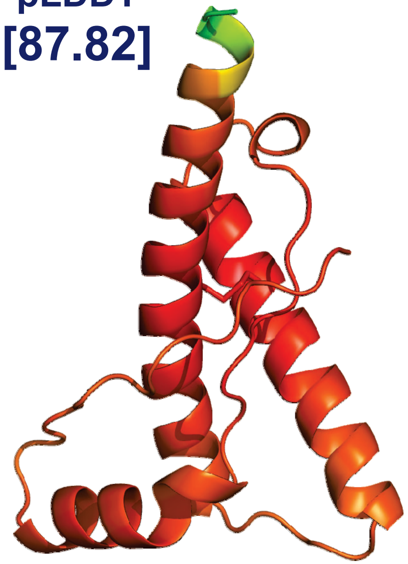
In vitro studies

TgVole (1x)	Not tested
Red-handed howler	Not tested

In vivo studies

TgVole (1x)	Not tested
Red-handed howler	Not tested

pLDDT
[87.82]



Protein code: 1383

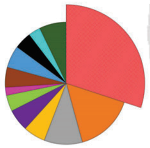
Gray-bellied night monkey

GenBank: AY765387

Aotus lemurinus

Primates 35/45
Aotidae 1/2

P29%



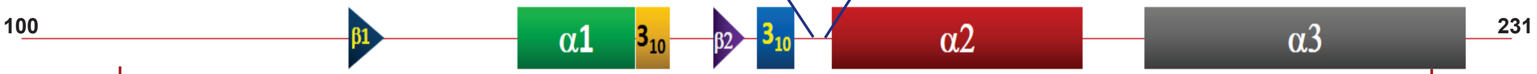
0

0

Nancy Ma's night monkey
Aotus nancymaae

1 species sharing the same primary sequence

β2-α2 LOOP
SNQNNF
273



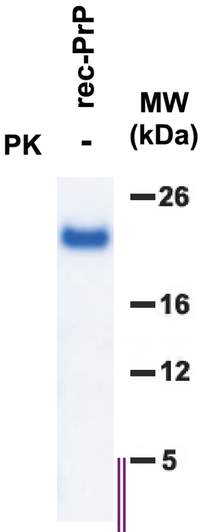
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYEKESQAYYQRGSS-
I V M W N N M V Q EGR

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: 1.07



210 AA

NO MISFOLDING

0
Conformers

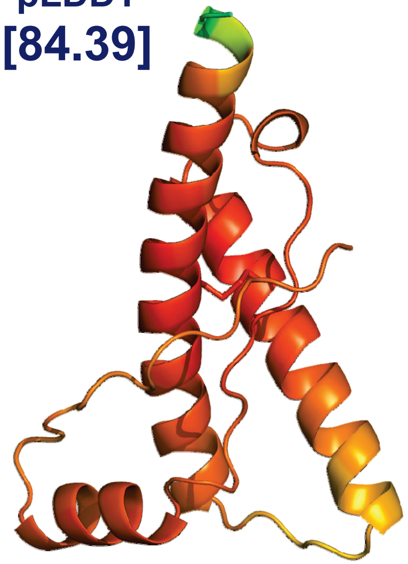
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[84.39]



Protein code: 1386

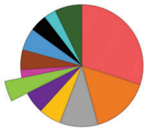
Three-striped night monkey

GenBank: U08293

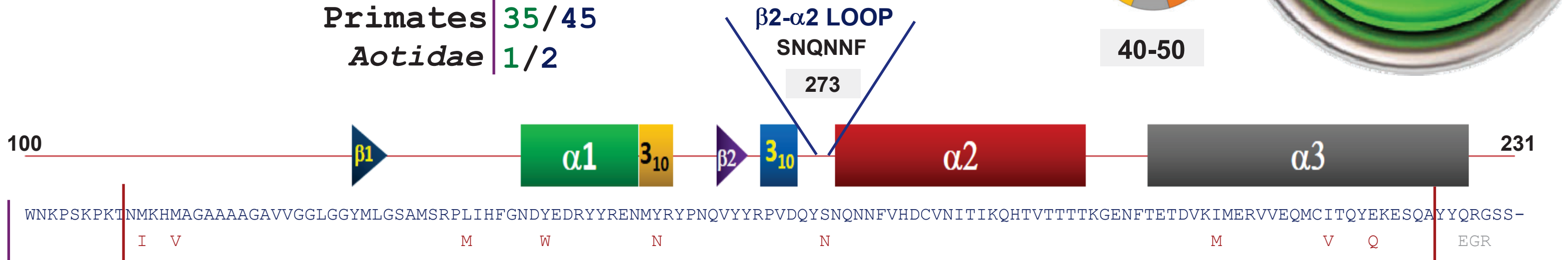
Aotus trivirgatus

Primates	35/45
Aotidae	1/2

P70% **46.1**



40-50



WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYEKESQAYYQRGSS-

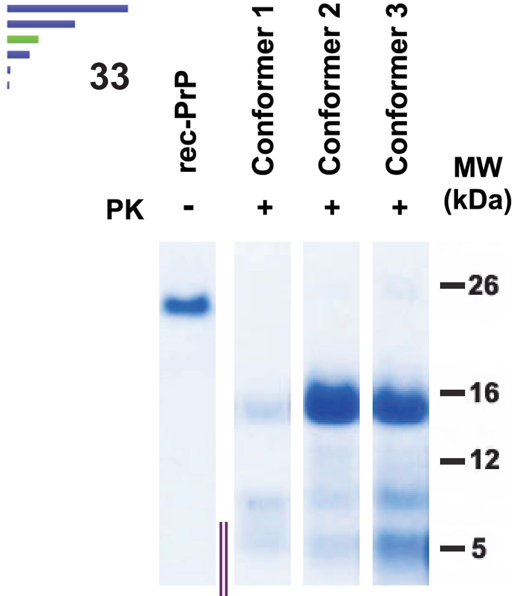
I V M W N N M V Q EGR

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

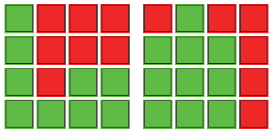
Distinct primary sequence across species

33



210 AA

3 Conformers



Tm^{Exp}: ND

ΔΔG: -5.5

***In vitro* studies**

TgVole (1x) Not tested

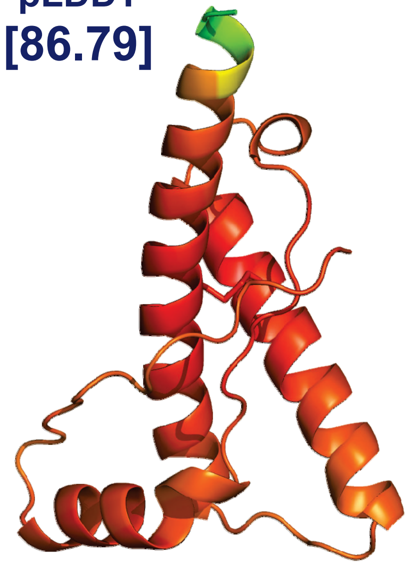
Three-striped night monkey Not tested

***In vivo* studies**

TgVole (1x) Not tested

Three-striped night monkey Not tested

pLDDT [86.79]



Protein code: 1385

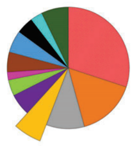
Geoffroy's spider monkey

GenBank: U08309

Ateles geoffroyi

Primates	35/45
Atelidae	3/5

P56%

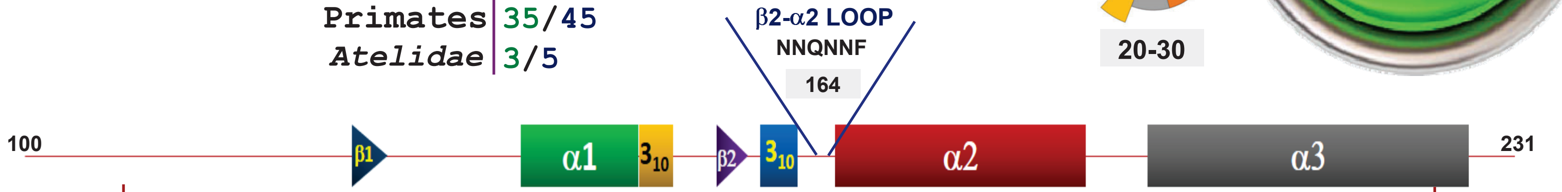


20-30

21.4

1 species sharing the same primary sequence

Brown spider monkey
Ateles hybridus

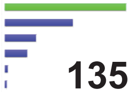


WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQRGSS-

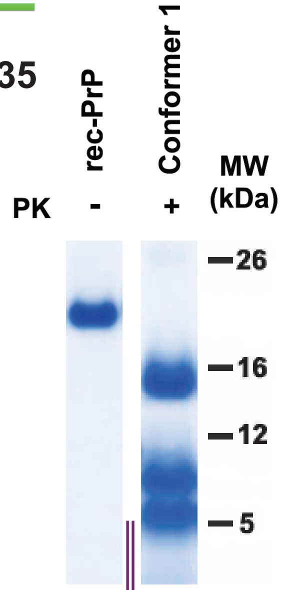
I V M W N V QK EGR

PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

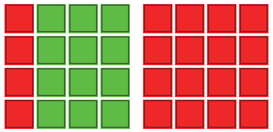


135



202 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -6.77

In vitro studies

TgVole (1x) Not tested

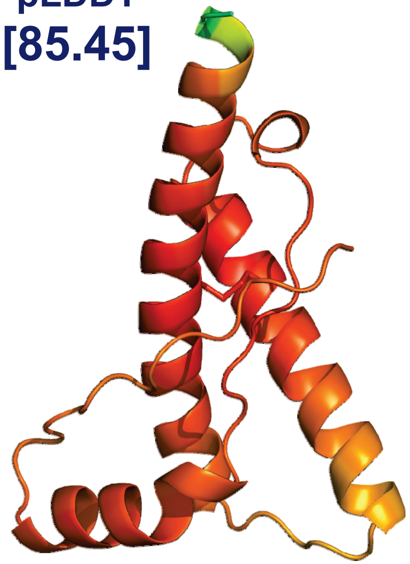
Geoffroy's spider monkey Not tested

In vivo studies

TgVole (1x) Not tested

Geoffroy's spider monkey Not tested

pLDDT
[85.45]



Protein code: 1417

Red-faced spider monkey

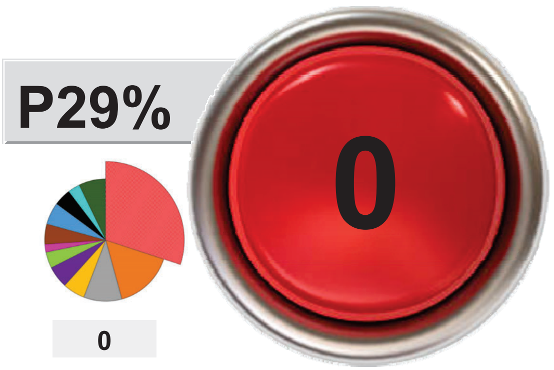
GenBank: U15164

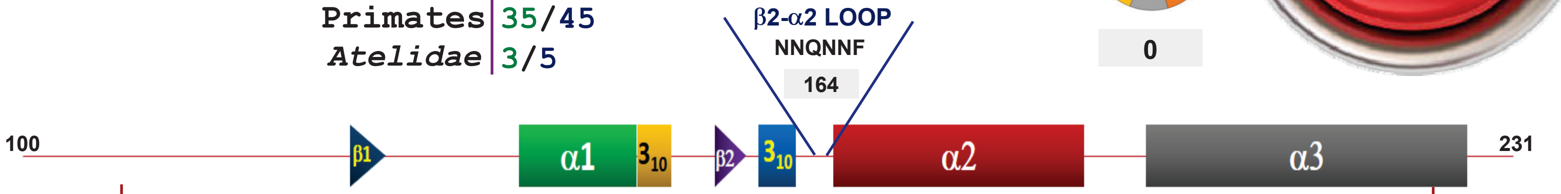
Ateles paniscus

Primates 35/45
Atelidae 3/5

Distinct primary sequence across species

P29%





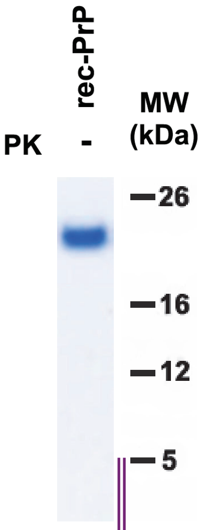
```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENLTETDVKMMERVVEQMCITQYERESQAYYQRGSS-
           I  V                             M      W          N                                           F                V    QK       EGR
```

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -5.68



210 AA

NO MISFOLDING

In vitro studies

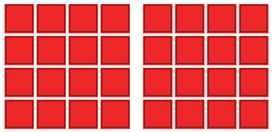
NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.16]

0
Conformers



Protein code: 1415

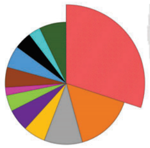
Southern muriqui

GenBank: AY765383

Brachyteles arachnoides

Primates	35/45
Atelidae	3/5

P29%



0

0

Distinct primary sequence across species

β2-α2 LOOP
NNQNNF
164

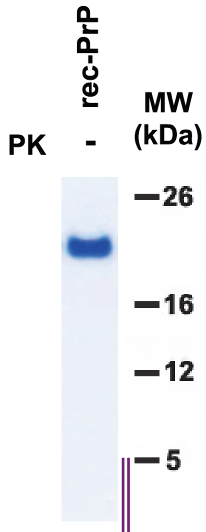
```
WSKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-
 N         I  V                                M      W          N                                                                                   V   Q          EGR
```

PrP sequence differs by 7 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -4.43



210 AA

NO MISFOLDING

0
Conformers

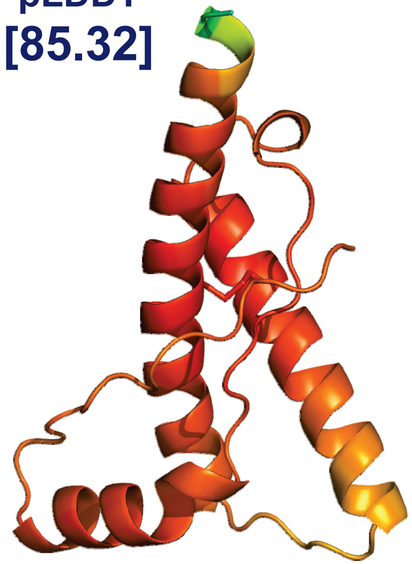
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[85.32]



Protein code: 1337

White-eared titi

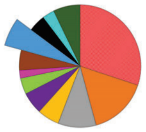
GenBank: BK064142

Callicebus donacophilus

Primates 35/45
Pitheciidae 3/4

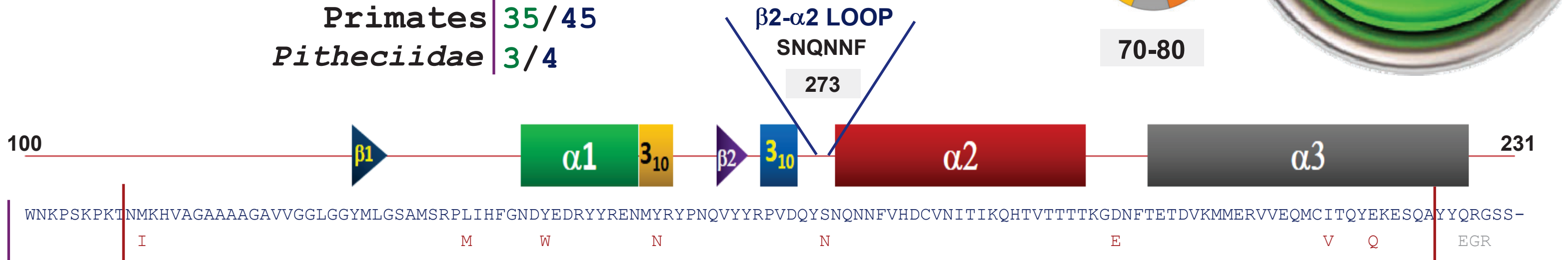
P82%

74.1



70-80

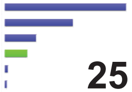
Distinct primary sequence across species



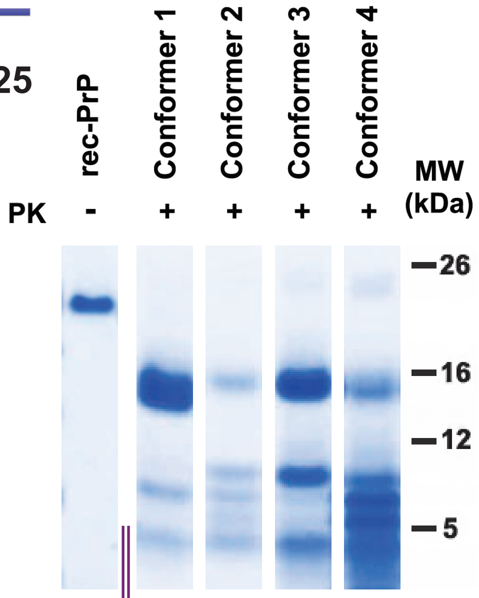
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGDNFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-

PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

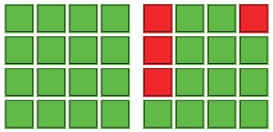


25



211 AA

4 Conformers



Tm^{Exp}: ND

ΔΔG: 4.73

In vitro studies

TgVole (1x) Not tested

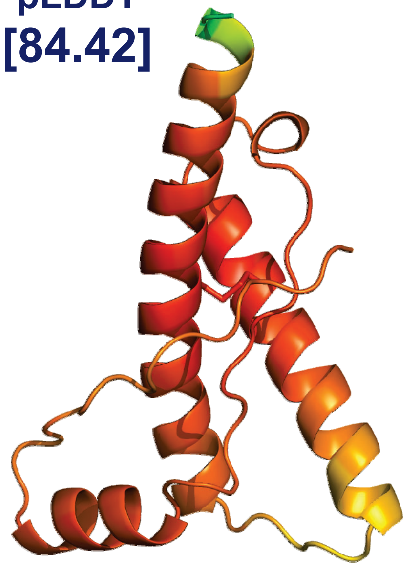
White-eared titi Not tested

In vivo studies

TgVole (1x) Not tested

White-eared titi Not tested

pLDDT
[84.42]



Protein code: 3329

Red-bellied titi

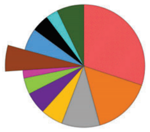
GenBank: U08312

Callicebus moloch

Distinct primary sequence across species

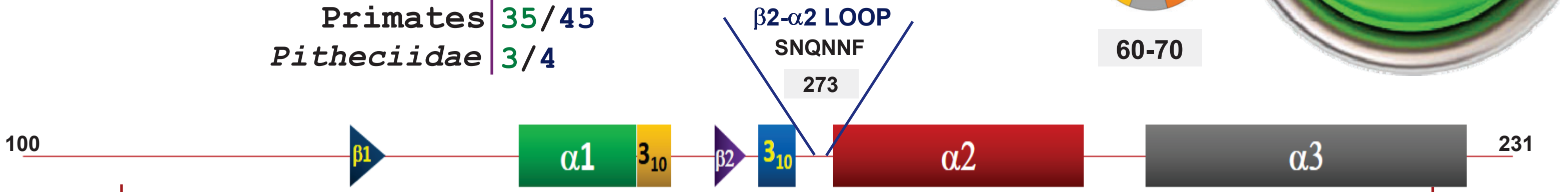
`Primates` **35/45**
`Pitheciidae` **3/4**

P76%



60-70

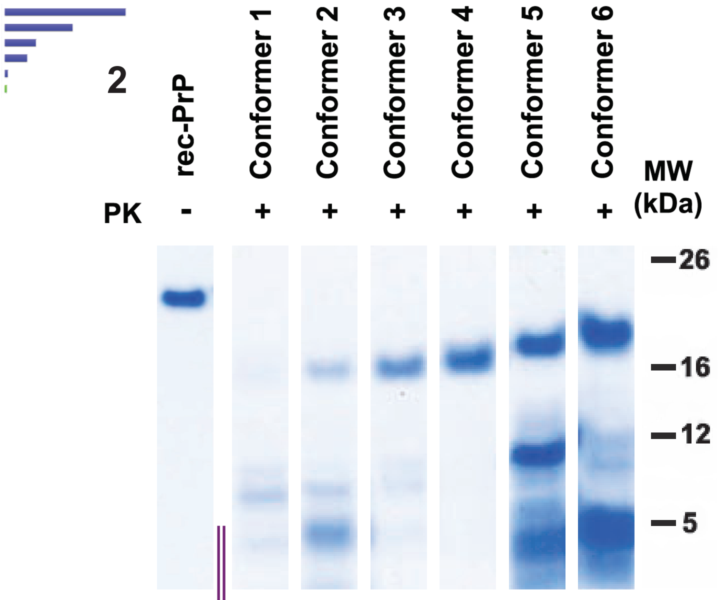
64.3



```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-
           I                         M     W        N           N                                        V   Q            EGR
```

PrP sequence differs by 7 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



211 AA

6
Conformers

🟩🟩🟩🟩 🟩🟩🟥🟥
🟩🟩🟩🟩 🟩🟩🟥🟥
🟩🟩🟩🟩 🟩🟩🟥🟥
🟩🟩🟩🟩 🟩🟩🟥🟥

Tm^{Exp}: ND

ΔΔG: 3.98

In vitro studies

TgVole (1x) Not tested

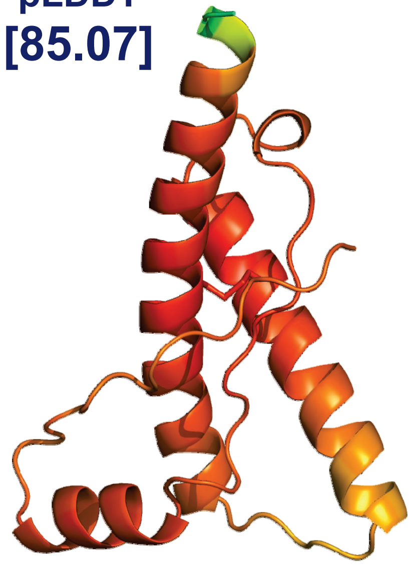
Red-bellied titi Not tested

In vivo studies

TgVole (1x) Not tested

Red-bellied titi Not tested

pLDDT
[85.07]



Protein code: 1429

Common marmoset

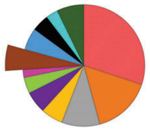
GenBank: XM_008995703

Callithrix jacchus

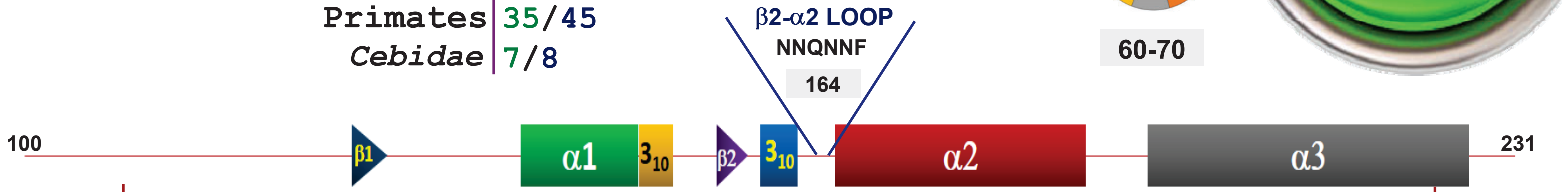
Primates 35/45
Cebidae 7/8

P77%

67.5



60-70



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQRGSS-

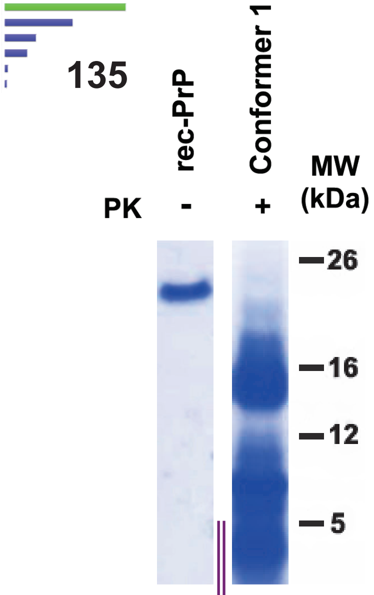
I M W N V QK EGR

PrP sequence differs by 7 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

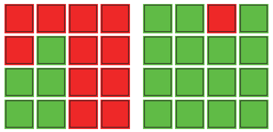
4 species sharing the same primary sequence

Goeldi's marmoset *Callimico goeldii*
Silvery marmoset *Callithrix argentata*
White-headed marmoset *Callithrix geoffroyi*
Pygmy marmoset *Callithrix pygmaea*



210 AA

1 Conformers



Tm^{Exp}: ND

ΔΔG: -4.16

In vitro studies

TgVole (1x) Not tested

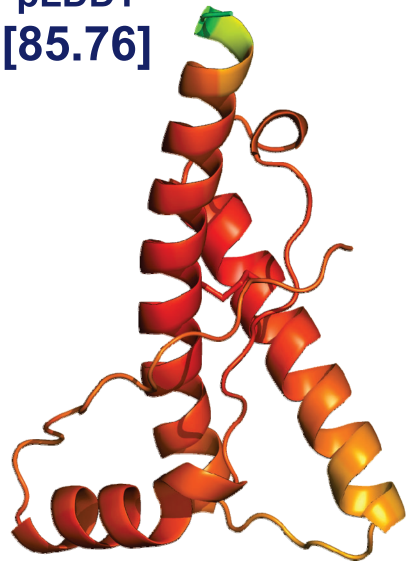
Common marmoset Not tested

In vivo studies

TgVole (1x) Not tested

Common marmoset Not tested

pLDDT [85.76]



Protein code: 1121

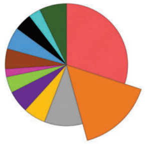
Panamanian white-faced capuchin

GenBank: XM_017524036

Cebus capucinus

Primates 35/45
Cebidae 7/8

P39%



0-10

3.9

2 species sharing the same primary sequence

H white-fronted capuchin
Cebus albifrons

Tufted capuchin
Cebus apella

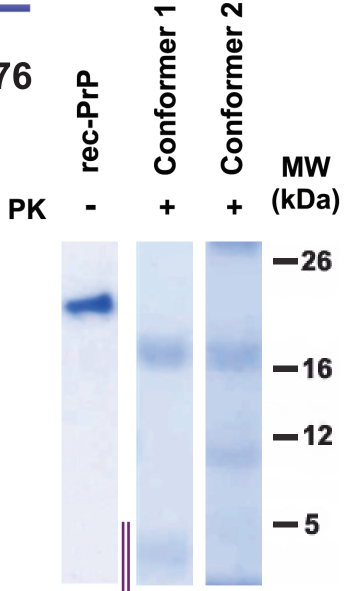
β2-α2 LOOP
SNQNNF
273

WNKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQRGSS-
NI M W N N V QK EGR

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

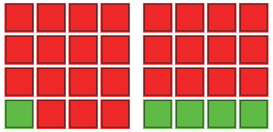
No deletions
No insertions
No polymorphic variants found

76



210 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -2.68

***In vitro* studies**

TgVole (1x) Not tested

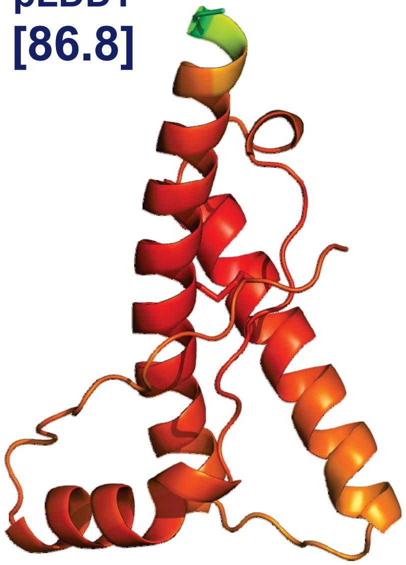
Panamanian white-faced Not tested

***In vivo* studies**

TgVole (1x) Not tested

Panamanian white-faced Not tested

pLDDT [86.8]



Protein code: 1084

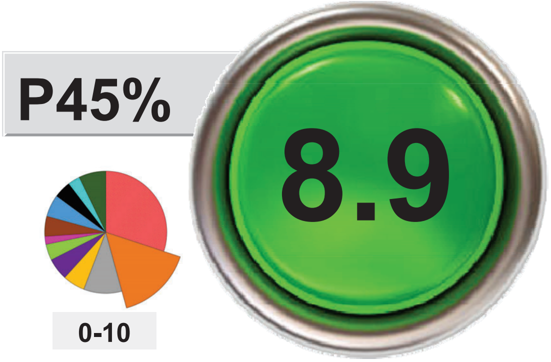
Sooty mangabey

GenBank: XM_012052159

Cercocebus atys

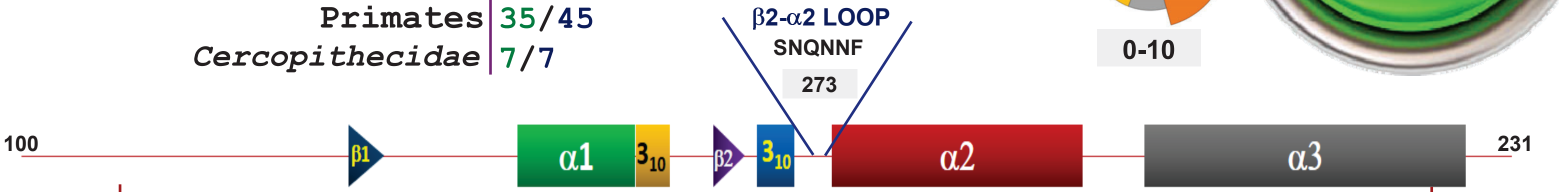
Primaries	35/45
Cercopithecidae	7/7

P45%



1 species sharing the same primary sequence

Collared mangabey
Cercocebus torquatus



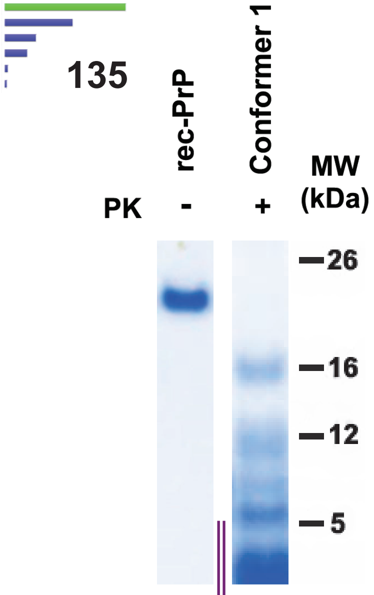
```
WHKPSKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNEYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-
 N        NI  V                               M      DW          N                 N                                                       V   Q         EGR
```

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

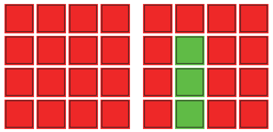
No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -9.39



211 AA



1
Conformers

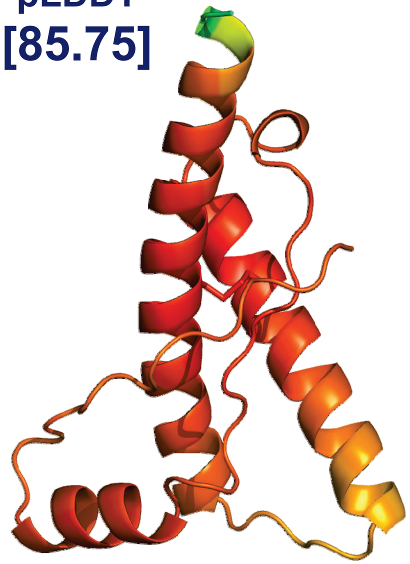
In vitro studies

TgVole (1x)	Not tested
Sooty mangabey	Not tested

In vivo studies

TgVole (1x)	Not tested
Sooty mangabey	Not tested

pLDDT
[85.75]



Protein code: 2057

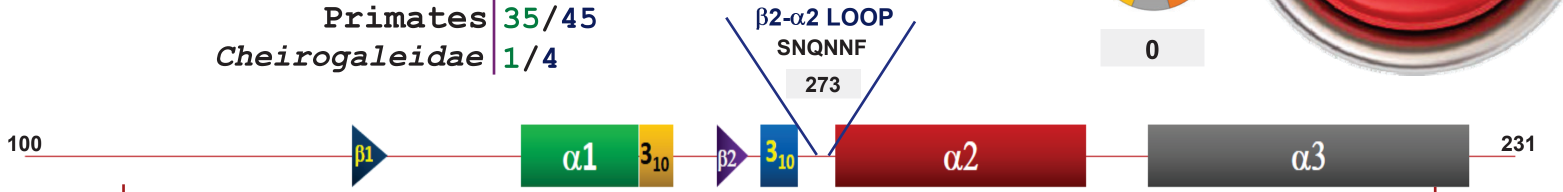
Fat-tailed dwarf lemur

GenBank: BK063936

Distinct primary sequence across species

Cheirogaleus medius

Primates	35/45
Cheirogaleidae	1/4



```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNDYEDRYYRENMNRYPNQVYYKPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKEYQAAYQRGSS-
          I                         MI    W                R     N                                                          S  Y EGR
```

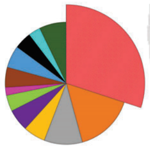
PrP sequence differs by 7 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

P29%



0

0

Tm^Exp^: ND

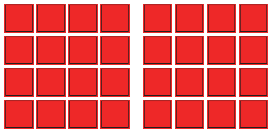
ΔΔG: 10.05

PK

212 AA

NO MISFOLDING

0
Conformers



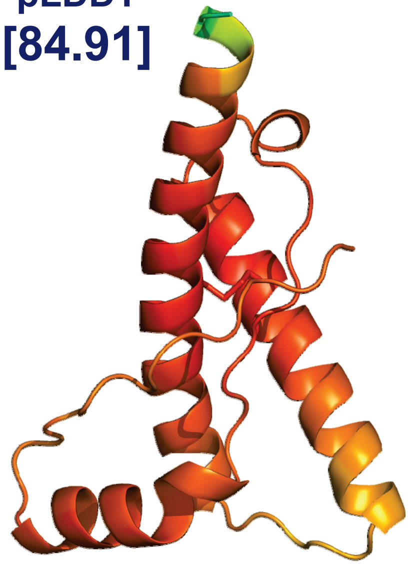
In vitro studies

NOT APPLICABLE

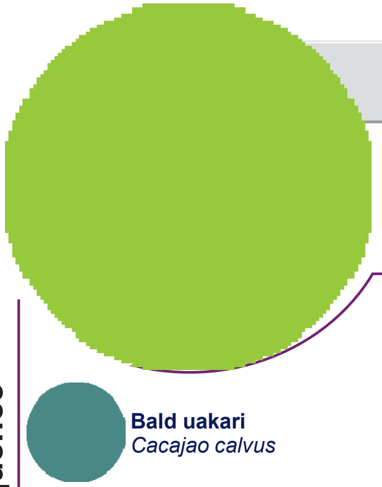
In vivo studies

NOT APPLICABLE

pLDDT [84.91]



Protein code: 3059



1 species sharing the same primary sequence

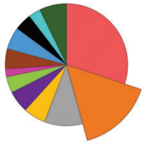
Black bearded saki

GenBank: AY765380

Chiropotes satanas

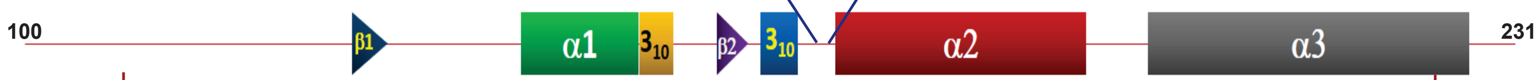
Primates	35/45
Pitheciidae	3/4

P31% **0.7**



0-10

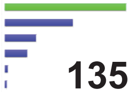
β2-α2 LOOP
SNQNNF
273



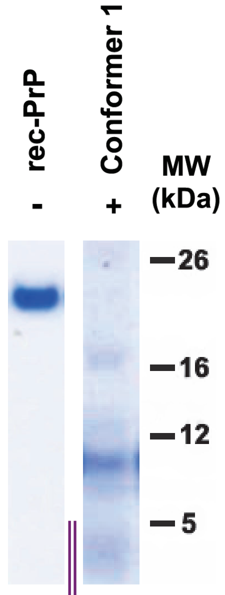
```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-
           I  V                          M       W          N               N                                            V    Q              EGR
```

PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

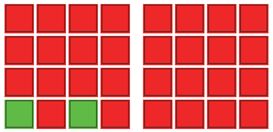


135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -3.52

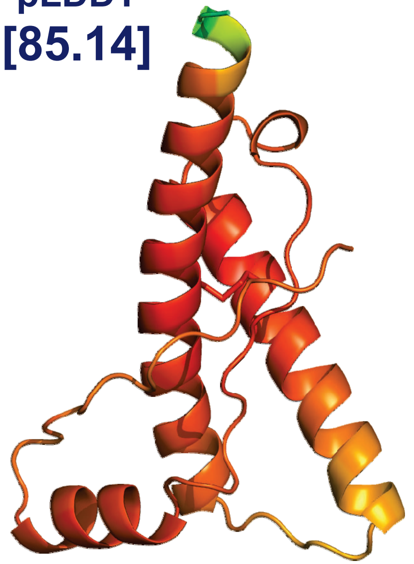
In vitro studies

TgVole (1x)	Not tested
Black bearded saki	Not tested

In vivo studies

TgVole (1x)	Not tested
Black bearded saki	Not tested

pLDDT
[85.14]



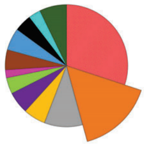
Protein code: 1431

Angola colobus

GenBank: XM_011941048

Colobus angolensis palliatus

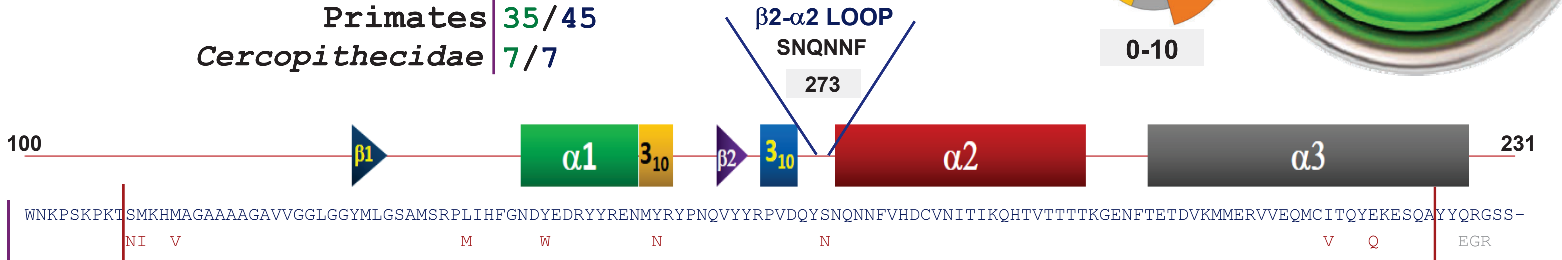
P42%



0-10

8.4

`Primates` 35/45
`Cercopithecidae` 7/7



PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions

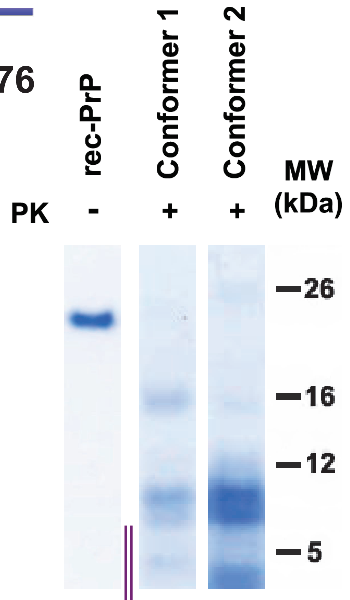
No insertions

No polymorphic variants found

11 species sharing the same primary sequence

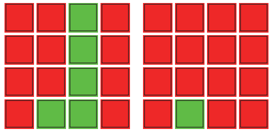
- ● **Black snub-nosed monkey** *Rhinopithecus bieti*
- ● **Angola colobus** *Colobus angolensis palliatus*
- ● **Mantled guereza** *Colobus guereza*
- ● **Francois' langur** *Trachypithecus francoisi*
- ● **Golden snub-nosed monkey** *Rhinopithecus roxellana*
- ● **Northern plains gray langur** *Semnopithecus entellus*
- ● **Proboscis monkey** *Nasalis larvatus*
- ● **Red-shanked douc** *Pygathrix nemaeus*
- ● **Phayre's leaf monkey** *Trachypithecus phayrei crepuscula*
- ● **Black-shanked douc** *Pygathrix nigripes*
- ● **Myanmar snub-nosed monkey** *Rhinopithecus strykeri*

76



211 AA

2 Conformers



Tm^{Exp}: ND

ΔΔG: -1.54

In vitro studies

TgVole (1x) Not tested

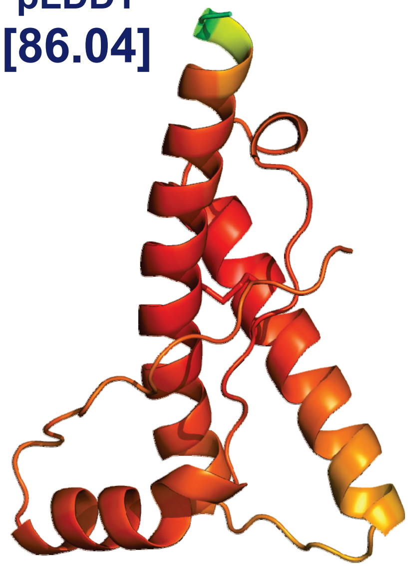
Angola colobus Not tested

In vivo studies

TgVole (1x) Not tested

Angola colobus Not tested

pLDDT [86.04]



Protein code: 1200

Distinct primary sequence across species

Aye-aye

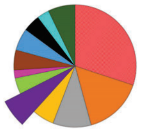
GenBank: BK064012

Daubentonia madagascariensis

Primates 35/45
Daubentoniidae 1/1

P63%

33



30-40

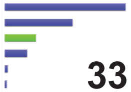
β2-α2 LOOP
SSQNSF
6

WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSSQNSFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQREYEAAAYQRGSS-

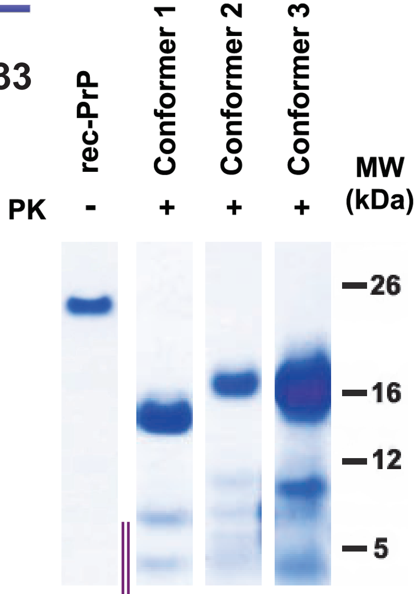
I M W N R NN N K SQ YYEG S

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

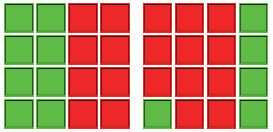


33



213 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: ND

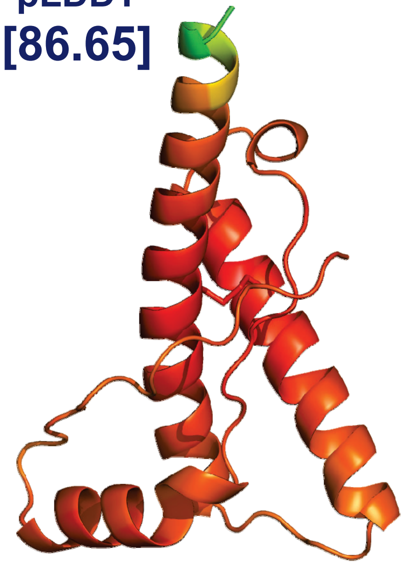
***In vitro* studies**

TgVole (1x)	Not tested
Aye-aye	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Aye-aye	Not tested

pLDDT [86.65]



Protein code: 3173

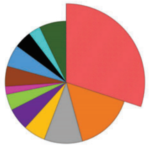
Mohol bushbaby

GenBank: BK064194

Galago moholi

Primates	35/45
Galagidae	1/2

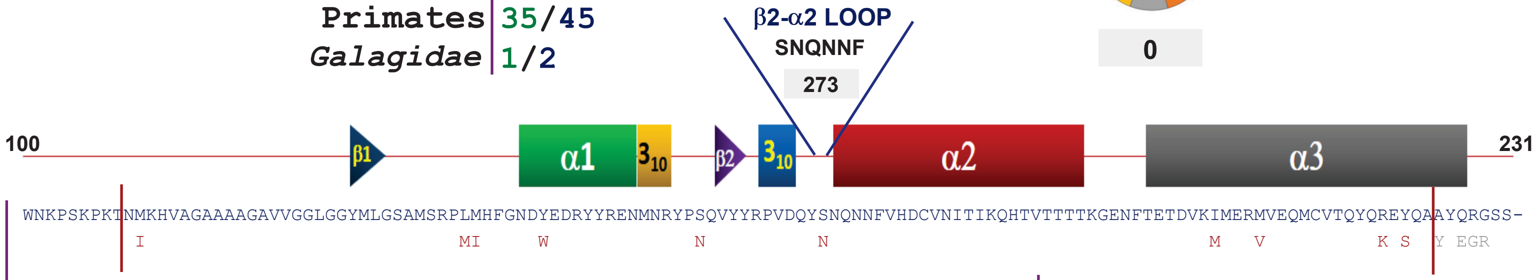
P29%



0

0

Distinct primary sequence across species



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNDYEDRYYRENMNRYPSQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKIMERMVEQMCVTQYQREYQAAYQRGSS-

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

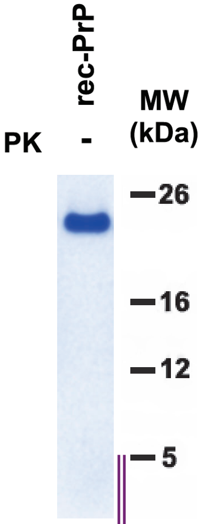
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -7.11

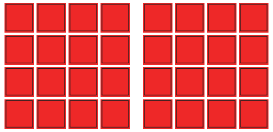


217 AA

NO MISFOLDING

0

Conformers



In vitro studies

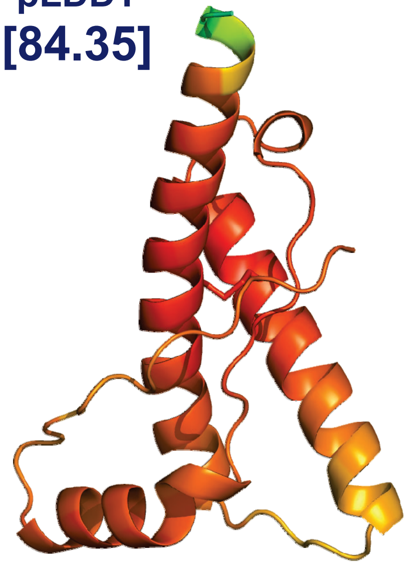
NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT

[84.35]



Protein code: 4523

Distinct primary sequence across species

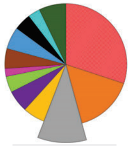
Western gorilla

GenBank: U08300

Gorilla gorilla

Primates	35/45
Hominidae	4/4

P51%


10-20

β2-α2 LOOP
SNQNNF
273

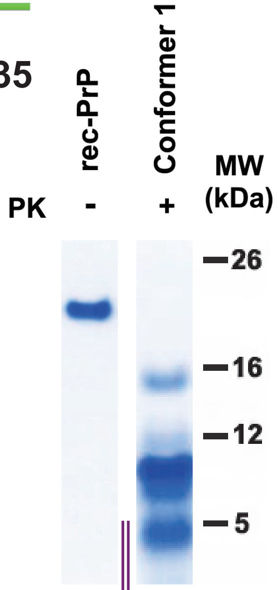
`WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPIIHFGSDYEDRYYRENMHRYPNQVYYRPMDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQRGSS-`

`I V M N W N V N V QK EGR`

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

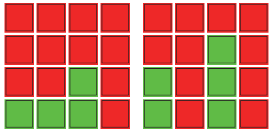
No deletions
No insertions
No polymorphic variants found

135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -5.87

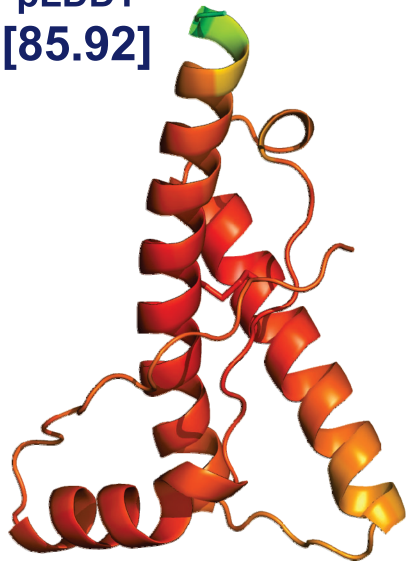
In vitro studies

TgVole (1x)	Not tested
Western gorilla	Not tested

In vivo studies

TgVole (1x)	Not tested
Western gorilla	Not tested

pLDDT
[85.92]



Protein code: 1148

Distinct primary sequence across species

Human

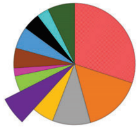
GenBank: NM_001080123

Homo sapiens

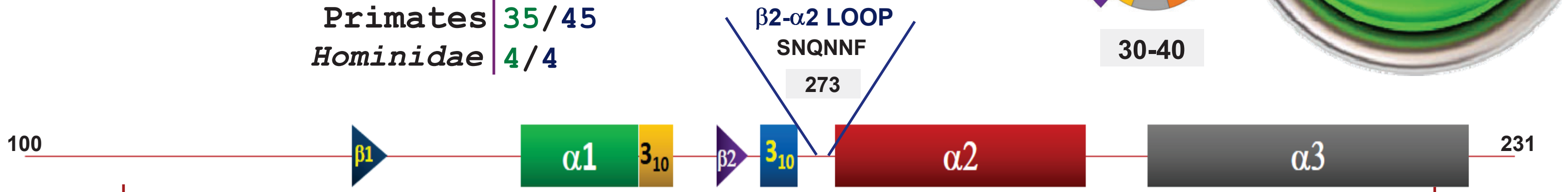
Primates	35/45
Hominidae	4/4

P61%

30.4



30-40



WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPIIHFGSDYEDRYYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQRGSS-

I V M N W N V Q N V QK EGR

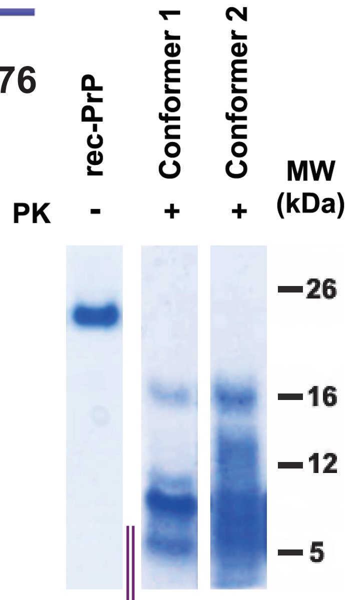
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

It shows polymorphic variants

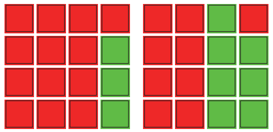
76



211 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: -11.6

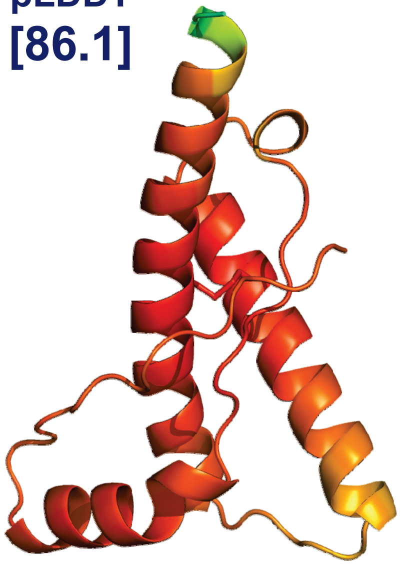
In vitro studies

TgVole (1x)	Propagate
Human	Ongoing

In vivo studies

TgVole (1x)	Infectious
TgHuman	Ongoing

pLDDT
[86.1]



Protein code: 0178

Eastern hoolock gibbon

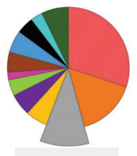
GenBank: BK064201

Hoolock leuconedys

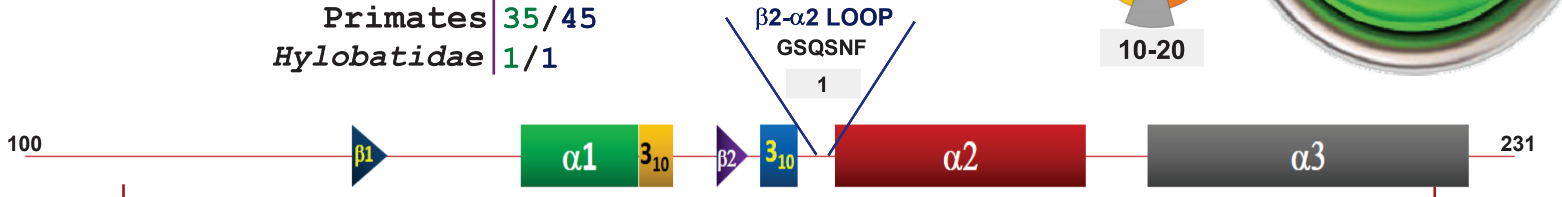
Distinct primary sequence across species

Primates	35/45
Hylobatidae	1/1

P50% **13.9**



10-20



```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPIIHFGSDYEDRYYRENMHRYPNQVYYRPVDQYGSQSNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQRGSS-
           I  V                        M    N W      N           NN N                                     V    QK       EGR
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

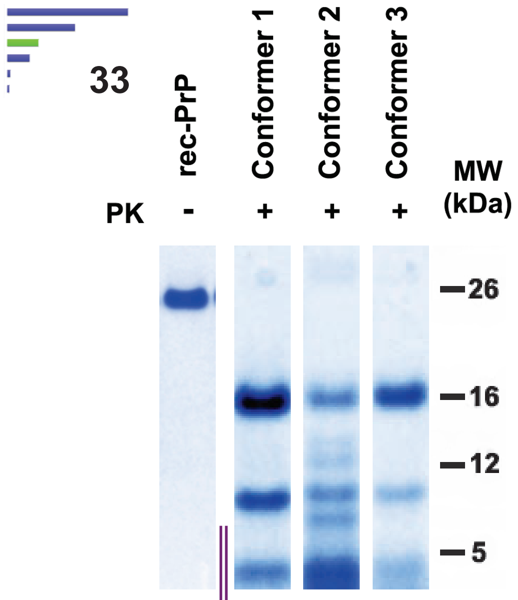
No deletions

No insertions

No polymorphic variants found

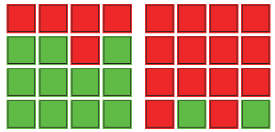
Tm^{Exp}: ND

ΔΔG: -11.24



211 AAs

3 Conformers



In vitro studies

TgVole (1x) Not tested

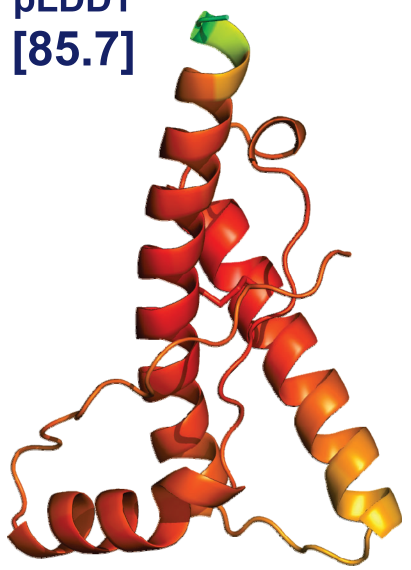
Eastern hoolock gibbon Not tested

In vivo studies

TgVole (1x) Not tested

Eastern hoolock gibbon Not tested

pLDDT [85.7]



Protein code: 4530

Distinct primary sequence across species

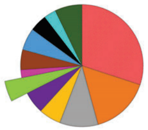
Indri

GenBank: **BK064058**

Indri indri

Primates	35/45
Indridae	2/2

P70% **47.9**



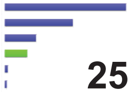
40-50

β2-α2 LOOP
SNQNSF
36

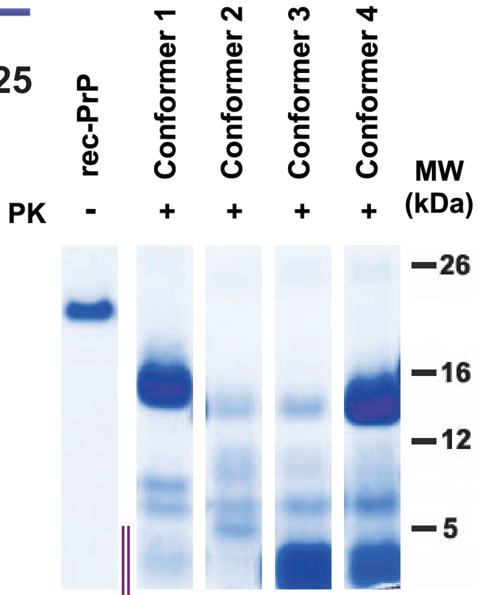
WNKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNSFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQREYEAAYQRGSS-
NI M W N R N N K SQ Y EGR

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

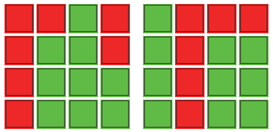


25



212 AA

4 Conformers



Tm^{Exp}: ND

ΔΔG: -10.04

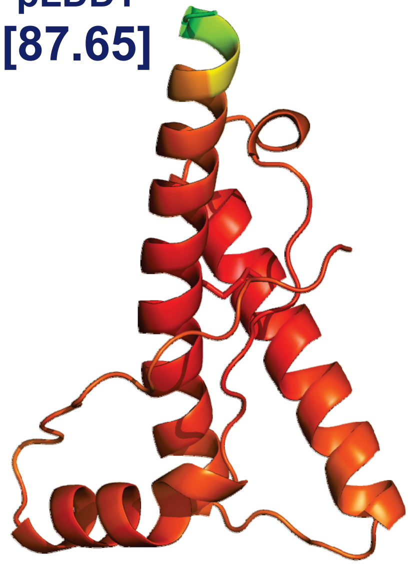
In vitro studies

TgVole (1x)	Not tested
Indri	Not tested

In vivo studies

TgVole (1x)	Not tested
Indri	Not tested

pLDDT [87.65]



Protein code: 3227

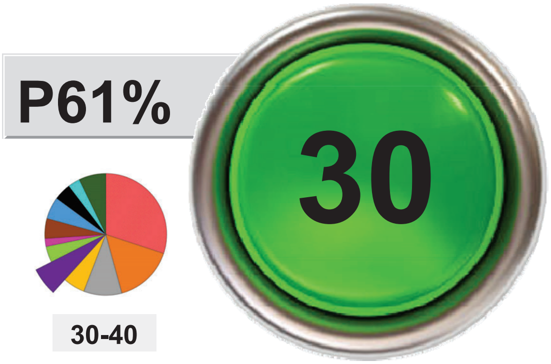
Brown woolly monkey

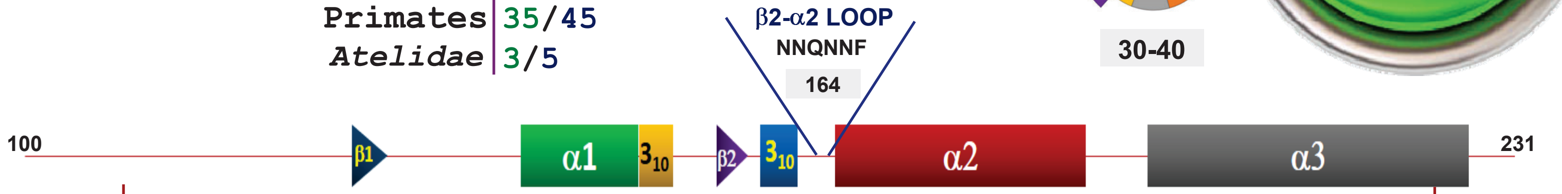
GenBank: AY765384

Lagothrix lagotricha

Primates	35/45
Atelidae	3/5

Distinct primary sequence across species





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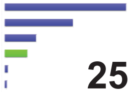
WNKPSKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNEYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQRGSS-
          NI  V                                M      DW          N                                                                              V    QK          EGR
```

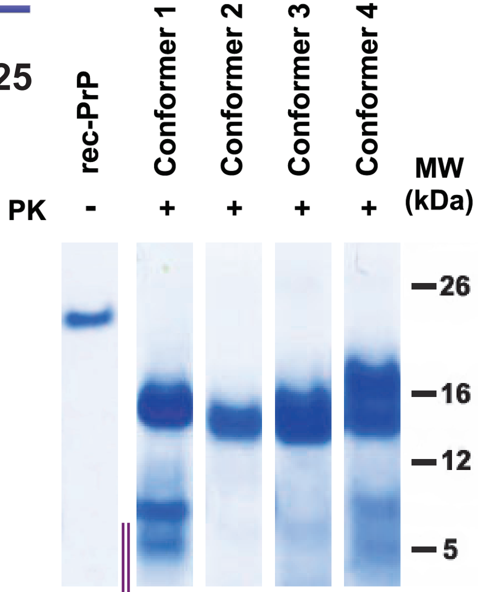
PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

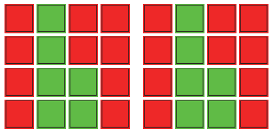
No polymorphic variants found





210 AA

4 Conformers



Tm^{Exp}: ND

ΔΔG: -7.89

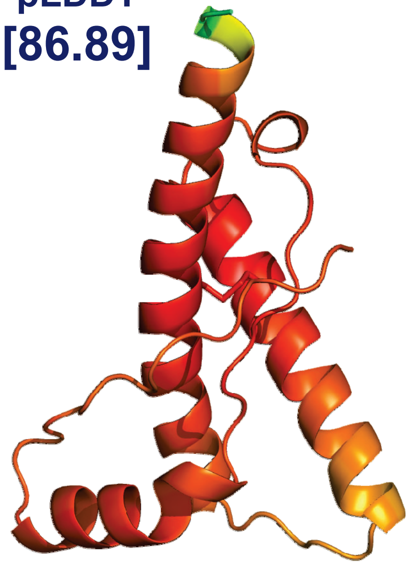
In vitro studies

TgVole (1x)	Not tested
Brown woolly monkey	Not tested

In vivo studies

TgVole (1x)	Not tested
Brown woolly monkey	Not tested

pLDDT [86.89]



Protein code: 1389

Golden lion tamarin

GenBank: BK063917

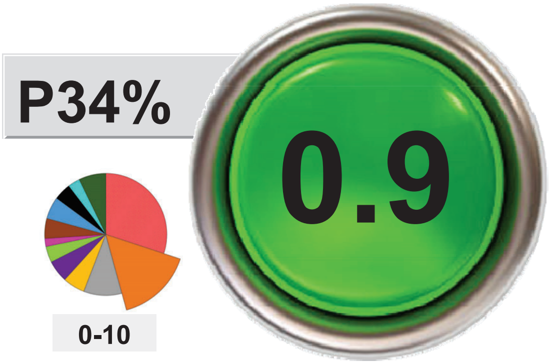
Leontopithecus rosalia

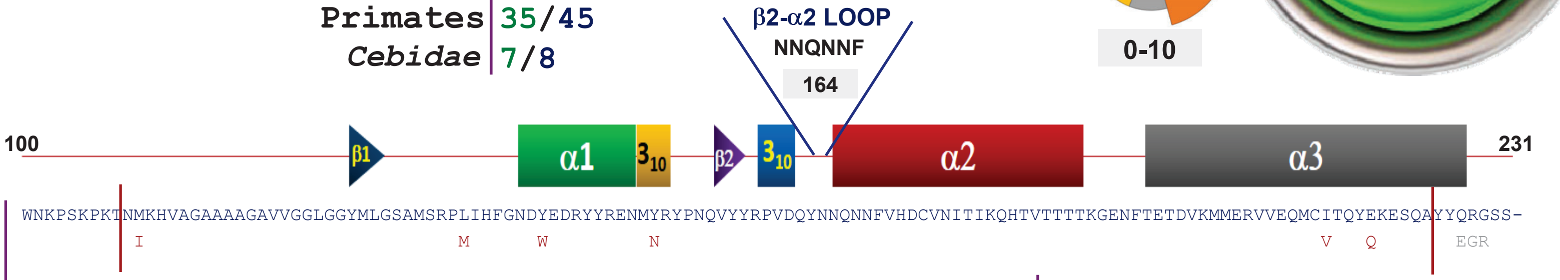
Primates	35/45
Cebidae	7/8

1 species sharing the same primary sequence

Golden-headed lion tamarin
Leontopithecus chrysomelas

P34%





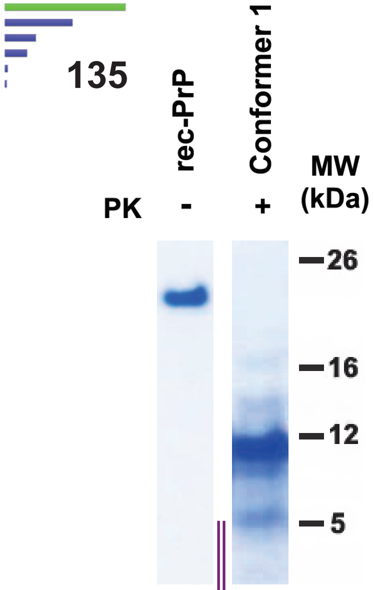
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-

PrP sequence differs by 6 amino acids from the bank vole PrP (see in red)

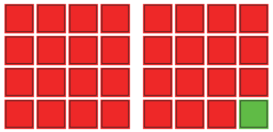
No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -4.23



210 AA



1
Conformers

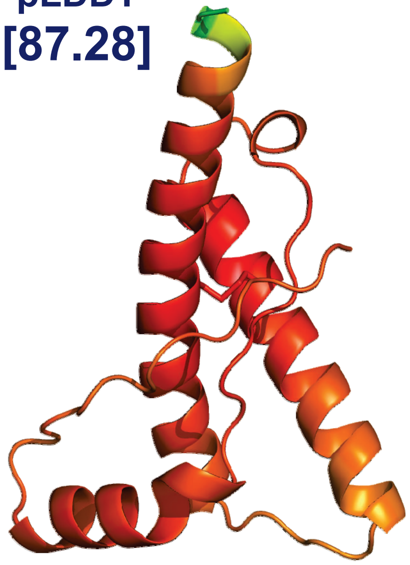
In vitro studies

TgVole (1x)	Not tested
Golden lion tamarin	Not tested

In vivo studies

TgVole (1x)	Not tested
Golden lion tamarin	Not tested

pLDDT
[87.28]



Protein code: 1437

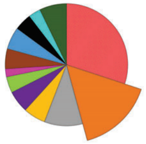
Red slender loris

GenBank: BK064198

Loris tardigradus

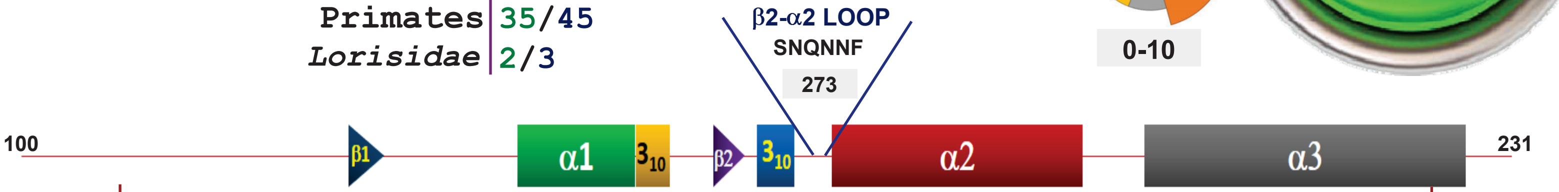
Primates	35/45
Lorisidae	2/3

P39%



0-10

4.8

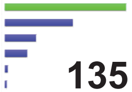


```
WNKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPGQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKIMERMVEQMCVTQYQREYQAAYQRGSS-
         NI                               M      W              N           N                                   M   V          K S  Y EGR
```

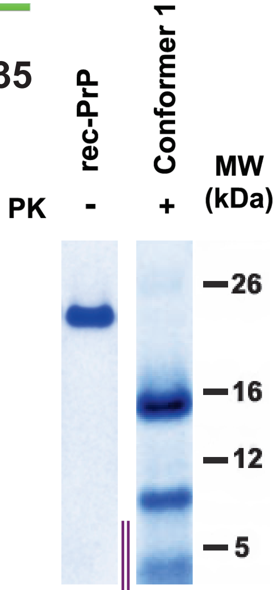
PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

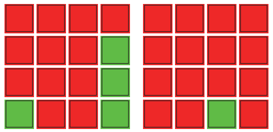


135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: 10.2

In vitro studies

TgVole (1x) Not tested

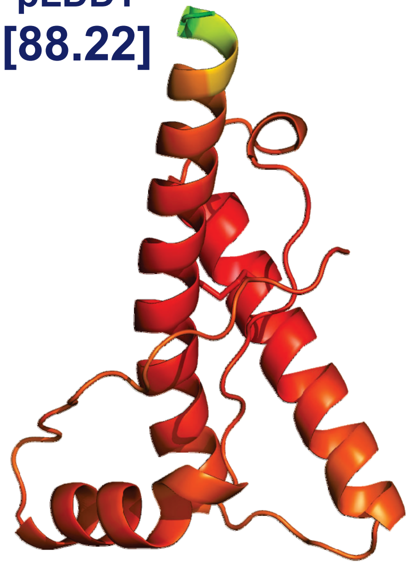
Red slender loris Not tested

In vivo studies

TgVole (1x) Not tested

Red slender loris Not tested

pLDDT
[88.22]



Protein code: 4527

Pigtail macaque

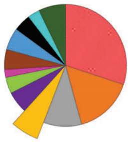
GenBank: XM_011741222

Macaca nemestrina

Primates 35/45
Cercopithecidae 7/7

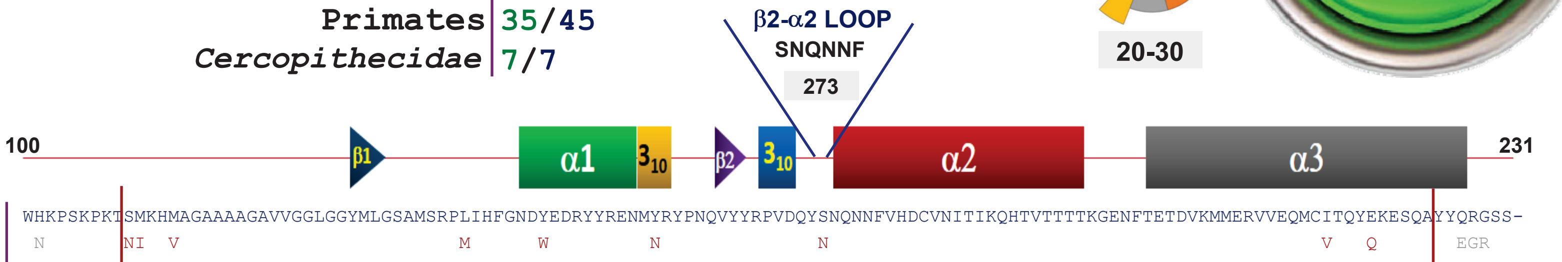
P59%

26.8


20-30

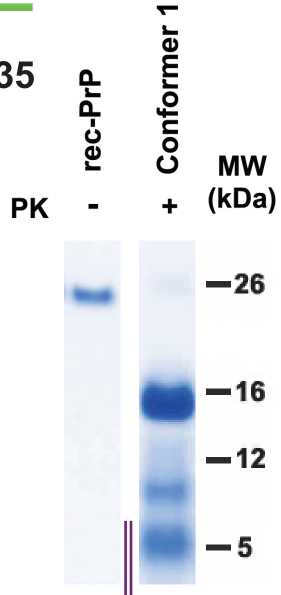
20 species sharing the same primary sequence

- ● **Hamadryas baboon** *Papio hamadryas*
- ● **Olive baboon** *Papio anubis*
- ● **Assam macaque** *Macaca assamensis*
- ● **Barbary macaque** *Macaca sylvanus*
- ● **Stump-tailed macaque** *Macaca arctoides*
- ● **Rhesus macaque** *Macaca mulatta*
- ● **Japanese macaque** *Macaca fuscata*
- ● **Grivet** *Chlorocebus aethiops*
- ● **Black crested mangabey** *Lophocebus aterrimus*
- ● **DeBrazza's monkey** *Cercopithecus neglectus*
- ● **Guenons** *Cercopithecus diana*
- ● **Mona monkey** *Cercopithecus mona*
- ● **Green monkey** *Chlorocebus sabaeus*
- ● **Pigtail macaque** *Macaca nemestrina*
- ● **Allen's swamp monkey** *Allenopithecus nigroviridis*
- ● **Patas monkey** *Erythrocebus patas*
- ● **Guinea baboon** *Papio papio*
- ● **Sykes' monkey** *Cercopithecus albogularis*
- ● **Lion-tailed macaque** *Macaca silenus*
- ● **Formosan rock macaque** *Macaca cyclopis*



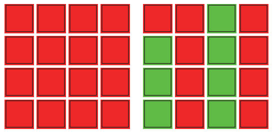
PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



219 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -6.33

In vitro studies

No propagation
TgVole (1x)

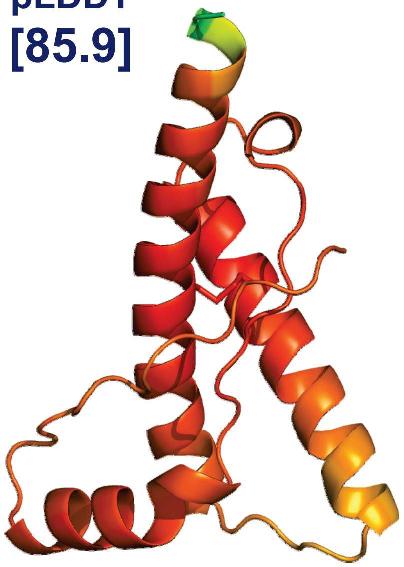
Not tested
Pigtail macaque

In vivo studies

Ongoing
TgVole (1x)

Not tested
Pigtail macaque

pLDDT [85.9]



Protein code: 1970

Drill

GenBank: XM_011975232

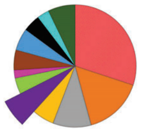
Mandrillus leucophaeus

Primates 35/45
Cercopithecidae 7/7

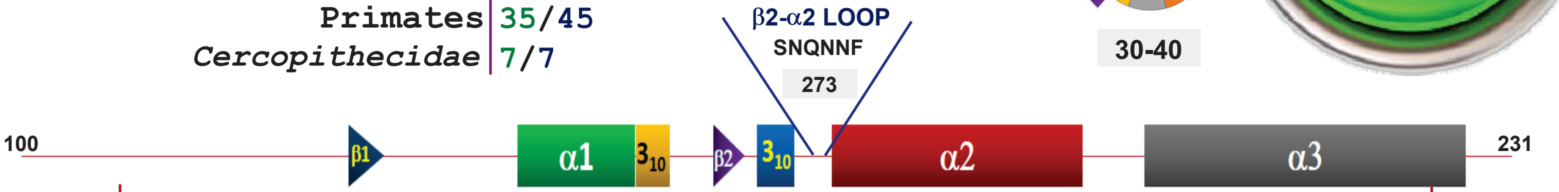
Distinct primary sequence across species

P64%

35.7



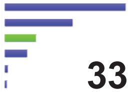
30-40

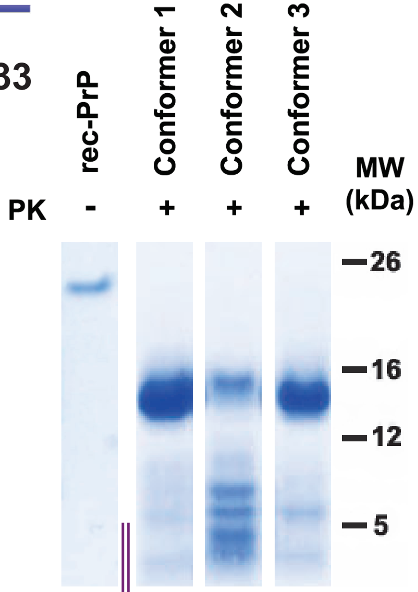


```
WHKPNKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNEYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-
  N  S   NI  V                                  M     DW         N                N                                      V   Q          EGR
```

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

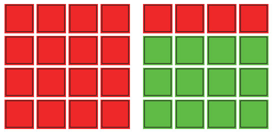
No deletions
No insertions
No polymorphic variants found





219 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: -10.7

In vitro studies

TgVole (1x) Not tested

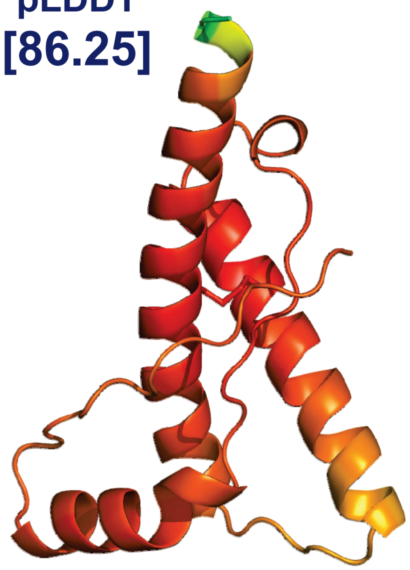
Drill Not tested

In vivo studies

TgVole (1x) Not tested

Drill Not tested

pLDDT
[86.25]



Protein code: 2078

Distinct primary sequence across species

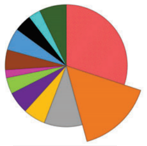
Mandrill

GenBank: U08303

Mandrillus sphinx

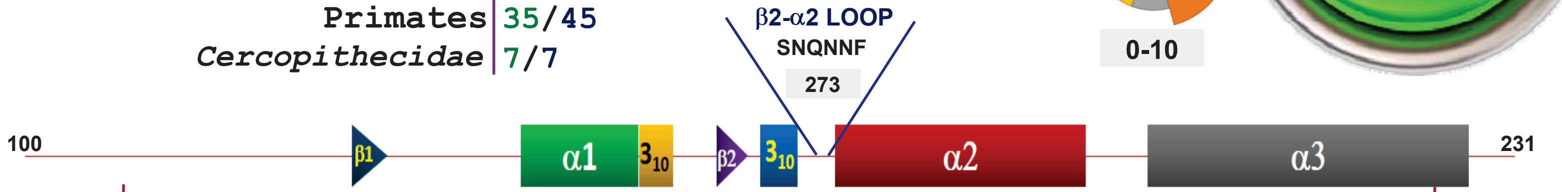
Primates	35/45
Cercopithecidae	7/7

P34%



0-10

0.9



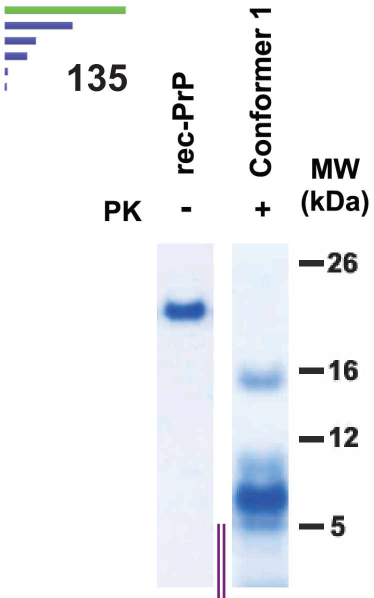
```
WHKPNKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-
 N  S    NI  V                         M      W         N              N                                            V   Q       EGR
```

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

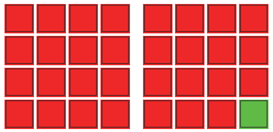
No polymorphic variants found



211 AA

1

Conformers



Tm^{Exp}: ND

ΔΔG: -6.05

***In vitro* studies**

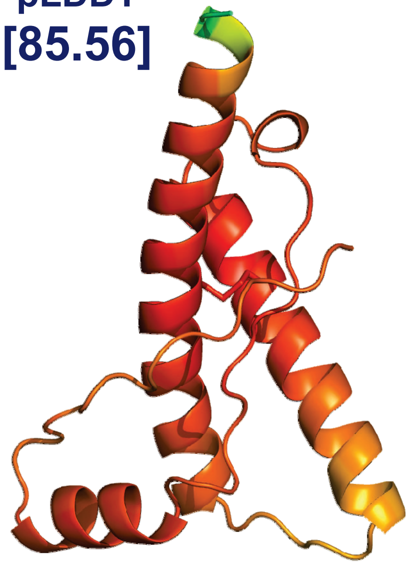
TgVole (1x)	Not tested
Mandrill	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Mandrill	Not tested

pLDDT

[85.56]



Gray mouse lemur

GenBank: NM_001309920

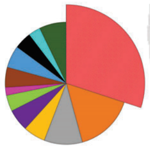
Microcebus murinus

Primates	35/45
Cheirogaleidae	1/4

3 species sharing the same primary sequence

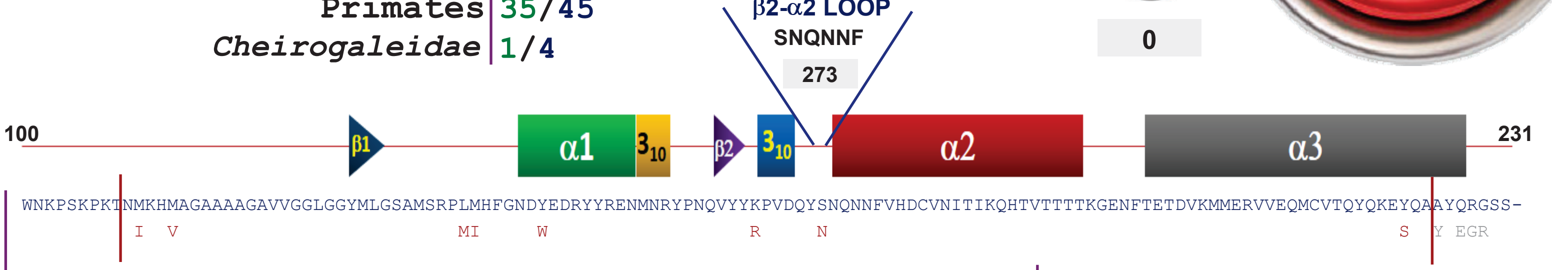
- **Reddish-gray mouse lemur** *Microcebus griseorufus*
- **Mittermeier's mouse lemur** *Microcebus mittermeieri*
- **Northern rufous mouse lemur** *Microcebus tavaratra*

P29%



0

0



PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

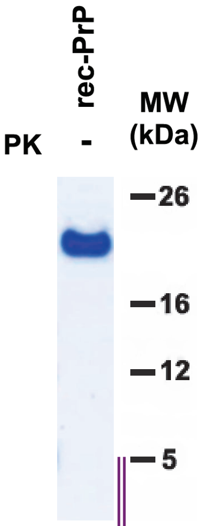
No deletions

No insertions

No polymorphic variants found

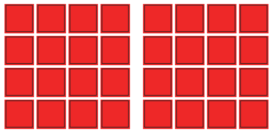
Tm^{Exp}: ND

ΔΔG: 1.62



212 AA

NO MISFOLDING



0

Conformers

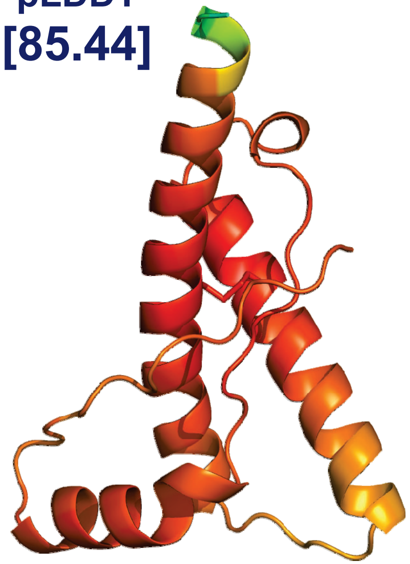
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [85.44]



Protein code: 0933

Distinct primary sequence across species

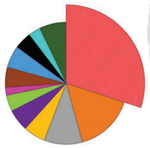
Golden-brown mouse lemur

GenBank: BK064086

Microcebus ravelobensis

Primates	35/45
Cheirogaleidae	1/4

P29%



0

0

β2-α2 LOOP
SNQNNF
273

```
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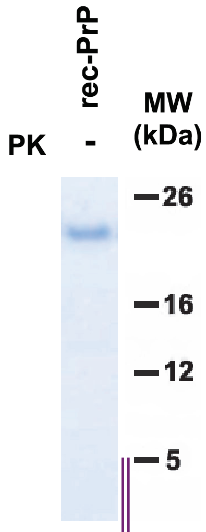
           I  V                                MI      W          N         R      N                                                                  S   Y EGR
```

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -0.56



212 AA

NO MISFOLDING

0
Conformers

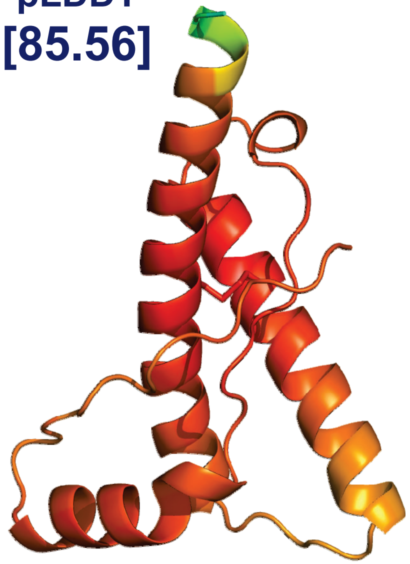
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[85.56]

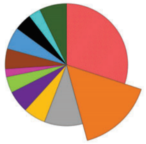


Protein code: 3265

Angolan talapoin

GenBank: BK064818

P41%

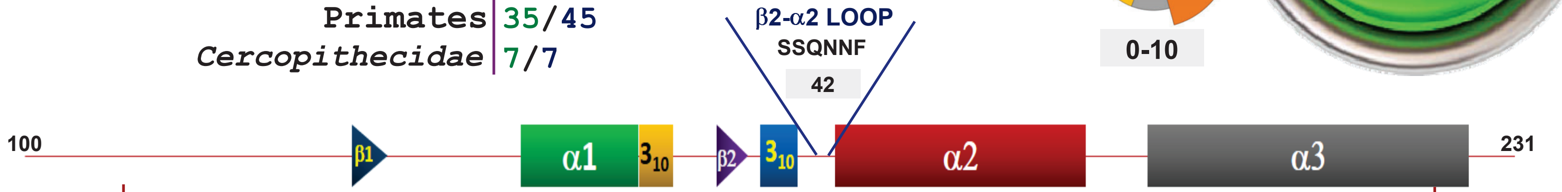


7.5

Distinct primary sequence across species

Miopithecus talapoin

Primates	35/45
Cercopithecidae	7/7



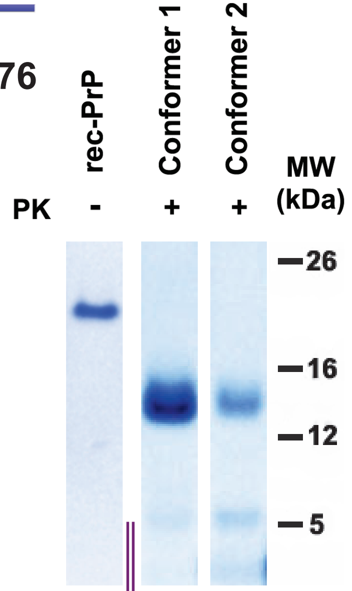
WHKPSKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSSQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-

N NI V M W N NN V Q EGR

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

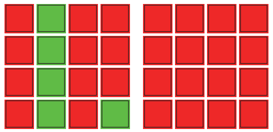
No deletions
No insertions
No polymorphic variants found

76



211 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -10.99

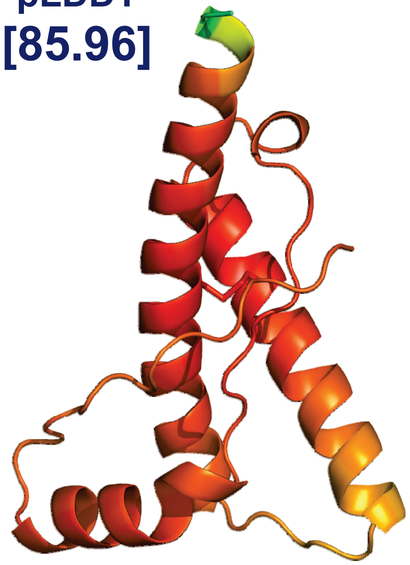
In vitro studies

TgVole (1x)	Not tested
Angolan talapoin	Not tested

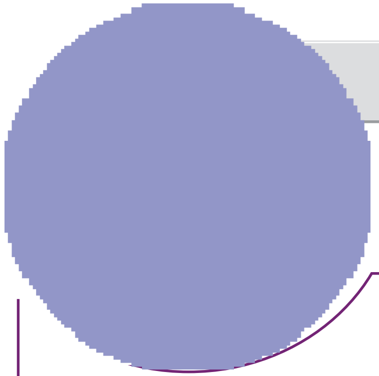
In vivo studies

TgVole (1x)	Not tested
Angolan talapoin	Not tested

pLDDT
[85.96]



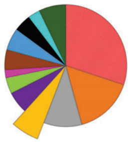
Protein code: 4508



Coquerel's giant mouse lemur

GenBank: BK064094

P60% **27.9**



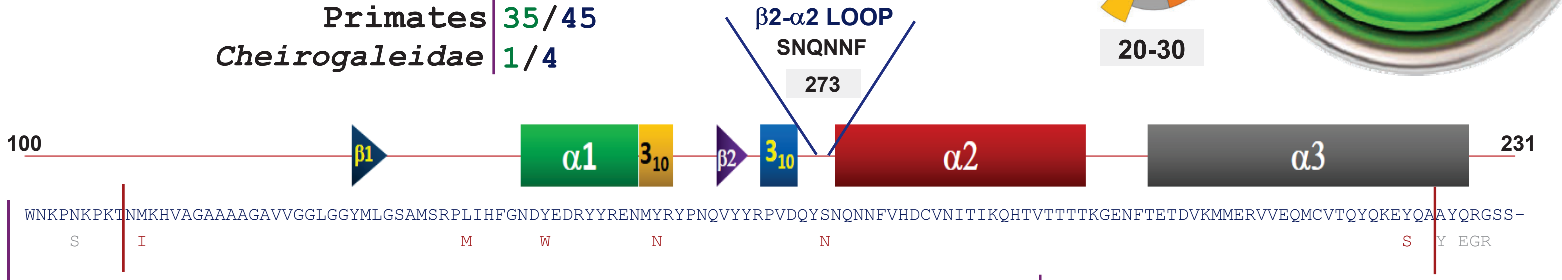
20-30

Mirza coquereli

`Primates` **35/45**
`Cheirogaleidae` **1/4**

1 species sharing the same primary sequence

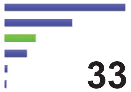
Northern giant mouse lemur
Mirza zaza



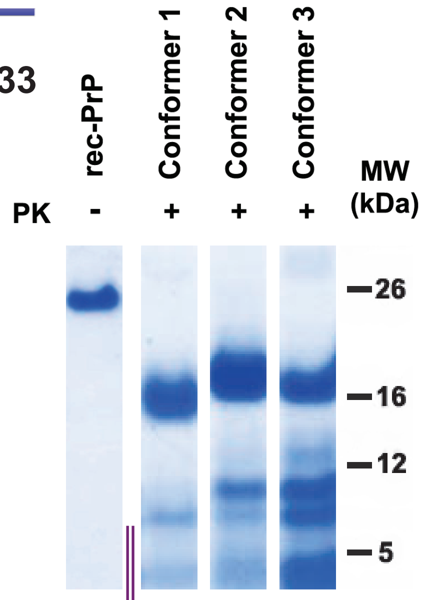
```
WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKEYQAAYQRGSS-
    S    I                          M     W        N             N                                                           S   Y EGR
```

PrP sequence differs by 6 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

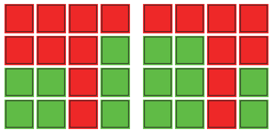


33



212 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: 4.23

***In vitro* studies**

Not tested
TgVole (1x)

Not tested
Coquerel's giant mouse lemur

***In vivo* studies**

Not tested
TgVole (1x)

Not tested
Coquerel's giant mouse lemur

pLDDT
[85.02]

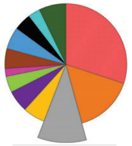
Protein code: 3273

Sunda slow loris

GenBank: BK064114

P46%

10.7



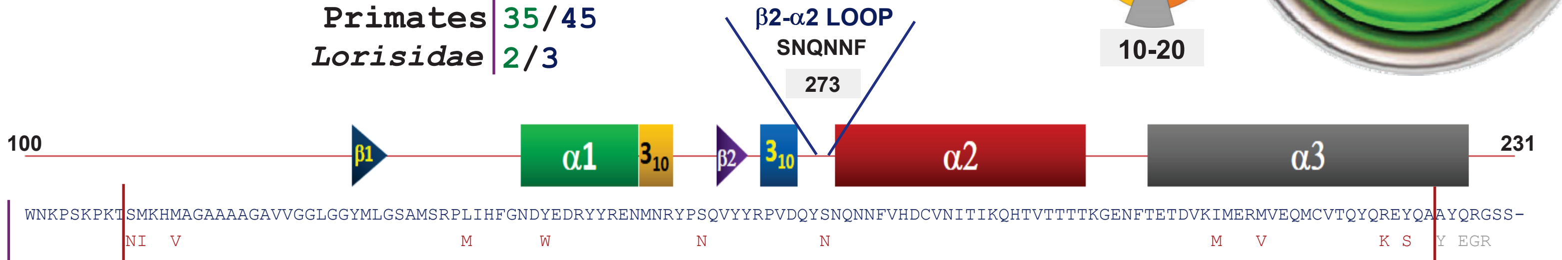
10-20

Nycticebus coucang

Primates 35/45
Lorisidae 2/3

1 species sharing the same primary sequence

Bengal slow loris
Nycticebus bengalensis



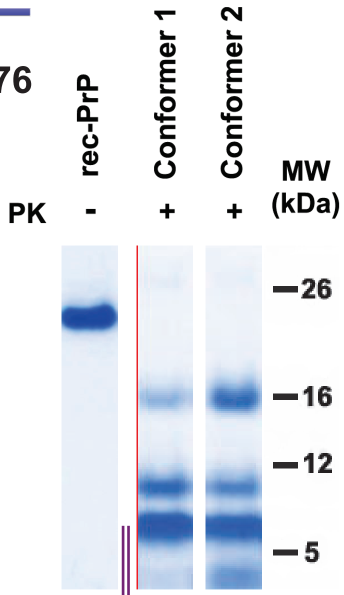
WNKPSKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPSQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKIMERMVEQMCVTQYQREYQAAYQRGSS-

NI V M W N N M V K S Y EGR

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

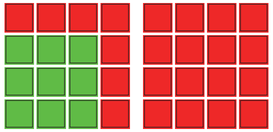
No deletions
No insertions
No polymorphic variants found

76



211 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -1.87

In vitro studies

TgVole (1x) Not tested

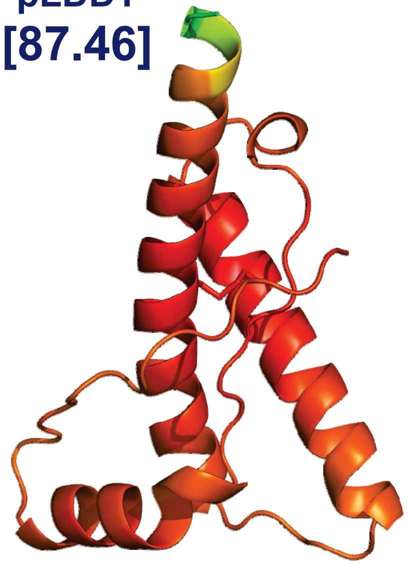
Sunda slow loris Not tested

In vivo studies

TgVole (1x) Not tested

Sunda slow loris Not tested

pLDDT
[87.46]



Protein code: 3294

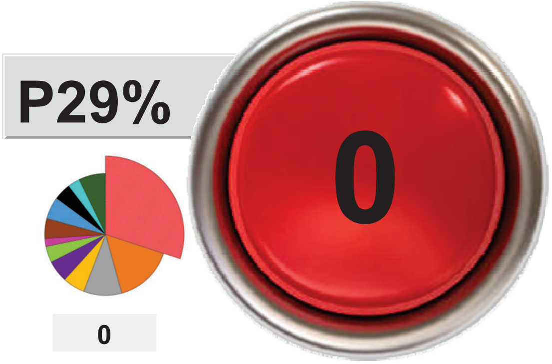
Pygmy slow loris

GenBank: OR47281

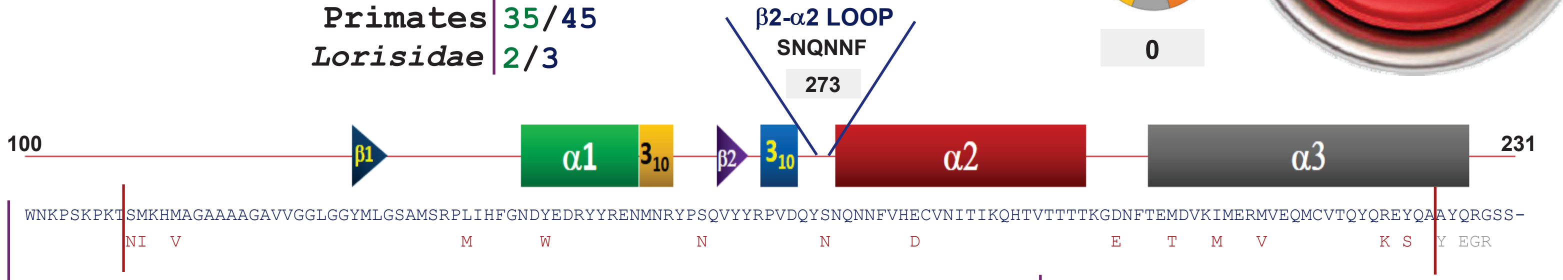
Nycticebus pygmaeus

Primates	35/45
Lorisidae	2/3

P29%



Distinct primary sequence across species



```
WNKPSKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPSQVYYRPVDQYSNQNNFVHECVNITIKQHTVTTTTKGDNFTEMDVKIMERMVEQMCVTQYQREYQAAYQRGSS-
         NI  V                         M      W             N          N       D                 E    T   M   V          K S  Y EGR
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

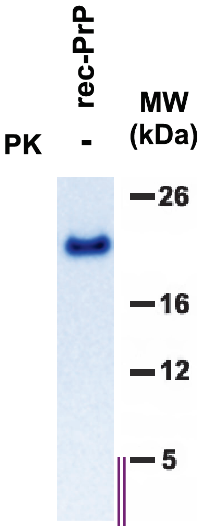
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -6.58



211 AA

NO MISFOLDING

0 Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [90.2]

Protein code: 4835

Northern greater galago

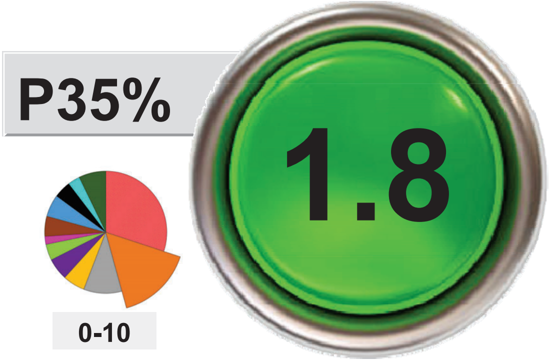
GenBank: XM_003788036

Otolemur garnettii

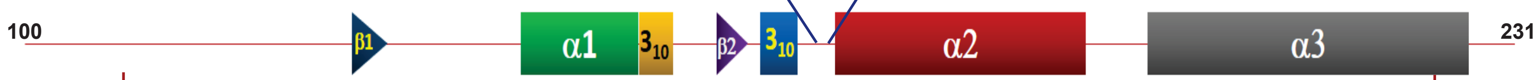
Distinct primary sequence across species

Primates	35/45
Galagidae	1/2

P35%



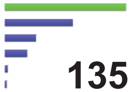
β2-α2 LOOP
SNQNNF
273

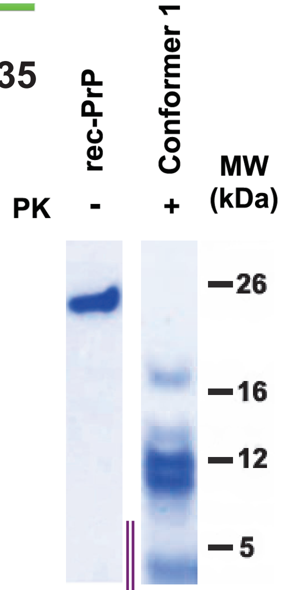


```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPSQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKIMERMVEQMCVTQYQREYQAAYQRGSS-
           I                        M       W              N          N                                  M    V           K S  Y EGR
```

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

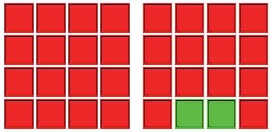
No deletions
No insertions
No polymorphic variants found





217 AA

1 Conformers



Tm^{Exp}: ND

ΔΔG: -2.15

***In vitro* studies**

TgVole (1x) — Not tested

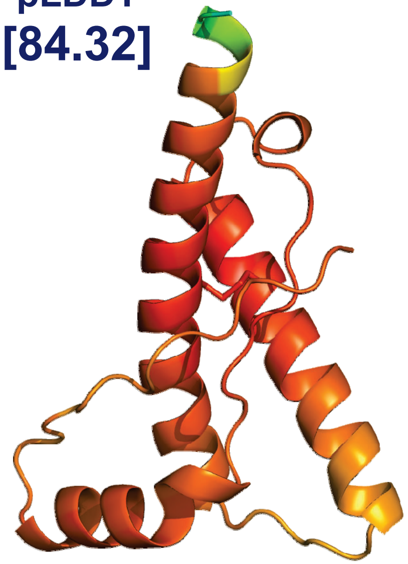
Northern greater galago — Not tested

***In vivo* studies**

TgVole (1x) — Not tested

Northern greater galago — Not tested

pLDDT [84.32]



Protein code: 1105

Chimpanzee

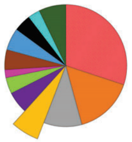
GenBank: U08296

Pan troglodytes

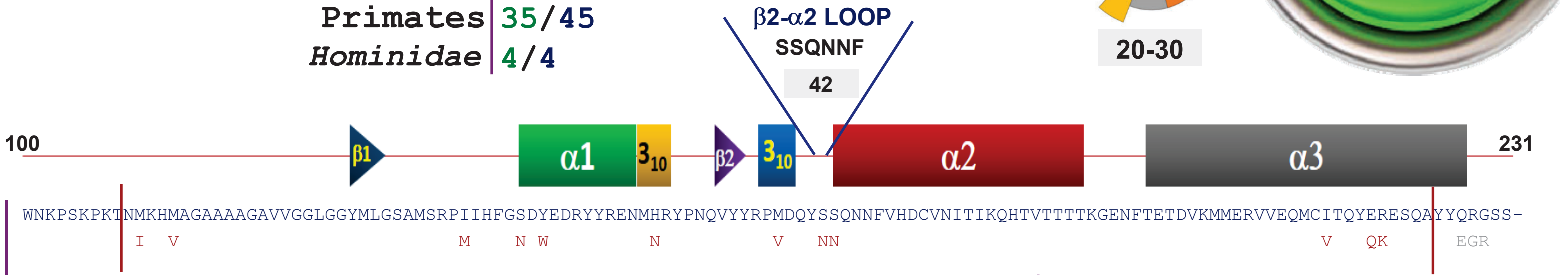
Primates 35/45
Hominidae 4/4

P55%

20.7



20-30



WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPIIHFGSDYEDRYYRENMHRYPNQVYYRPMDQYSSQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQRGSS-

I V M N W N V NN V QK EGR

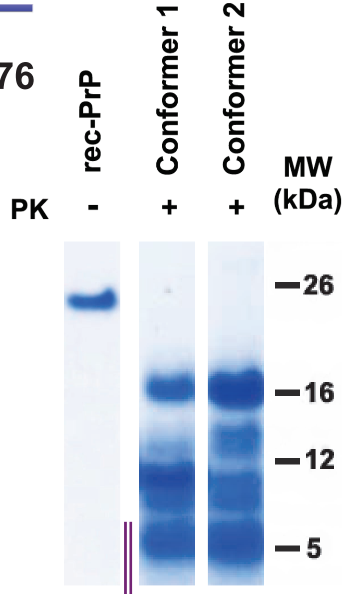
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

9 species sharing the same primary sequence

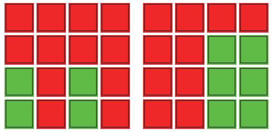
- **Agile gibbon** *Hylobates agilis*
- **Lar gibbon** *Hylobates lar*
- **Silvery gibbon** *Hylobates moloch*
- **Müller's gibbon** *Hylobates muelleri*
- **Pileated gibbon** *Hylobates pileatus*
- **N white-cheeked gibbon** *Nomascus leucogenys*
- **S white-cheeked gibbon** *Nomascus siki*
- **Bonobo** *Pan paniscus*
- **Siamang** *Symphalangus syndactylus*

76



211 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -9.88

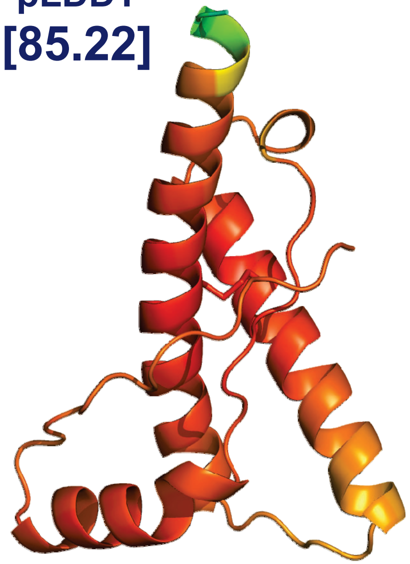
In vitro studies

TgVole (1x)	Not tested
Chimpanzee	Not tested

In vivo studies

TgVole (1x)	Not tested
Chimpanzee	Not tested

pLDDT [85.22]



Protein code: 1134

Rio Tapajós saki

GenBank: AY765379

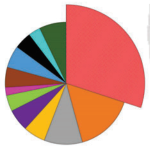
Pithecia irrorata

Primates	35/45
Pitheciidae	3/4

1 species sharing the same primary sequence

White-faced saki
Pithecia pithecia

P29%



0

0

β2-α2 LOOP
SNQNNF
273

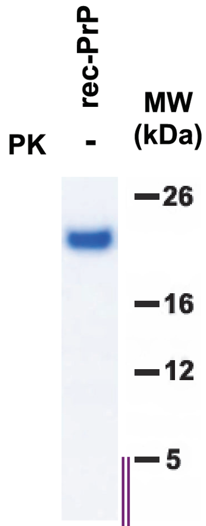
```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQRGSS-
           I  V                           M      W          N             N                                           V   QK       EGR
```

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -6.48



211 AA

NO MISFOLDING

0
Conformers

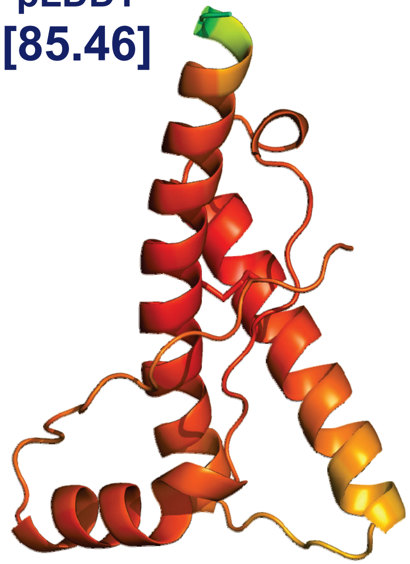
In vitro studies

NOT APPLICABLE

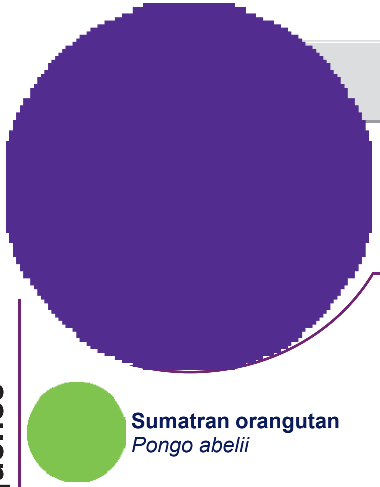
In vivo studies

NOT APPLICABLE

pLDDT
[85.46]



Protein code: 1411



Bornean orangutan

GenBank: U08305

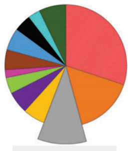
Pongo pygmaeus

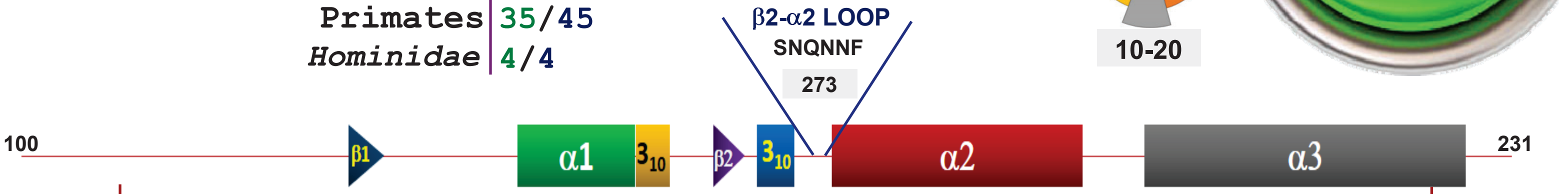
1 species sharing the same primary sequence

Sumatran orangutan
Pongo abelii

Primates	35/45
Hominidae	4/4

P47%

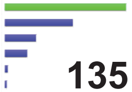


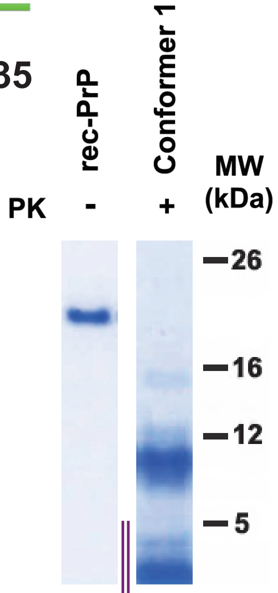


```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPIIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQRGSS-
           I  V                                  M      W         N             N                                          V    QK      EGR
```

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

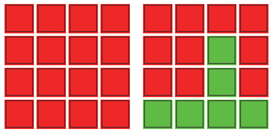
No deletions
No insertions
No polymorphic variants found





211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -10.55

In vitro studies

TgVole (1x) Not tested

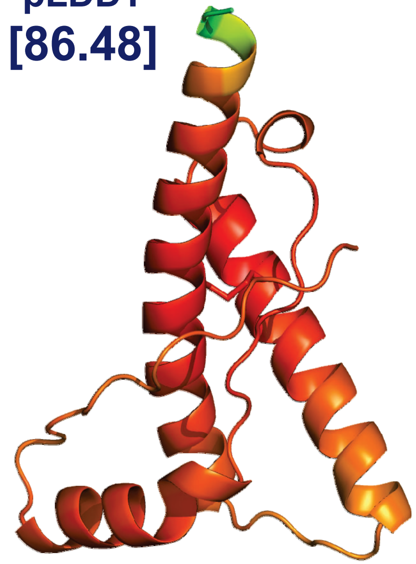
Bornean orangutan Not tested

In vivo studies

TgVole (1x) Not tested

Bornean orangutan Not tested

pLDDT
[86.48]



Protein code: 0926

Greater bamboo lemur

GenBank: BK063921

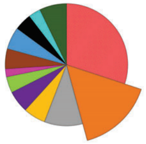
Prolemur simus

Primates	35/45
Lemuridae	1/1

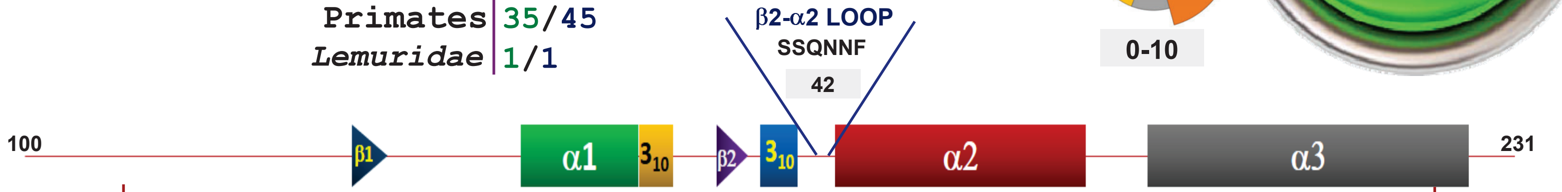
5 species sharing the same primary sequence

- **White-headed lemur** *Eulemur albifrons*
- **Common brown lemur** *Eulemur fulvus*
- **Black lemur** *Eulemur macaco*
- **Mongoose lemur** *Eulemur mongoz*
- **Ring-tailed lemur** *Lemur catta*

P34% **0.9**



0-10



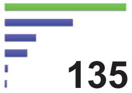
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSSQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQREYEAAYQRGSS-
           I                                M      W          N         R      NN                                                         K SQ Y EGR
```

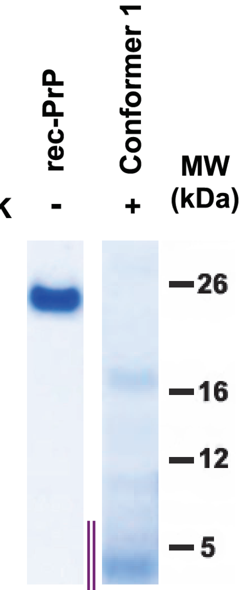
PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

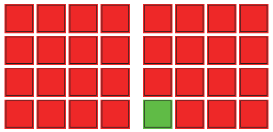
No polymorphic variants found





211 AA

1 Conformers



Tm^{Exp}: ND

ΔΔG: -6.96

In vitro studies

Not tested
TgVole (1x)

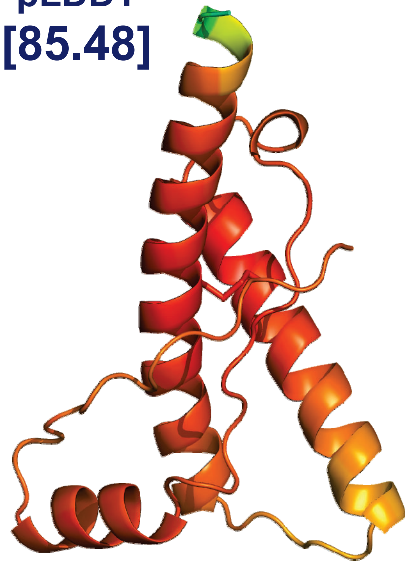
Not tested
Greater bamboo lemur

In vivo studies

Not tested
TgVole (1x)

Not tested
Greater bamboo lemur

pLDDT
[85.48]



Protein code: 2028

Coquerel's sifaka

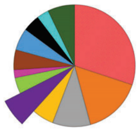
GenBank: XM_012639270

Propithecus coquereli

Primates 35/45
Indridae 2/2

P64%

33.9



30-40

Distinct primary sequence across species

β2-α2 LOOP
SSQNSF
6

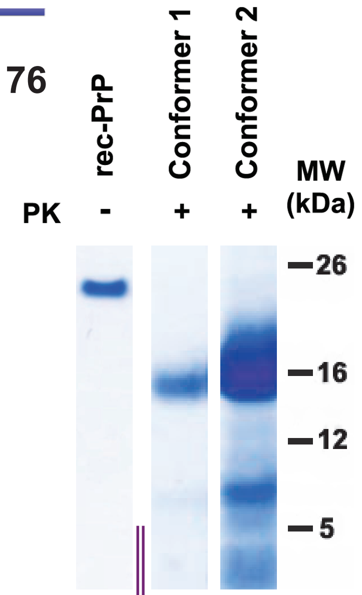
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSSQNSFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQREYEAAYQRGSS-

I M W N R NN N K SQ Y EGR

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

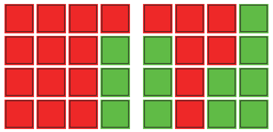
No deletions
No insertions
No polymorphic variants found

76



212 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -3.69

***In vitro* studies**

TgVole (1x) Not tested

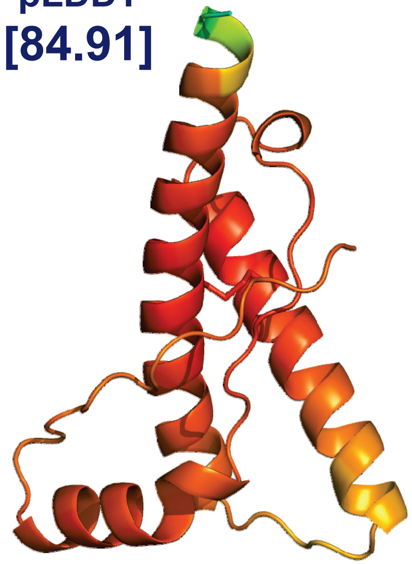
Coquerel's sifaka Not tested

***In vivo* studies**

TgVole (1x) Not tested

Coquerel's sifaka Not tested

pLDDT
[84.91]



Protein code: 1127

Pied tamarin

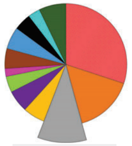
GenBank: AY765388

Saguinus bicolor

Primates 35/45
Cebidae 7/8

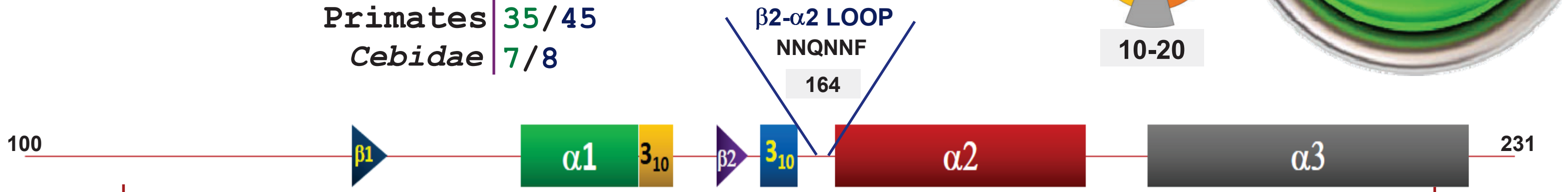
Distinct primary sequence across species

P54%



10-20

18.8



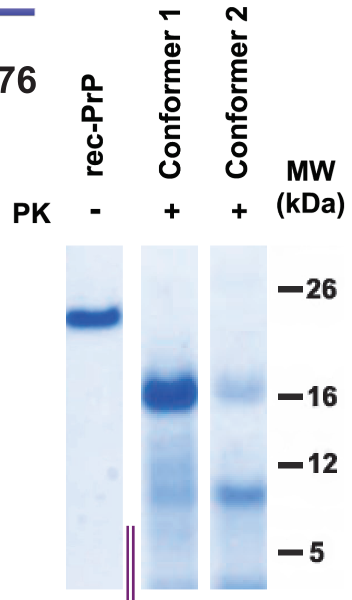
`WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEGRYYRENMYRYPNQVYYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-`

`I M WD N V Q EGR`

PrP sequence differs by 7 amino acids from the bank vole PrP (see in red)

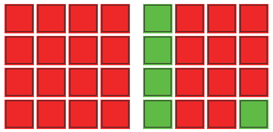
No deletions
No insertions
No polymorphic variants found

76



210 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: 6.16

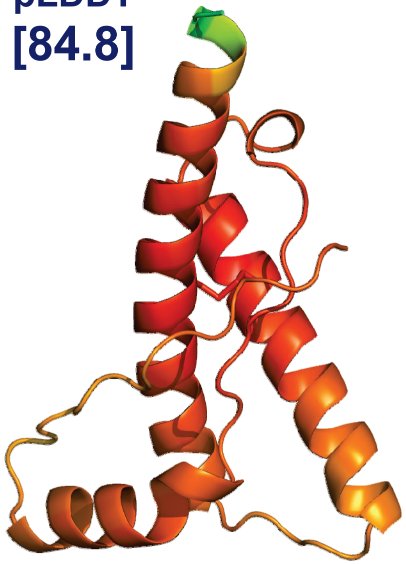
***In vitro* studies**

TgVole (1x)	Not tested
Pied tamarin	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Pied tamarin	Not tested

pLDDT [84.8]



Protein code: 1456

Emperor tamarin

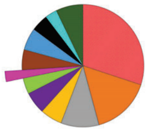
GenBank: BK064034

Saguinus imperator

Primates	35/45
Cebidae	7/8

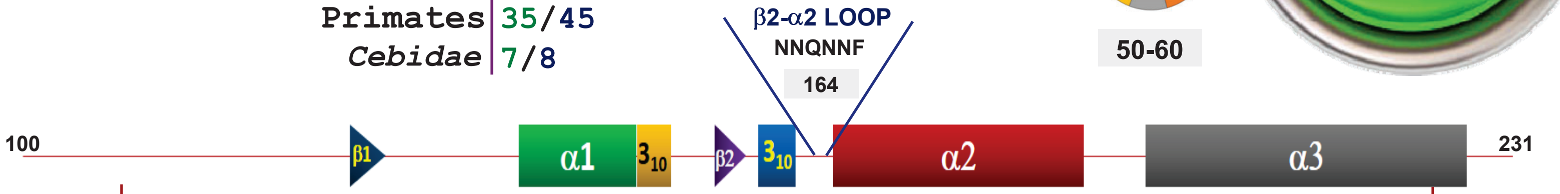
P73%

53.6



50-60

Distinct primary sequence across species



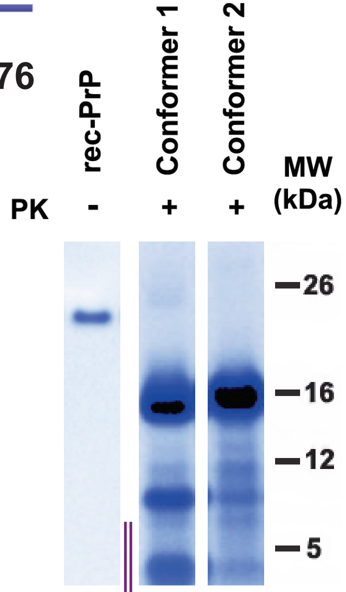
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-
          I                          M      W         N                                                                       V   Q          EGR
```

PrP sequence differs by 6 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

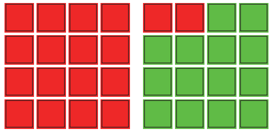
No polymorphic variants found



210 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: 4.37

In vitro studies

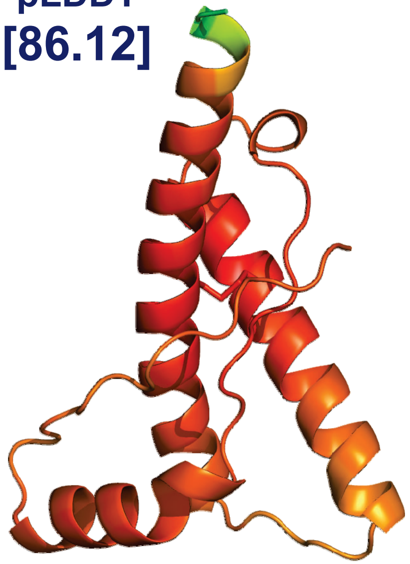
TgVole (1x)	Not tested
Emperor tamarin	Not tested

In vivo studies

TgVole (1x)	Not tested
Emperor tamarin	Not tested

pLDDT

[86.12]



Protein code: 3200

Distinct primary sequence across species

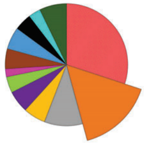
Golden-handed tamarin

GenBank: BK064187

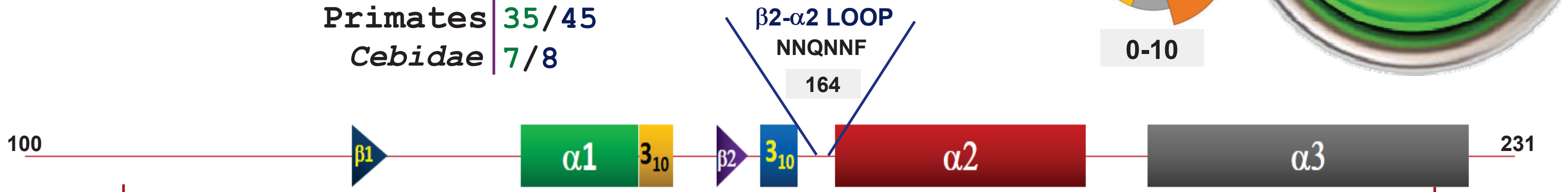
Saguinus midas

Primates	35/45
Cebidae	7/8

P41%



0-10



WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-

I V M W N V Q EGR

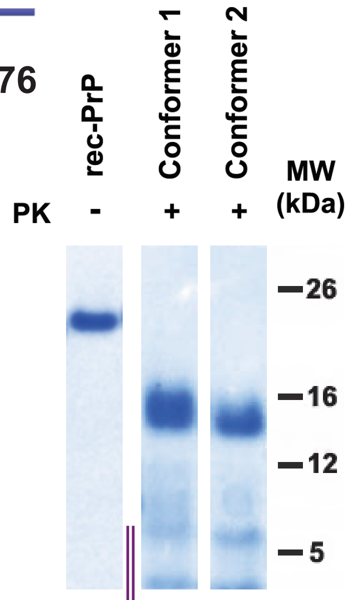
PrP sequence differs by 7 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

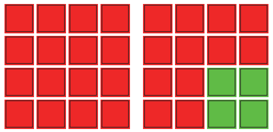
No polymorphic variants found

76



210 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -4.49

In vitro studies

TgVole (1x) Not tested

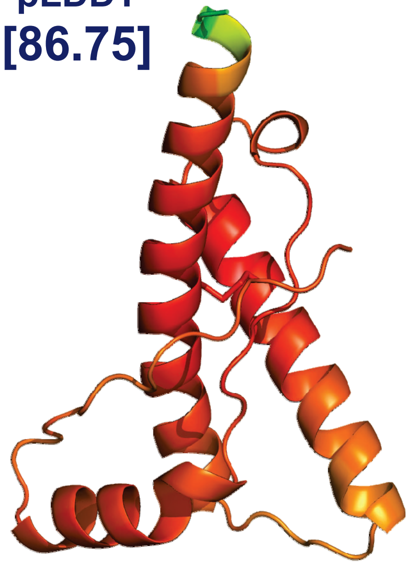
Golden-handed tamarin Not tested

In vivo studies

TgVole (1x) Not tested

Golden-handed tamarin Not tested

pLDDT
[86.75]



Protein code: 4093

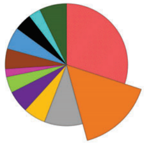
Black-capped squirrel monkey

GenBank: BK064035

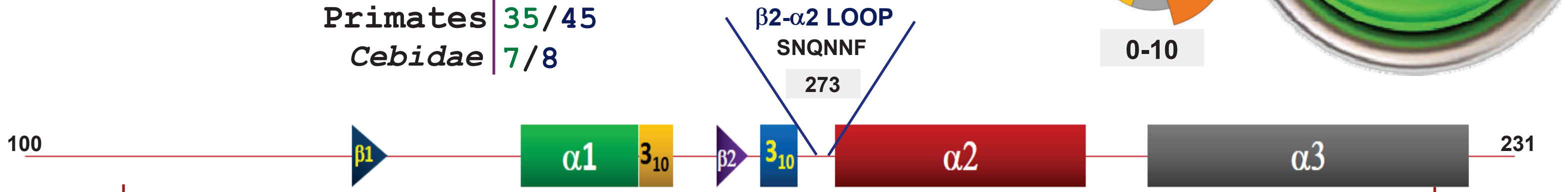
Saimiri boliviensis

Primates 35/45
Cebidae 7/8

P34%



0-10



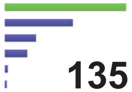
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPSQVYYKPVDQYSNQNNFVHDCVNVTIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-

I V M W N N R N I V Q EGR

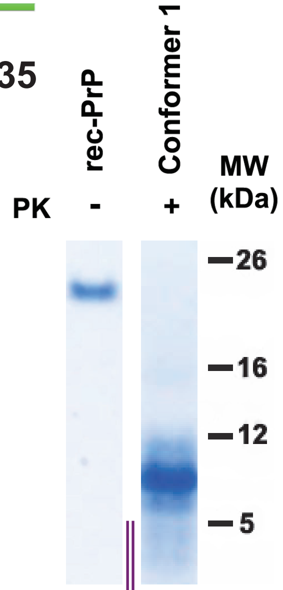
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

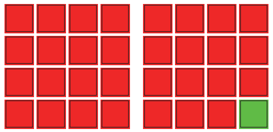


135



218 AA

1 Conformers



Tm^{Exp}: ND

ΔΔG: -5.19

In vitro studies

TgVole (1x) Not tested

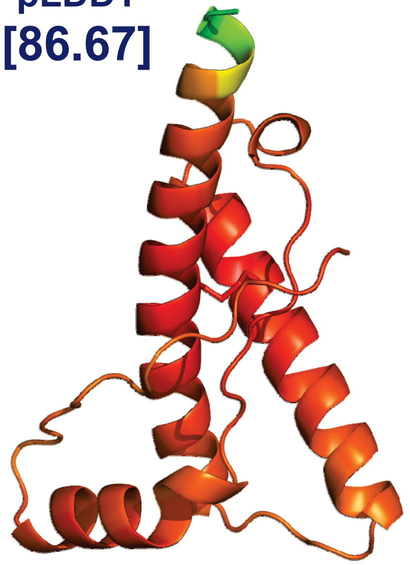
Black-capped squirrel monkey Not tested

In vivo studies

TgVole (1x) Not tested

Black-capped squirrel monkey Not tested

pLDDT [86.67]



Protein code: 1975

Squirrel monkey

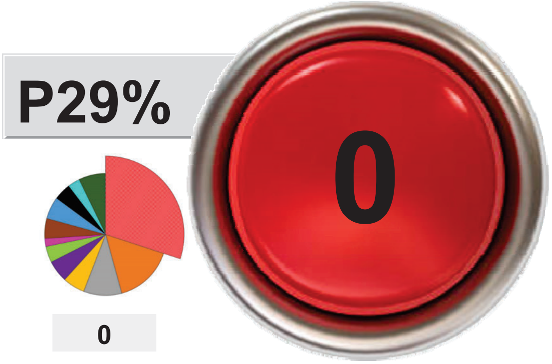
GenBank: U15165

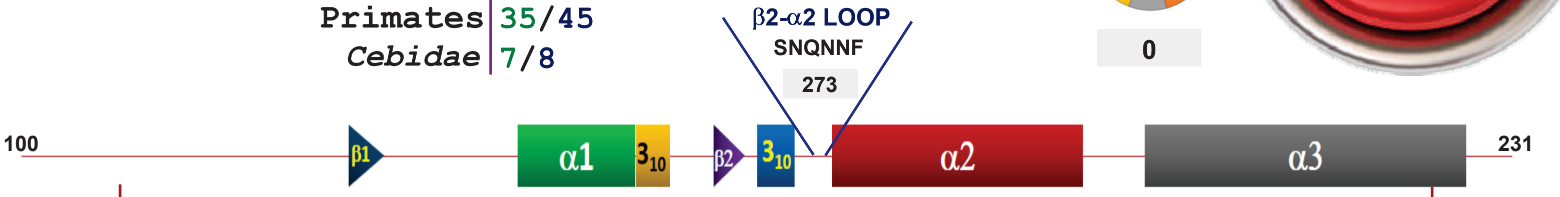
Saimiri sciureus

Primates	35/45
Cebidae	7/8

Distinct primary sequence across species

P29%





WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPSQVYYRPVDQYSNQNNFVHDCVNVTIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYEKESQAYYQRGSS-

I V M W N N N I V Q EGR

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

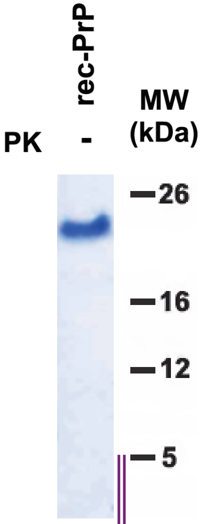
No deletions

No insertions

It shows polymorphic variants

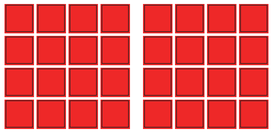
Tm^{Exp}: ND

ΔΔG: -5.63



218 AA

NO MISFOLDING



0 Conformers

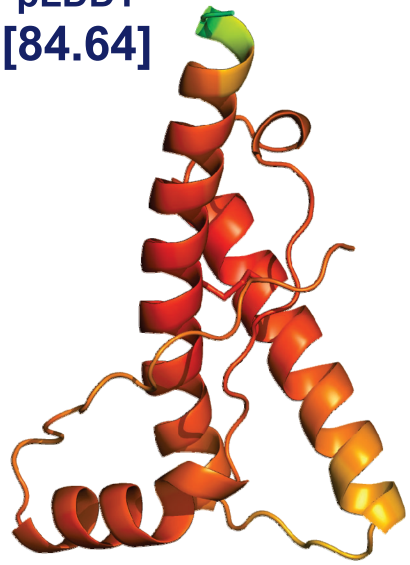
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [84.64]



Protein code: 0362

Philippine tarsier

GenBank: XM_021710036

Tarsius syrichta

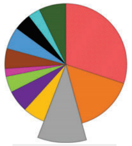
Primates 35/45
Tarsiidae 1/1

1 species sharing the same primary sequence

Horsfield's tarsier
Cephalopachus bancanus

P52%

17



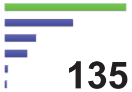
10-20

β2-α2 LOOP
NNQNNF
164

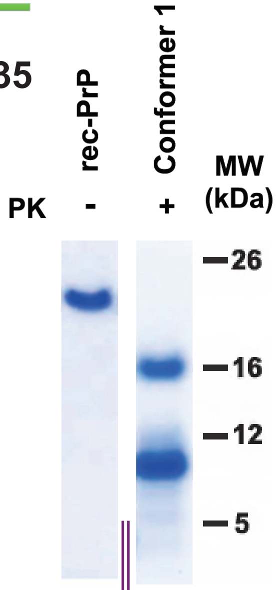
```
WSKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPMDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQKEYQASYHSGSN-
 N         I                            M      W          N          V                                        V           V      S  Y EGR S
```

PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

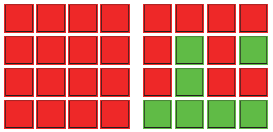


135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -9.49

In vitro studies

TgVole (1x) Not tested

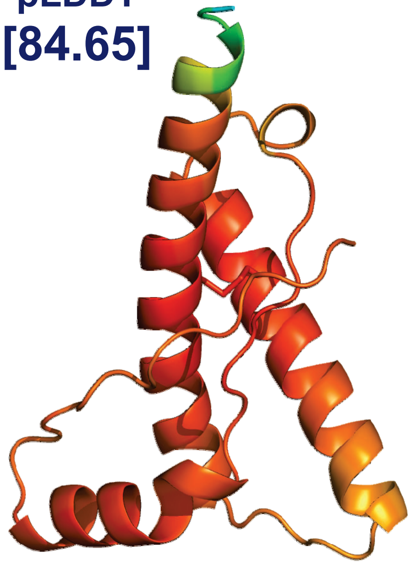
Philippine tarsier Not tested

In vivo studies

TgVole (1x) Not tested

Philippine tarsier Not tested

pLDDT
[84.65]



Gelada

GenBank: XM_025399776

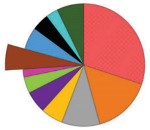
Theropithecus gelada

Primates	35/45
Cercopithecidae	7/7

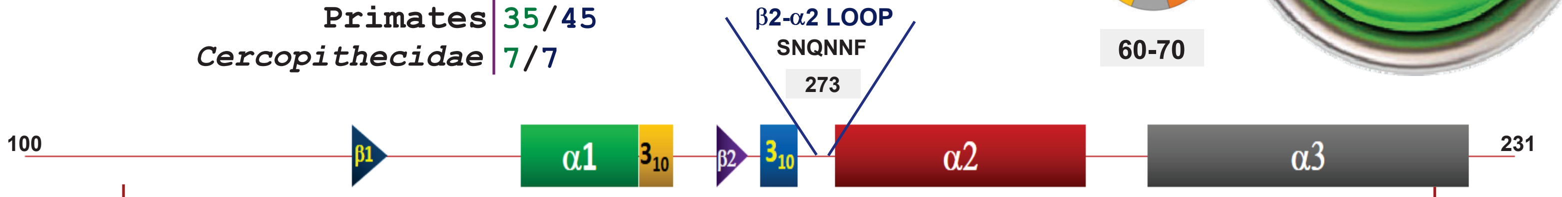
Distinct primary sequence across species

P78%

67.9



60-70



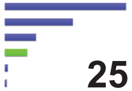
```
WHKPSKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQKESQAYYQRGSS-
 N       NI  V                            M      W         N               N                                                V        EGR
```

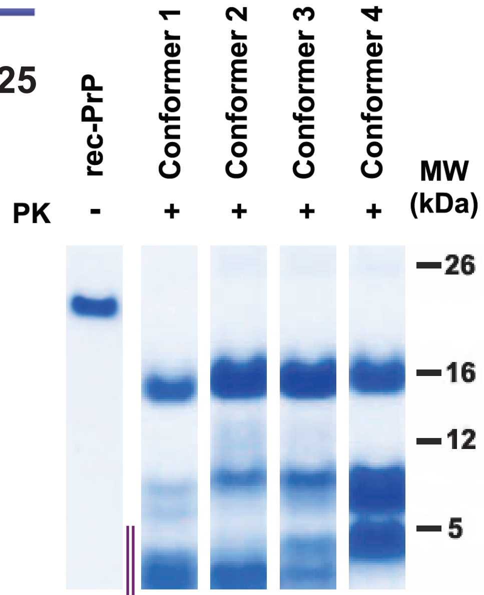
PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

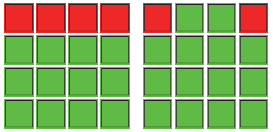




211 AA

4

Conformers



Tm^{Exp}: ND

ΔΔG: -8.22

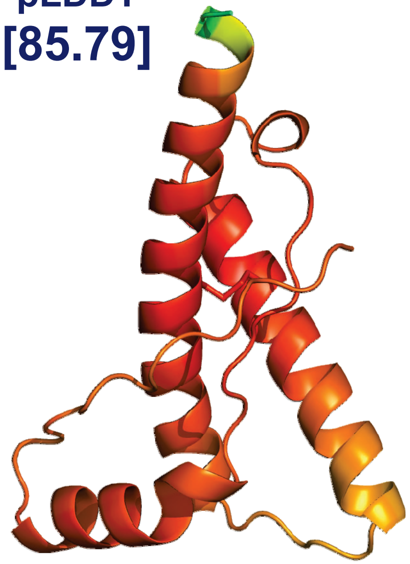
In vitro studies

TgVole (1x)	Not tested
Gelada	Not tested

In vivo studies

TgVole (1x)	Not tested
Gelada	Not tested

pLDDT
[85.79]



Elephant

GenBank: EU588731

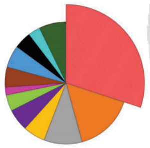
Loxodonta africana

Proboscidea 0/1
Elephantidae 0/1

Asian elephant
Elephas maximus

1 species sharing the same primary sequence

P29%



0

0

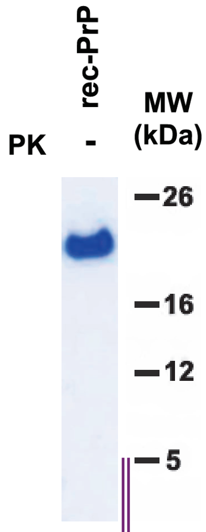
β2-α2 LOOP
SNENNF
2

```
WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVNEYSNENNFVHDCVNITVKQHTTTTITKGENFTETDTKIMERMVEQMCVTQYRKEFQAYQRGSS-
           I                         M      W         N          DQ N Q          I    V  T          V M   V         Q  S   YE R S
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

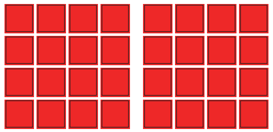
No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND
ΔΔG: ND



212 AA

NO MISFOLDING



0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[88.02]

Protein code: 0930

Cairo spiny mouse

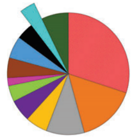
GenBank: EF467171

Acomys cahirinus

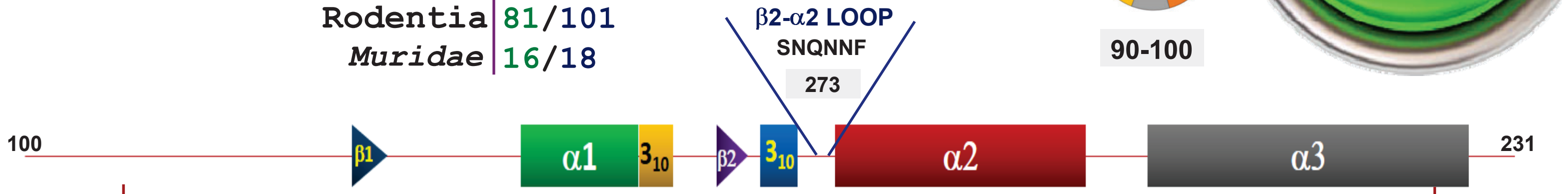
Rodentia 81/101
Muridae 16/18

P90%

91.1



90-100



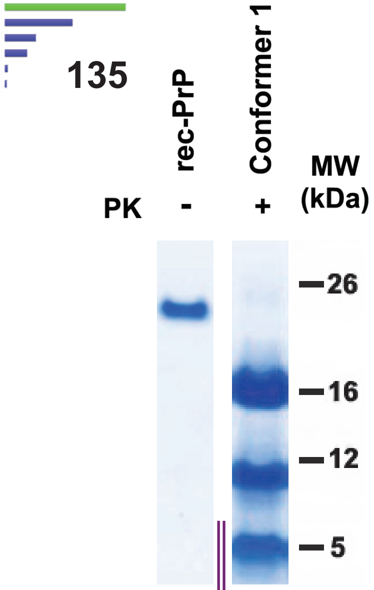
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-

N I N N E S

PrP sequence differs by 3 amino acids from the bank vole PrP (see in red)

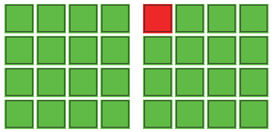
No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -2.04

In vitro studies

TgVole (1x) Not tested

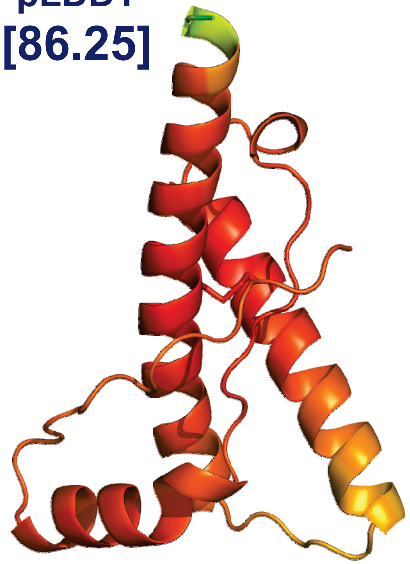
Cairo spiny mouse Not tested

In vivo studies

TgVole (1x) Not tested

Cairo spiny mouse Not tested

pLDDT
[86.25]

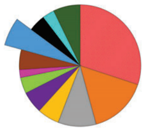


Protein code: 1370

Gobi jerboa

GenBank: BK064143

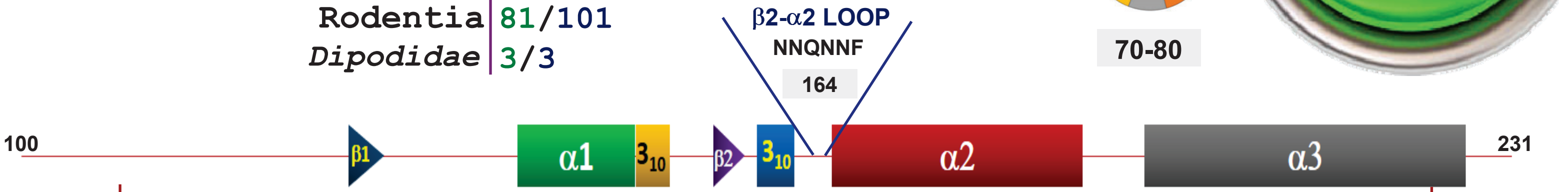
P84%



70-80

Allactaga bullata

Rodentia	81/101
Dipodidae	3/3

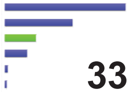


```
WNKPNKPKTSMKHMAGAAAAGAVAGGLGGYMLGSAMSRPSMNFGNDYEDRYYRENMNRYPSQVYYKPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQKESQAYLEGRRS-
    S   NI  V         V               MIH   W            N    R                I                    M         V          Y   S
```

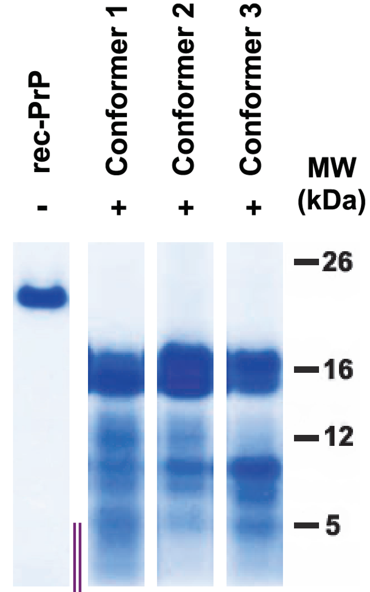
PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

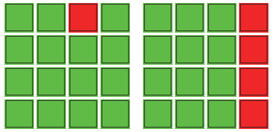


33



213 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: -10.12

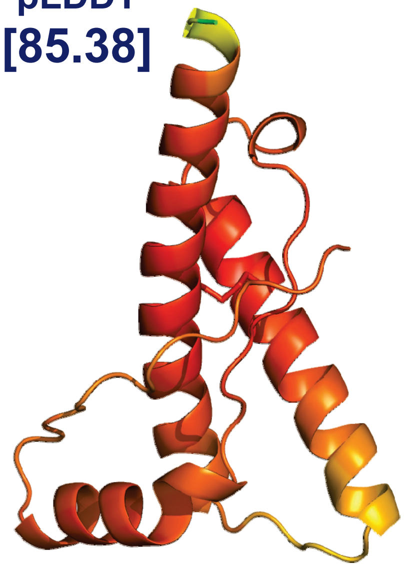
In vitro studies

TgVole (1x)	Not tested
Gobi jerboa	Not tested

In vivo studies

TgVole (1x)	Not tested
Gobi jerboa	Not tested

pLDDT
[85.38]



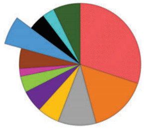
Protein code: 3330

Mountain beaver

GenBank: BK064070

P79%

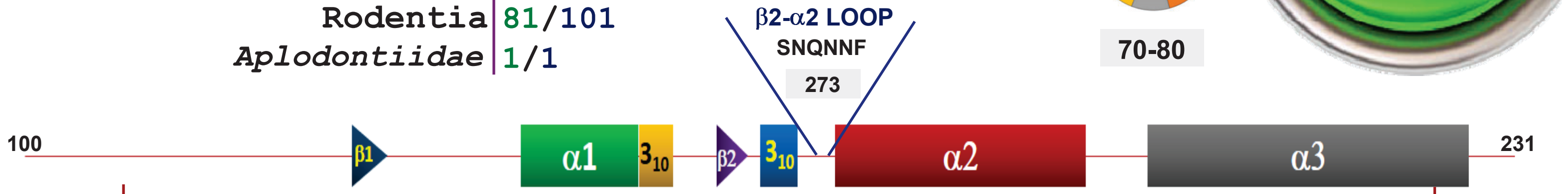
71.1



70-80

Aplodontia rufa

`Rodentia` 81/101
`Aplodontiidae` 1/1

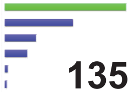


```
WNKPKKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQEAQAYYQRGSS-
    S    I                            M      W          N         R     N            I                           V M         V     K S     EGR
```

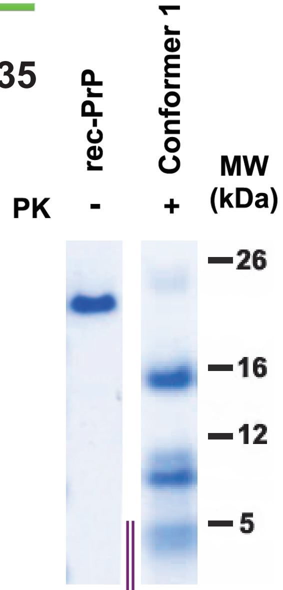
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

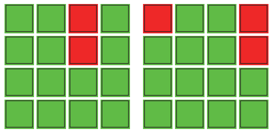


135



213 AA

1
Conformers



🟩🟩🟥🟩 🟥🟩🟩🟥
🟩🟩🟥🟩 🟩🟩🟩🟥
🟩🟩🟩🟩 🟩🟩🟩🟩
🟩🟩🟩🟩 🟩🟩🟩🟩

Tm^{Exp}: ND

ΔΔG: -11.28

***In vitro* studies**

TgVole (1x) **Not tested**

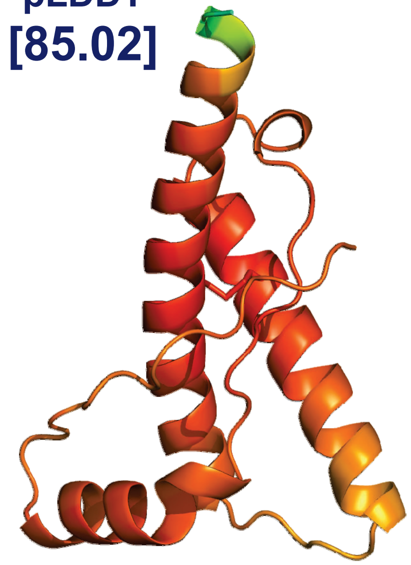
Mountain beaver **Not tested**

***In vivo* studies**

TgVole (1x) **Not tested**

Mountain beaver **Not tested**

pLDDT
[85.02]



Protein code: 3247

Distinct primary sequence across species

Steppe field mouse

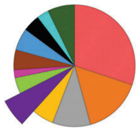
GenBank: KF466953

Apodemus fulvipectus

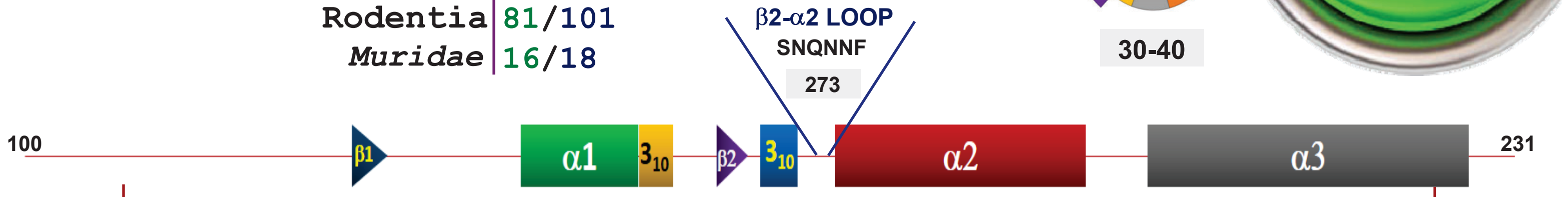
Rodentia	81/101
Muridae	16/18

P61%

30.4



30-40



WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTNGENFTETDVKMMERVVDQMCVTQYHKESQAYYDGRRS-

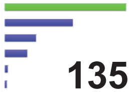
I N N E Q E S

PrP sequence differs by 5 amino acids from the bank vole PrP (see in red)

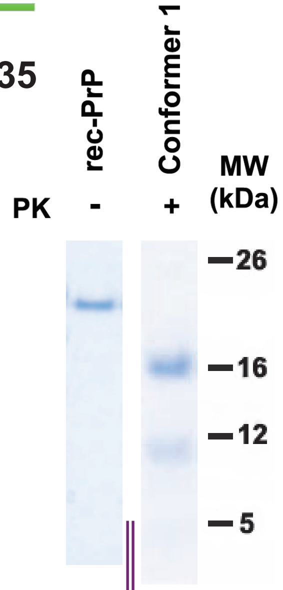
No deletions

No insertions

No polymorphic variants found



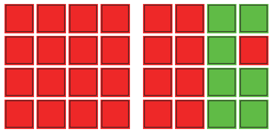
135



211 AA

1

Conformers



Tm^{Exp}: ND

ΔΔG: -11.57

***In vitro* studies**

TgVole (1x) Not tested

Steppe field mouse Not tested

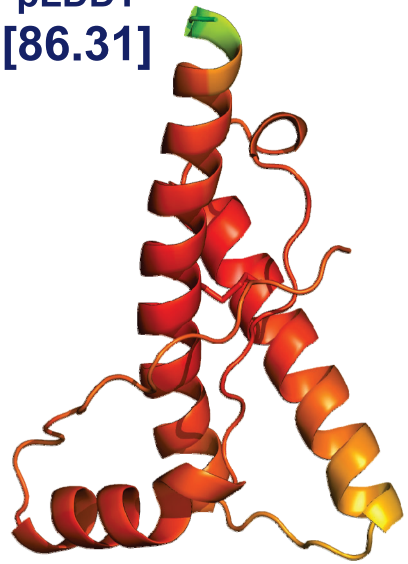
***In vivo* studies**

TgVole (1x) Not tested

Steppe field mouse Not tested

pLDDT

[86.31]



Protein code: 1395

African grass rat

GenBank: XM_034493892

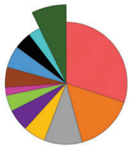
Arvicanthis niloticus

Rodentia 81/101
Muridae 16/18

Distinct primary sequence across species

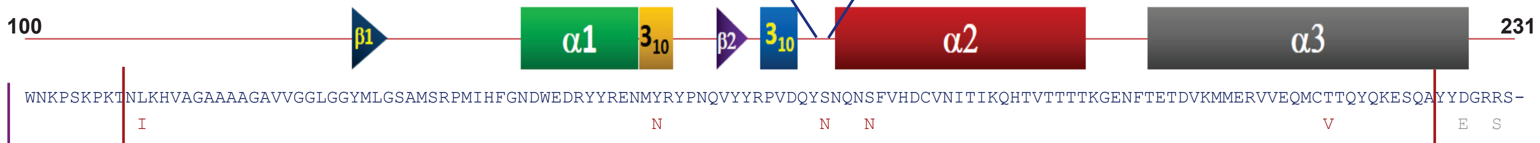
P100%

100



100

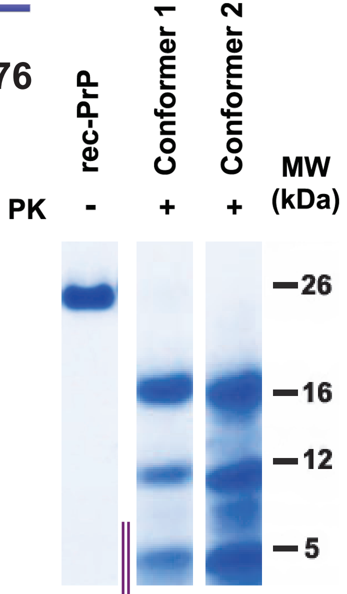
β2-α2 LOOP
SNQNSF
36



PrP sequence differs by 5 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

76



211 AA

2
Conformers

Tm^{Exp}: ND

ΔΔG: -5.57

In vitro studies

TgVole (1x) Not tested

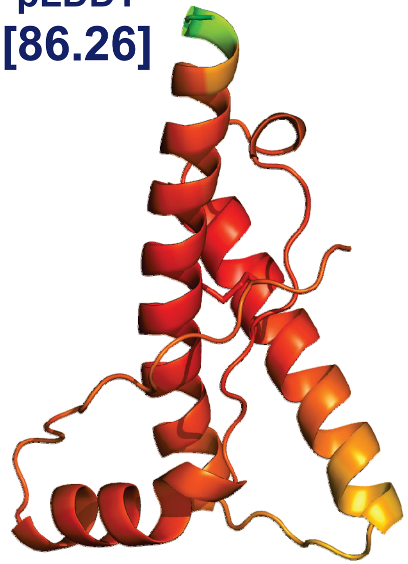
African grass rat Not tested

In vivo studies

TgVole (1x) Not tested

African grass rat Not tested

pLDDT
[86.26]



Protein code: 2544

European water vole

GenBank: BK063953

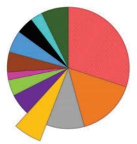
Arvicola amphibius

Rodentia 81/101
Cricetidae 25/27

Gerbe's vole
Microtus gerbei

1 species sharing the same primary sequence

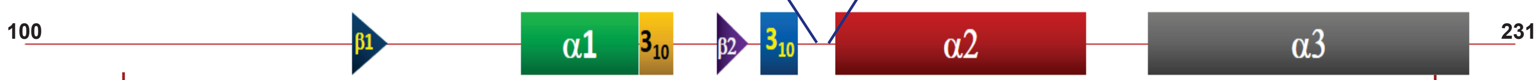
P60%



20-30

27.7

β2-α2 LOOP
NNQNNF
164



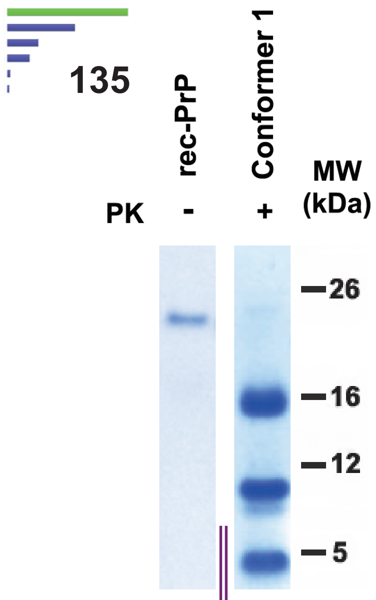
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRYS-
I S

PrP sequence differs by 1 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

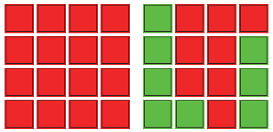
Tm^{Exp}: ND

ΔΔG: -0.51



210 AA

1
Conformers



In vitro studies

TgVole (1x) Not tested

European water vole Not tested

In vivo studies

TgVole (1x) Not tested

European water vole Not tested

pLDDT
[88.37]

Protein code: 3080

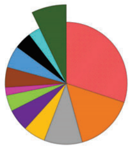
Greater bandicoot rat

GenBank: KF466950

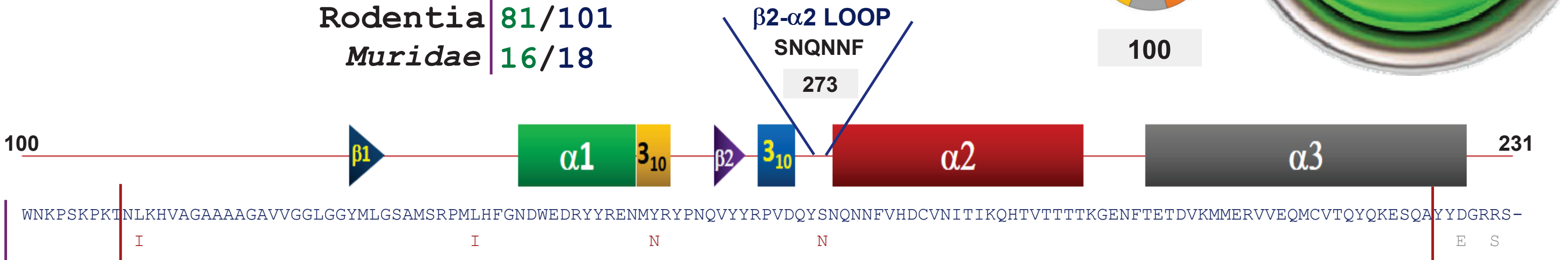
Bandicota indica

Rodentia	81/101
Muridae	16/18

P100%



100



WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-

I I N N E S

PrP sequence differs by 4 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

5 species sharing the same primary sequence

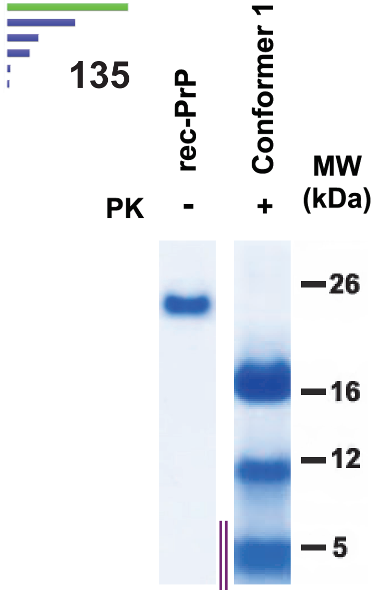
● **Savile's bandicoot rat** *Bandicota savilei*

● **Small white-toothed rat** *Berylmys berdmorei*

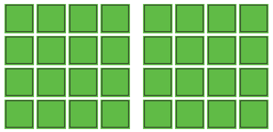
● **Edwards's long-tailed giant rat** *Leopoldamys edwardsi*

● **Long-tailed giant rat** *Leopoldamys sabanus*

● **Polynesian rat** *Rattus exulans*



210 AA

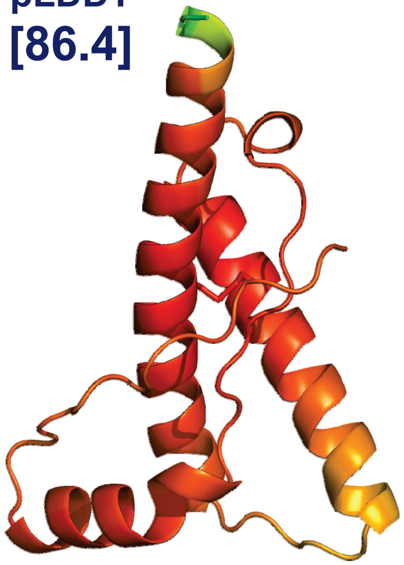


1 Conformers

Tm^{Exp}: ND

ΔΔG: -9.35

pLDDT [86.4]



***In vitro* studies**

TgVole (1x)	Not tested
Greater bandicoot rat	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Greater bandicoot rat	Not tested

Protein code: 1340

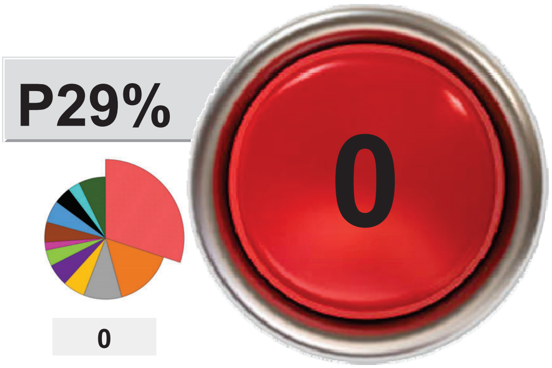
Desmarest's hutia

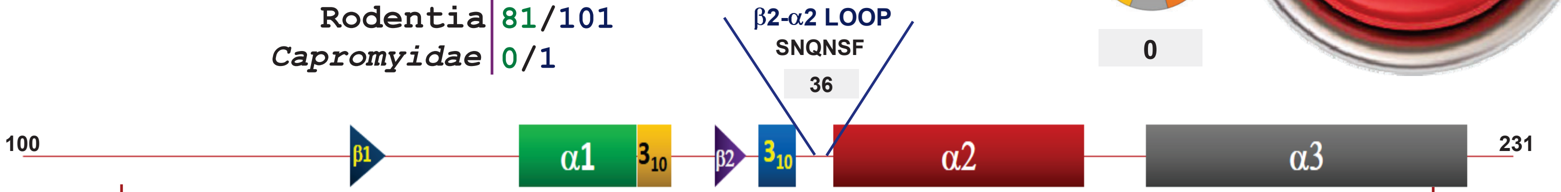
GenBank: BK064046

Capromys pilorides

Rodentia	81/101
Capromyidae	0/1

P29%





WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLQQMCTTQYQKESQAYYYHGRAG-

I M W N N N H M VE V EGRSS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions

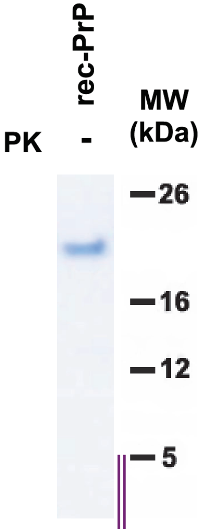
No insertions

No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

ΔΔG: ND



202 AA

NO MISFOLDING

0
Conformers

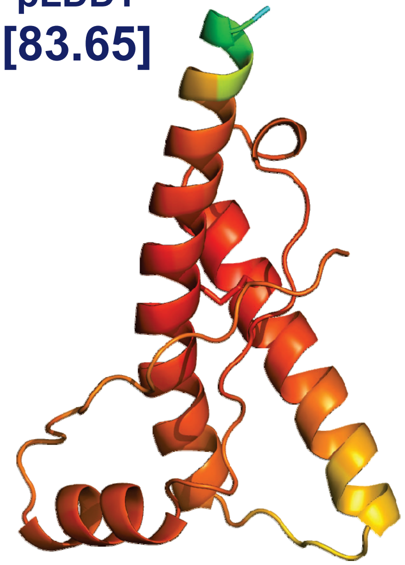
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[83.65]



Protein code: 3213

North American beaver

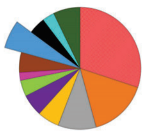
GenBank: XM_020184027

Castor canadensis

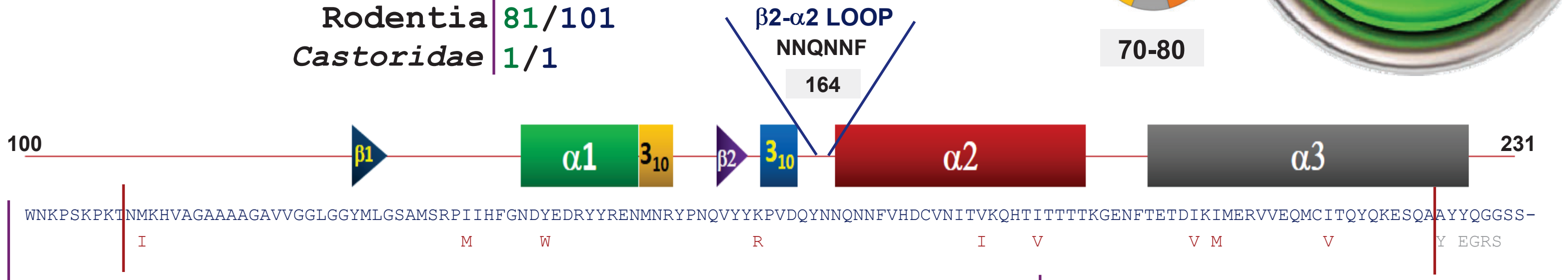
Rodentia 81/101
Castoridae 1/1

P84%

78.2



70-80

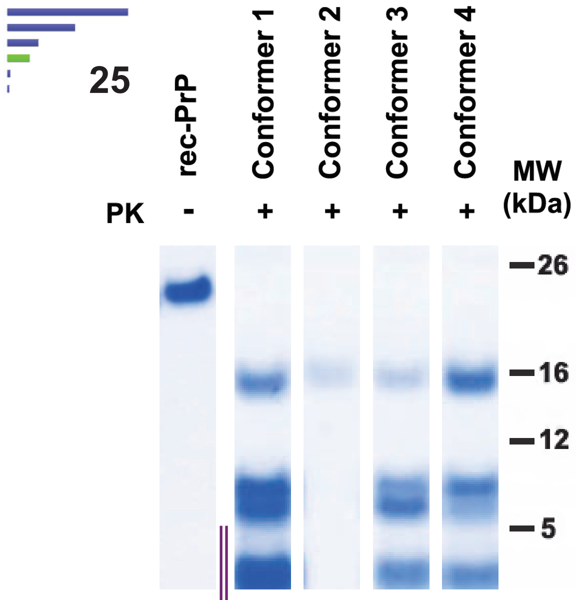


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPIIHFGNDYEDRYYRENMNRYPNQVYYKPVDQYNNQNNFVHDCVNITVKQHTITTTTKGENFTETDIKIMERVVEQMCITQYQKESQAAYYQGGSS-

I M W R I V V M V Y EGRS

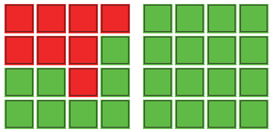
PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



225 AA

4
Conformers



Tm^{Exp}**: ND**

ΔΔG: ND

***In vitro* studies**

TgVole (1x) Not tested

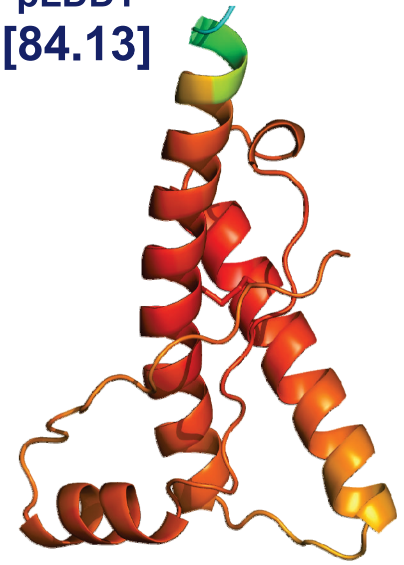
North American beaver Not tested

***In vivo* studies**

TgVole (1x) Not tested

North American beaver Not tested

pLDDT
[84.13]



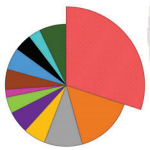
Distinct primary sequence across species

Protein code: 0940

Brazilian guinea pig

GenBank: KM357834

P29%



0

0

Cavia aperea

Rodentia	81/101
Caviidae	1/5

β2-α2 LOOP
SNQNSF
36

```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYKPVDQYSNQNSFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAYYYHGRAG-
           I  V                                M     N W          N        R     N   N  H                                    M    V    V             EGRSS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

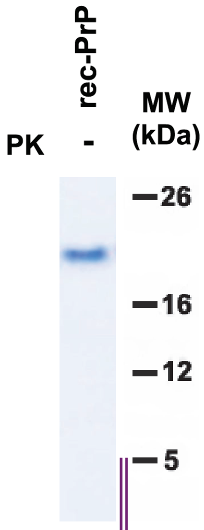
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



202 AA

NO MISFOLDING

0
Conformers

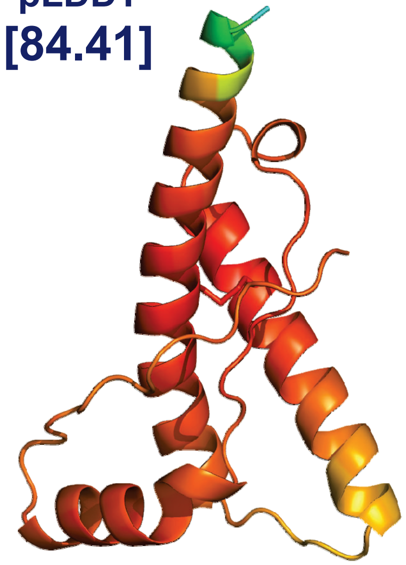
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[84.41]



Distinct primary sequence across species

Protein code: 1470

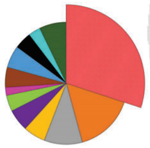
Guinea pig

GenBank: XM_003476602

Cavia porcellus

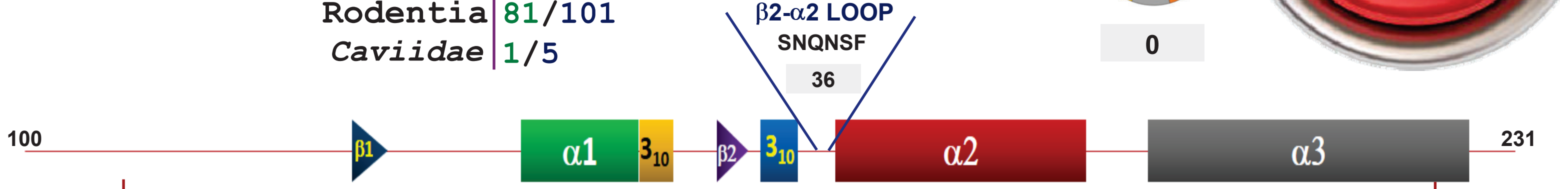
Rodentia	81/101
Caviidae	1/5

P29%



0

0



```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYKPVDQYSNQNSFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAYYYHGRA-
          I  V                         M    N W         N        R     N   N  H                           M    V    V           EGRSS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

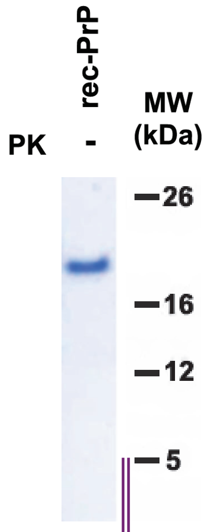
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔG: -6.62



201 AA

NO MISFOLDING

0

Conformers

***In vitro* studies**

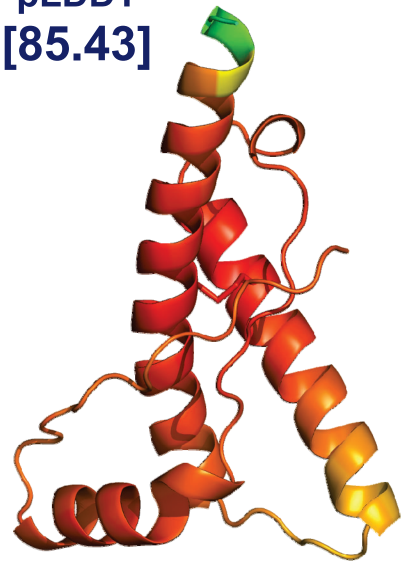
NOT APPLICABLE

***In vivo* studies**

NOT APPLICABLE

pLDDT

[85.43]



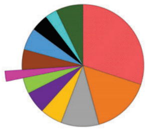
Distinct primary sequence across species

Montane guinea pig

GenBank: BK063938

P72%

53.2



50-60

Cavia tschudii

Rodentia	81/101
Caviidae	1/5

β2-α2 LOOP
SNQNSF
36

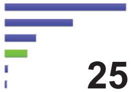
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYKPVDQYSNQNSFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAYYYHGRAG-

I M N W N R N N H M V V EGRSS

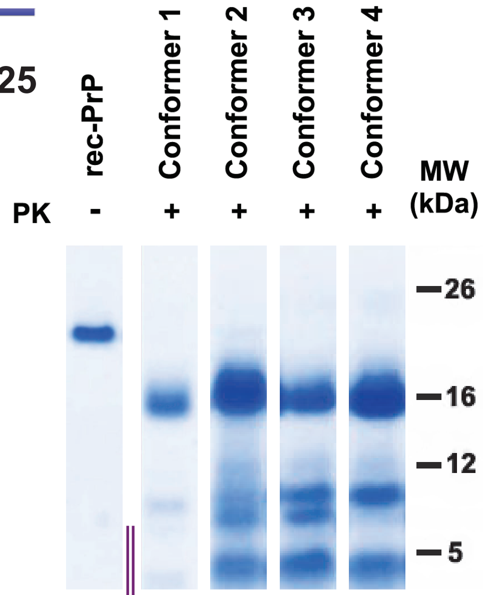
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

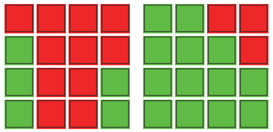


25



202 AA

4
Conformers



Tm^{Exp}: ND

ΔΔG: ND

***In vitro* studies**

TgVole (1x) — Propagate

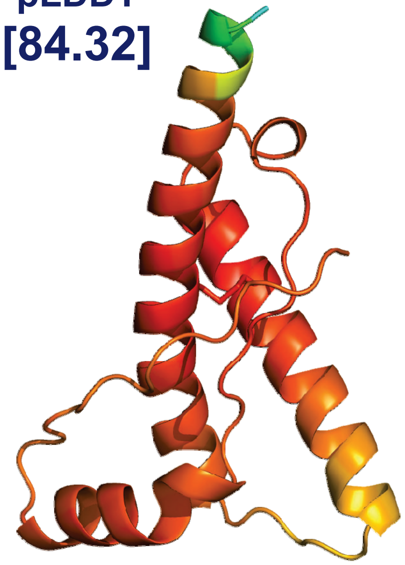
Montane guinea pig — Ongoing

***In vivo* studies**

TgVole (1x) — Ongoing

Montane guinea pig — Not tested

pLDDT
[84.32]



Protein code: 3061

Distinct primary sequence across species

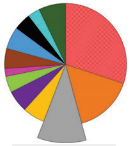
Long-tailed chinchilla

GenBank: XM_005380818

Chinchilla lanigera

Rodentia	81/101
Chinchillidae	1/1

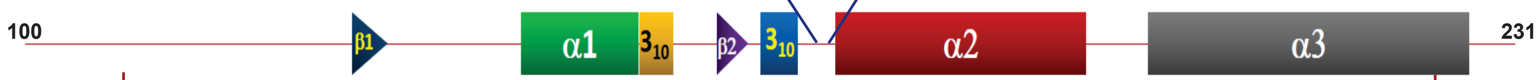
P54%



10-20

18.8

β2-α2 LOOP
NSQNSF
5

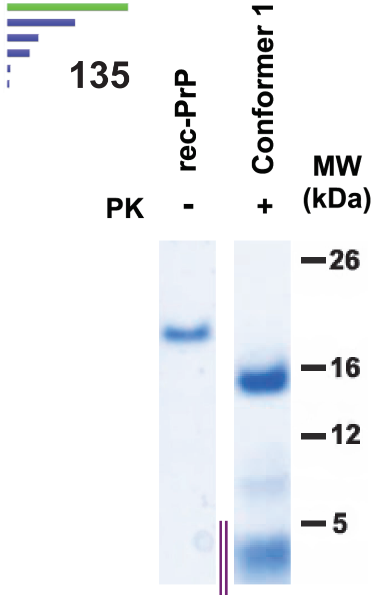


```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFSNDYEDRYYRENMYRYPNQVYYKPVDQYNSQNSFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESRAYYYHGRAG-
          I                            M   G  W         N        R      N  N  H                           M    V    V       Q   EGRSS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

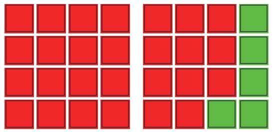
No deletions
No insertions
No polymorphic variants found

135



202 AA

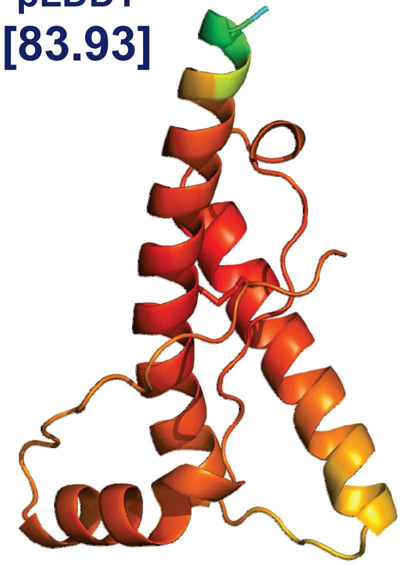
1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

pLDDT
[83.93]



In vitro studies

TgVole (1x)	Propagate
Long-tailed chinchilla	Ongoing

In vivo studies

TgVole (1x)	Ongoing
Long-tailed chinchilla	Not tested

Protein code: 1136

Brazilian porcupine

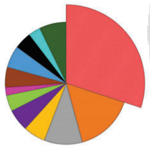
GenBank: OR47272

Coendou prehensilis

Rodentia	81/101
Erethizontidae	0/2

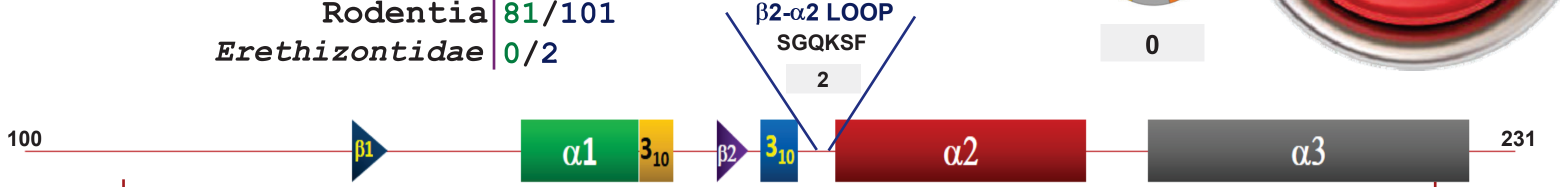
Distinct primary sequence across species

P29%



0

0



```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPDQVYYRPVDQYSGQKSFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAYYYRGRAG-
           I  V                                M     N W         N   N          NN NN  H                                M    V    V                EGRSS
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

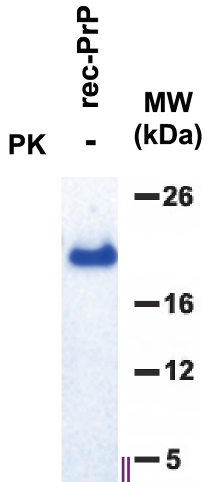
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



202 AA

NO MISFOLDING

0
Conformers

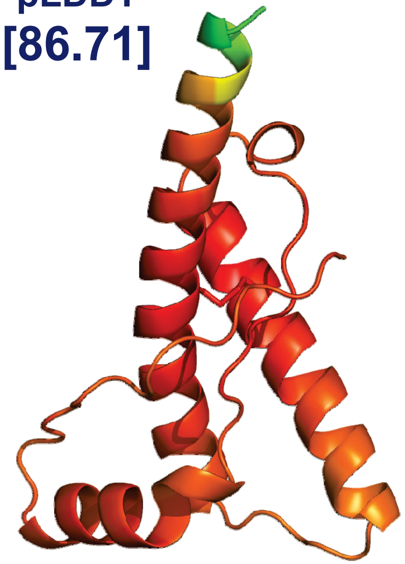
***In vitro* studies**

NOT APPLICABLE

***In vivo* studies**

NOT APPLICABLE

pLDDT
[86.71]



Protein code: 3785

Gambian pouched rat

GenBank: BK063941

Cricetomys gambianus

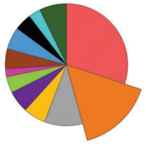
Rodentia 81/101
Nesomyidae 1/1

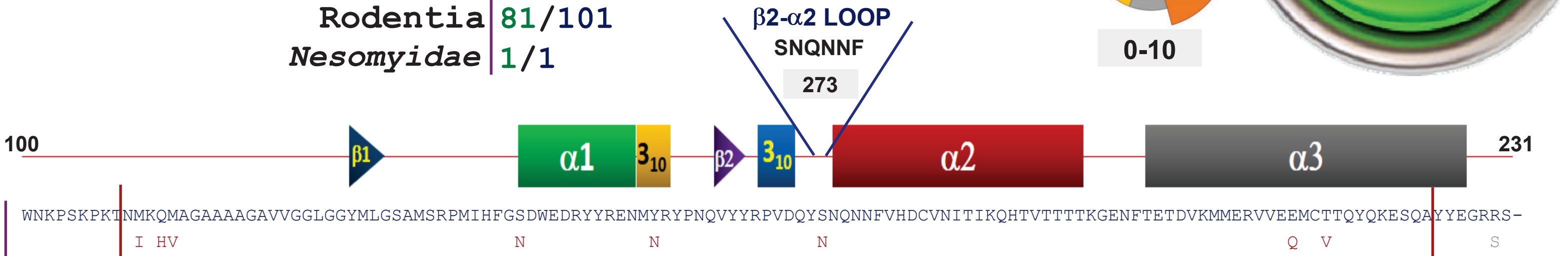
1 species sharing the same primary sequence

Southern giant pouched rat
Cricetomys ansorgei

P40%

5.5


0-10



WNKPSKPKTNMKQMAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGSDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEEMCTTQYQKESQAYYEGRRS-

I HV N N N Q V S

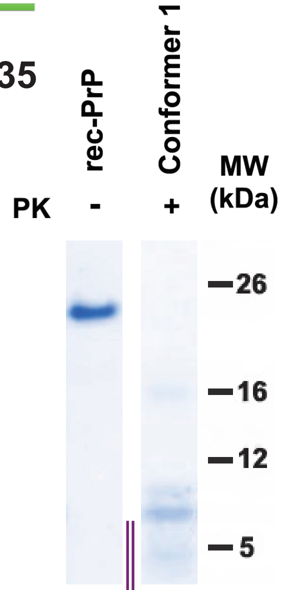
PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

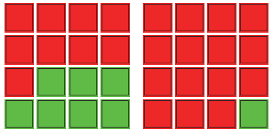
135



214 AA

1

Conformers



Tm^{Exp}: ND

ΔΔG: -4.31

In vitro studies

Not tested
TgVole (1x)

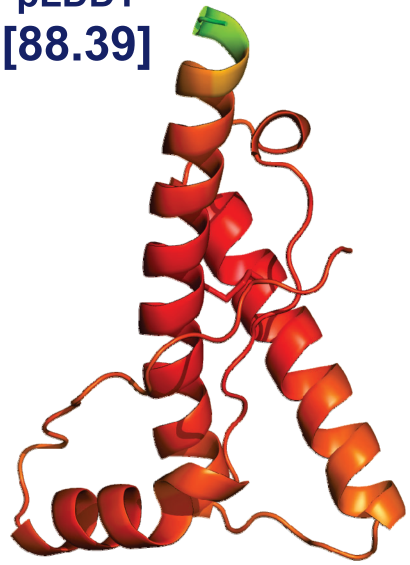
Not tested
Gambian pouched rat

In vivo studies

Not tested
TgVole (1x)

Not tested
Gambian pouched rat

pLDDT
[88.39]



Protein code: 3067

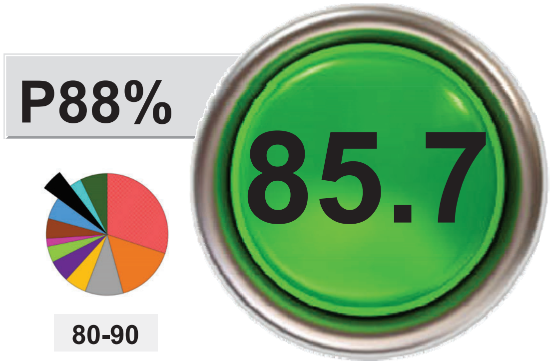
Distinct primary sequence across species

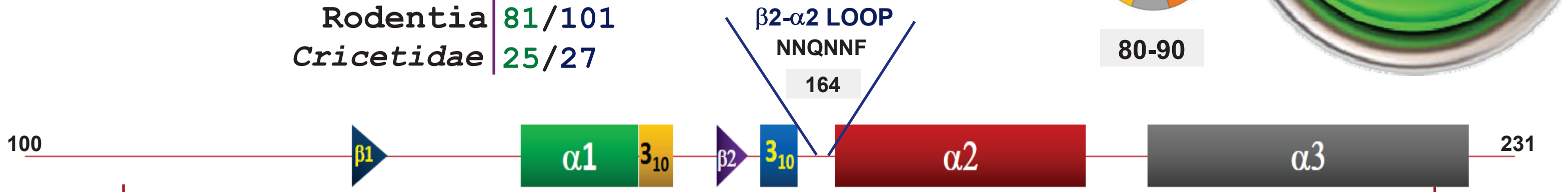
Chinese hamster

GenBank: M33958

Cricetulus barabensis

Rodentia	81/101
Cricetidae	25/27





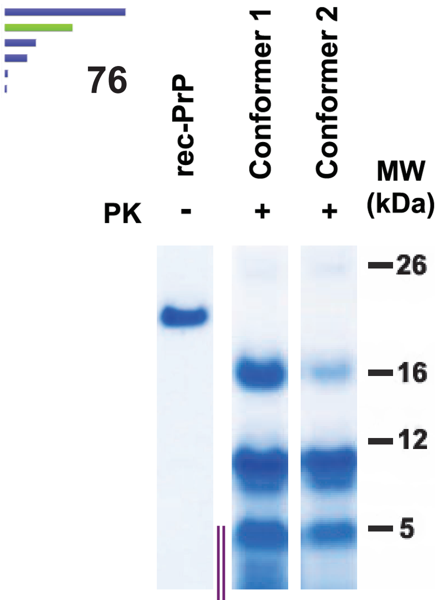
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-
           I                                 I                                                                                            E  S
```

PrP sequence differs by 2 amino acids from the bank vole PrP (see in red)

No deletions

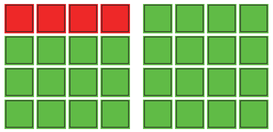
No insertions

No polymorphic variants found



211 AA

2 Conformers



Tm^{Exp}: ND

ΔΔG: -4.97

***In vitro* studies**

TgVole (1x) — Not tested

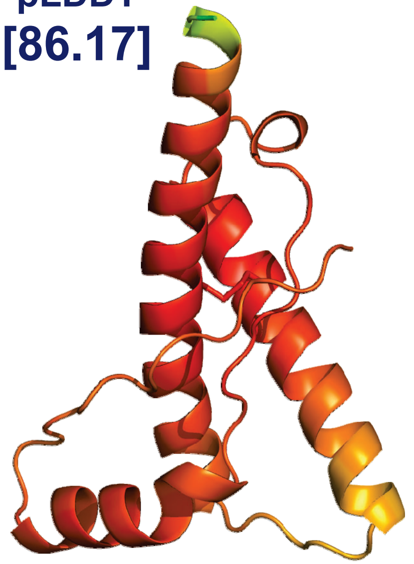
Chinese hamster — Not tested

***In vivo* studies**

TgVole (1x) — Not tested

Chinese hamster — Not tested

pLDDT [86.17]



Armenian hamster

GenBank: M33959

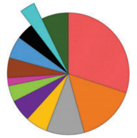
Cricetulus migratorius

Rodentia 81/101
Cricetidae 25/27

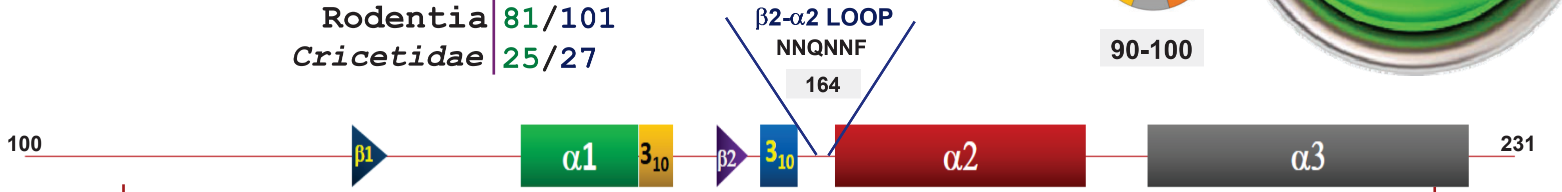
Distinct primary sequence across species

P91%

92.9



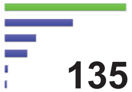
90-100



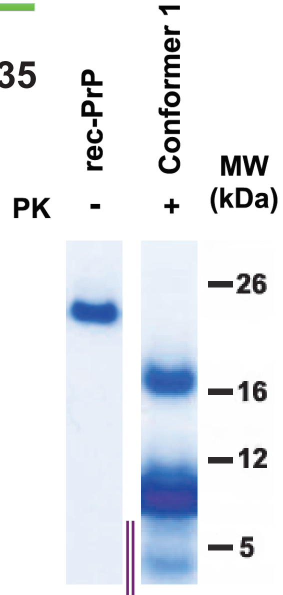
```
WNKPNKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-
    S     NI  V                         I                                                                                               E  S
```

PrP sequence differs by 4 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

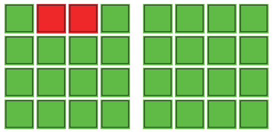


135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -7.18

In vitro studies

TgVole (1x) Not tested

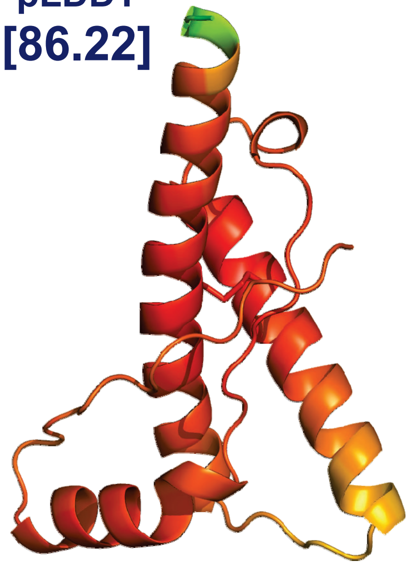
Armenian hamster Not tested

In vivo studies

TgVole (1x) Not tested

Armenian hamster Not tested

pLDDT
[86.22]



Damaraland mole-rat

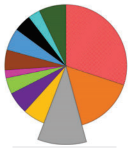
GenBank: XM_010607544

Cryptomys damarensis

Rodentia 81/101
Bathyergidae 2/3

P49%

13



10-20

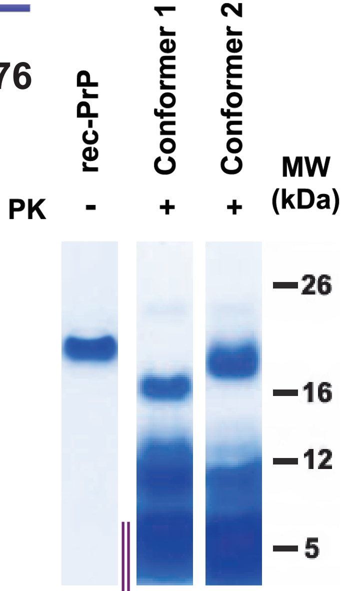
β2-α2 LOOP
SSQNNF
42

```
WNKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFSSDYEDRYYRENMYRYPNQVYYRPVDQYSSQNNFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAHYYRGRAG-
     S      I  V                          M   GN W         N                  NN     H                            M    V    V                Y EGRSS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

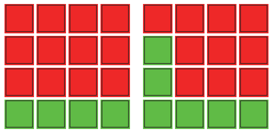
No deletions
No insertions
No polymorphic variants found

76



194 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

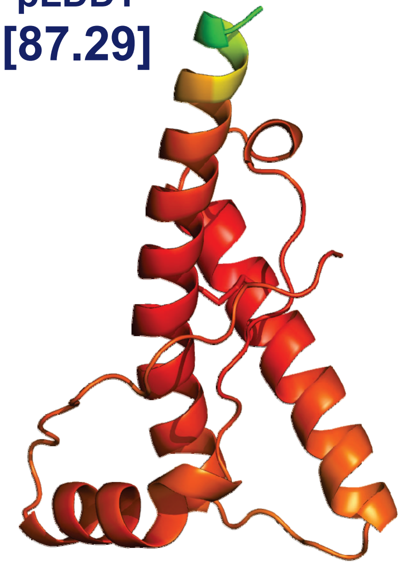
Damaraland mole-rat Not tested

In vivo studies

TgVole (1x) Not tested

Damaraland mole-rat Not tested

pLDDT
[87.29]



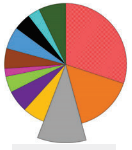
Distinct primary sequence across species

Protein code: 1130

Mashona mole-rat

GenBank: BK064181

P46%

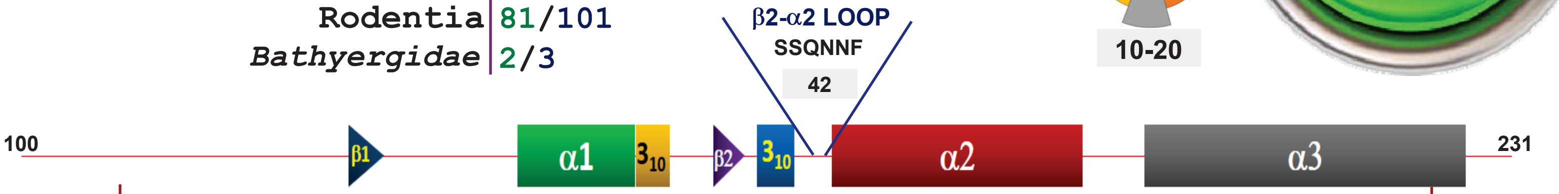


10.7

Cryptomys darlingi

Rodentia	81/101
Bathyergidae	2/3

Distinct primary sequence across species



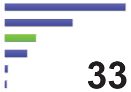
```
WNKPNKPKTNMKHMAGAAAAGAGVGGLGGYMLGSAMSRPLIHFSSDYEDRYYRENMYRYPNQVYYRPVDQYSSQNNFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAHYYRGRAG-
    S        I  V          V                 M   GN W          N               NN     H                            M    V    V            Y EGRSS
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

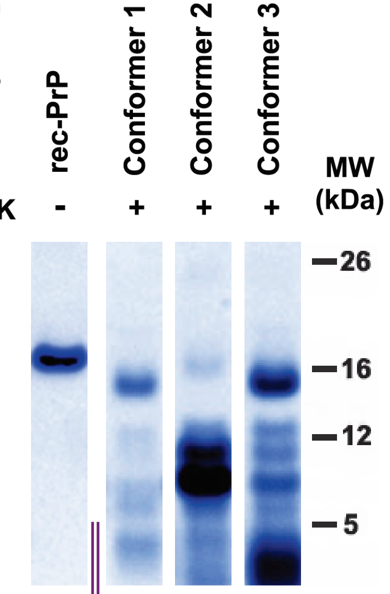
No deletions

No insertions

No polymorphic variants found

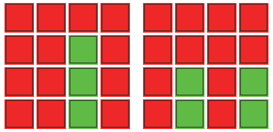


33



178 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

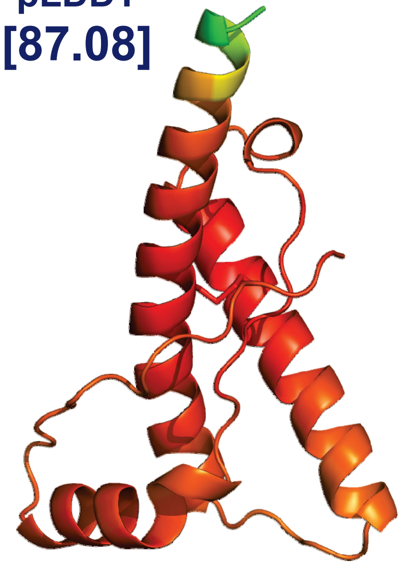
Mashona mole-rat Not tested

In vivo studies

TgVole (1x) Not tested

Mashona mole-rat Not tested

pLDDT
[87.08]



Protein code: 4004

Common gundi

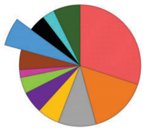
GenBank: BK063949

Ctenodactylus gundi

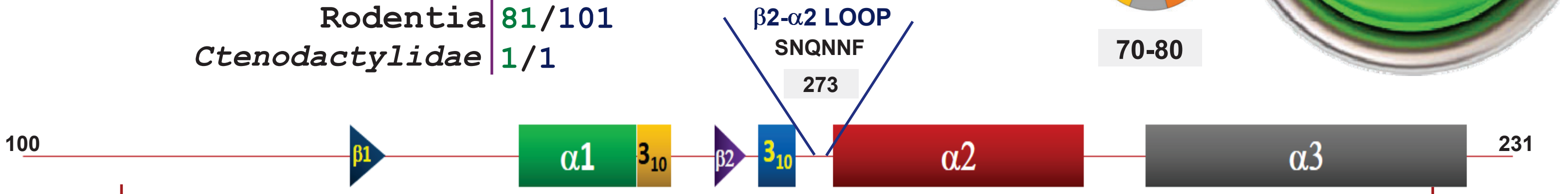
Rodentia 81/101
Ctenodactylidae 1/1

P79%

71.1



70-80



WNKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPNQVYYRPIDQYSNQNNFVHDCVNITIKQHTVTTTTKGDNFTETDIKIMERVVEQMCITQYQQEAQAYQYQGRS-

NI M W V N E V M V K S YEGRS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

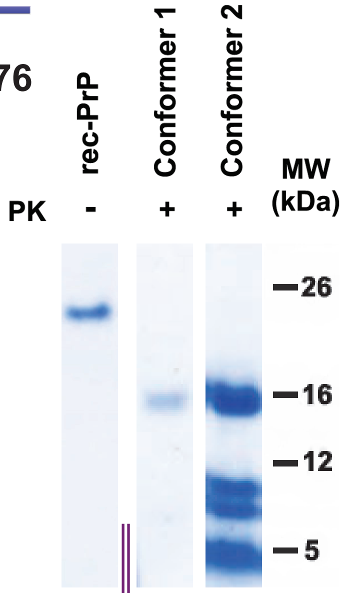
No deletions

No insertions

No polymorphic variants found

Distinct primary sequence across species

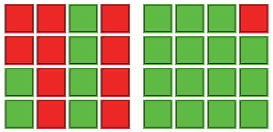
76



210 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: -6.5

In vitro studies

TgVole (1x) Not tested

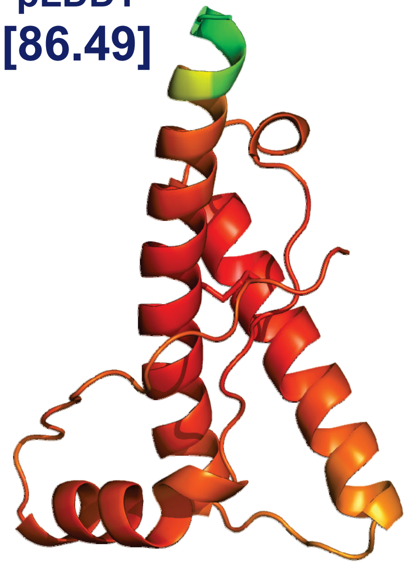
Common gundi Not tested

In vivo studies

TgVole (1x) Not tested

Common gundi Not tested

pLDDT
[86.49]



Protein code: 3076

Distinct primary sequence across species

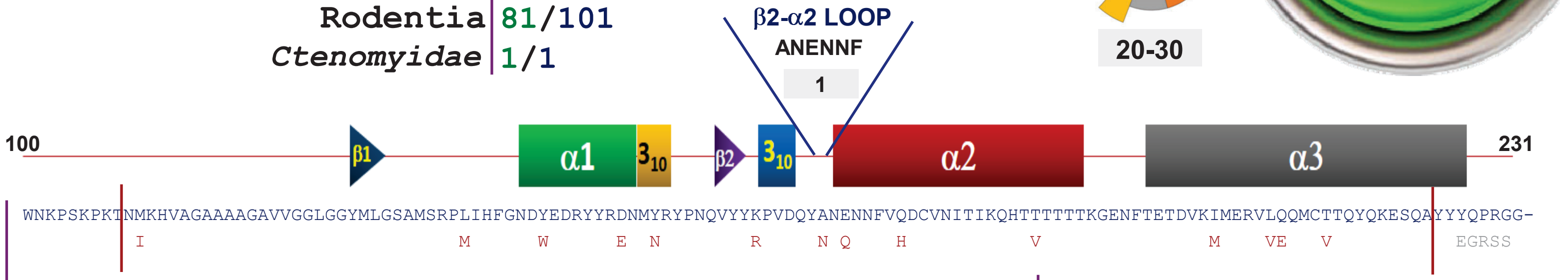
Social tuco-tuco

GenBank: BK063951

Ctenomys sociabilis

Rodentia 81/101
Ctenomyidae 1/1

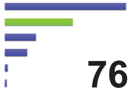
P60%

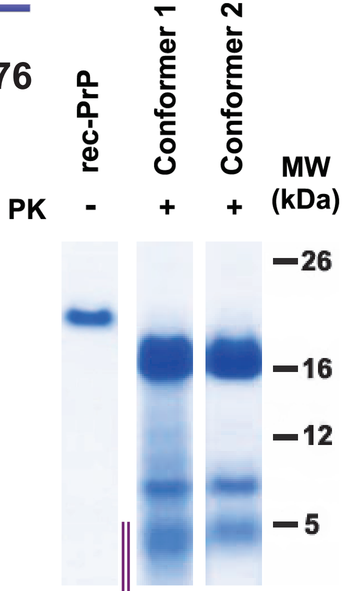


```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRDNMYRYPNQVYYKPVDQYANENNFVQDCVNITIKQHTTTTTTKGENFTETDVKIMERVLQQMCTTQYQKESQAYYYQPRGG-
           I                            M      W       E  N         R      N Q    H           V                 M     VE   V              EGRSS
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

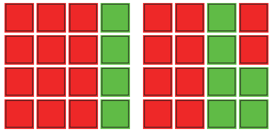
No deletions
No insertions
No polymorphic variants found





203 AA

2
Conformers



Tm^Exp: ND

ΔΔG: ND

***In vitro* studies**

TgVole (1x) Not tested

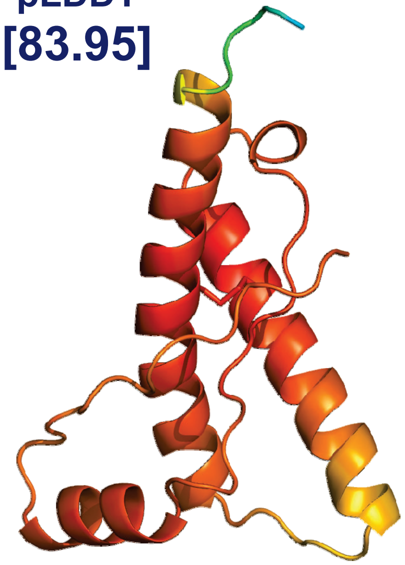
Social tuco-tuco Not tested

***In vivo* studies**

TgVole (1x) Not tested

Social tuco-tuco Not tested

pLDDT
[83.95]



Protein code: 3078

Distinct primary sequence across species

Central American agouti

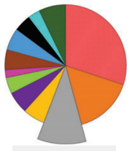
GenBank: BK063998

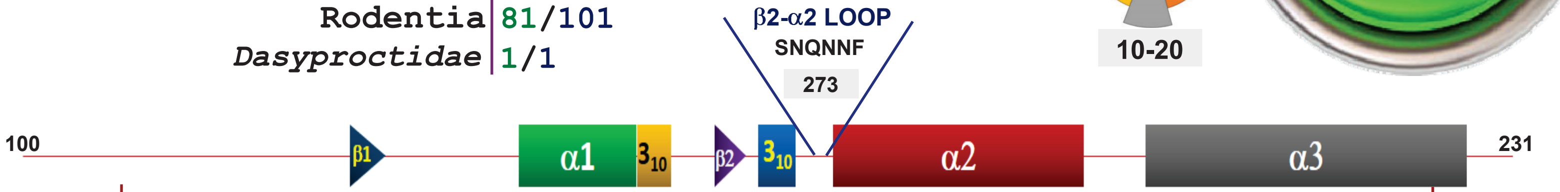
Dasyprocta punctata

Rodentia 81/101
Dasyproctidae 1/1

P45%

10.4

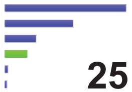


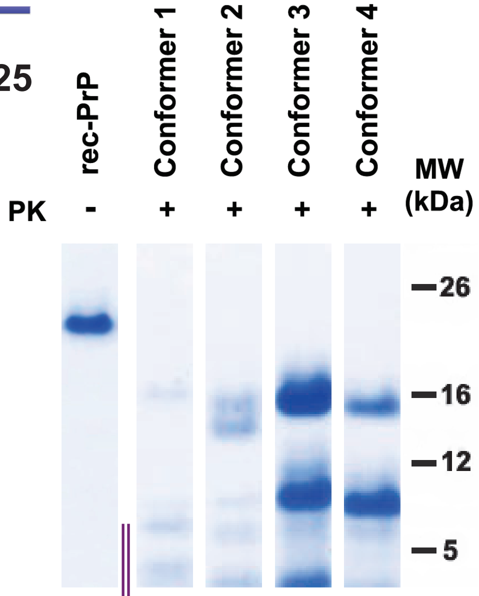


```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDFEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAYYSPGRAG-
           I  V                            M      W         N        R     N      H                                   M    V    V                EGRSS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

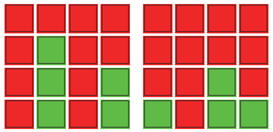
No deletions
No insertions
No polymorphic variants found





202 AA

4
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

Central American agouti Not tested

In vivo studies

TgVole (1x) Not tested

Central American agouti Not tested

pLDDT
[83.85]

Protein code: 3158

Pacarana

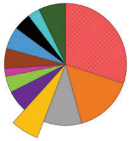
GenBank: BK063954

Dinomys branickii

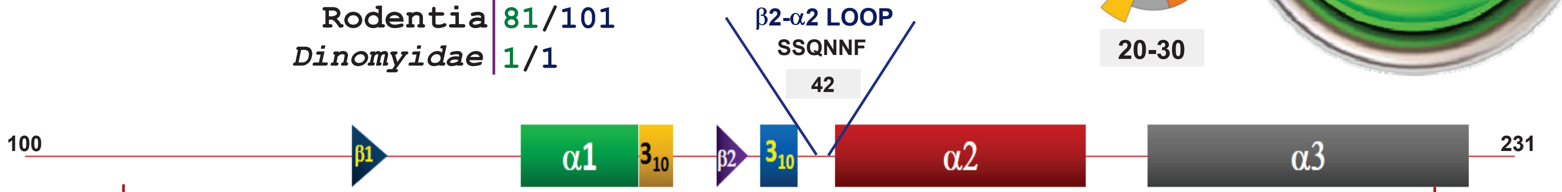
Rodentia	81/101
Dinomyidae	1/1

P59%

26.8



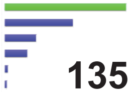
20-30



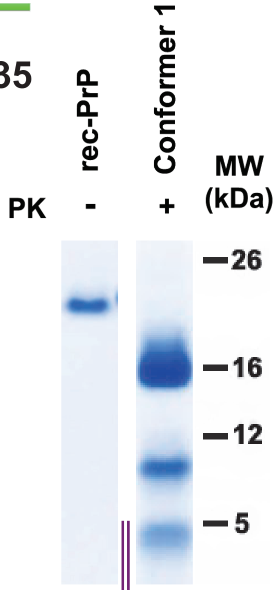
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYKPVDQYSSQNNFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCATQYQKESQAYYYHGRAG-
           I                         M    N W        N       R      NN    H                           M   V   V              EGRSS
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

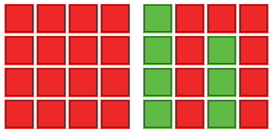


135



204 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

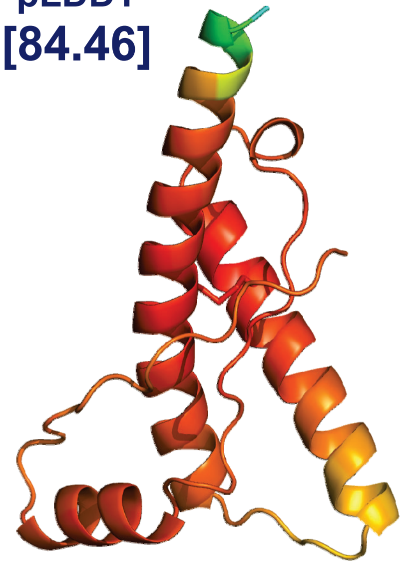
In vitro studies

TgVole (1x)	Not tested
Pacarana	Not tested

In vivo studies

TgVole (1x)	Not tested
Pacarana	Not tested

pLDDT
[84.46]



Distinct primary sequence across species

Protein code: 3082

Merriam's kangaroo rat

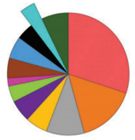
GenBank: BK064205

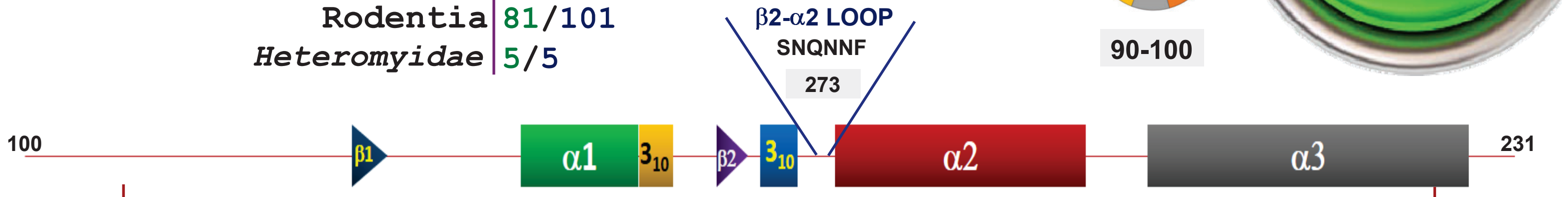
Dipodomys merriami

Rodentia 81/101
Heteromyidae 5/5

Distinct primary sequence across species

P91%

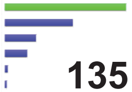

90-100

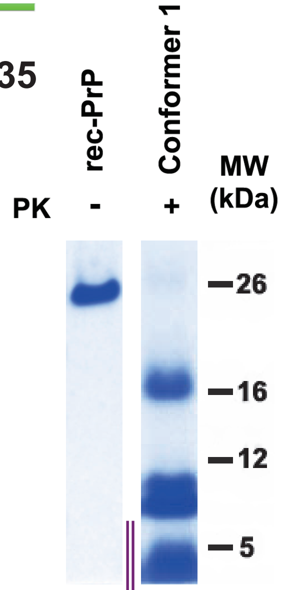


```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPSQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERMVEQMCITQYQKEAQASYYEPRS-
          I                        M      W              N   R    N          I                    M  V   V     S  Y EGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

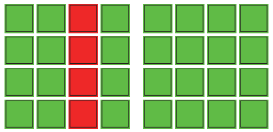
No deletions
No insertions
No polymorphic variants found


135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: 1.98

***In vitro* studies**

Not tested
TgVole (1x)

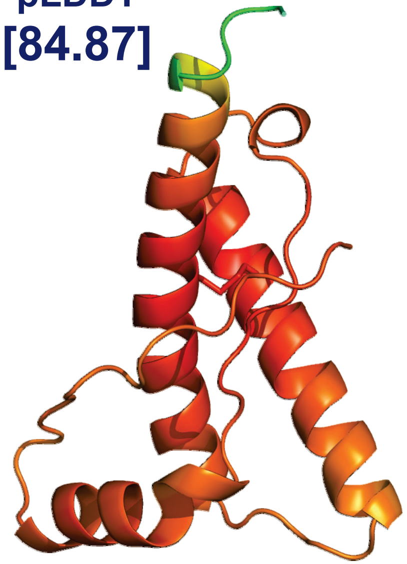
Not tested
Merriam's kangaroo rat

***In vivo* studies**

Not tested
TgVole (1x)

Not tested
Merriam's kangaroo rat

pLDDT
[84.87]



Protein code: 4560

Distinct primary sequence across species

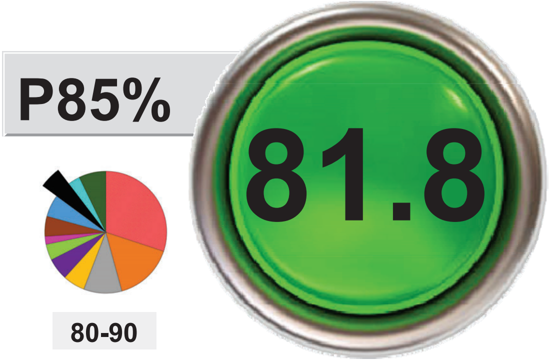
Ord's kangaroo rat

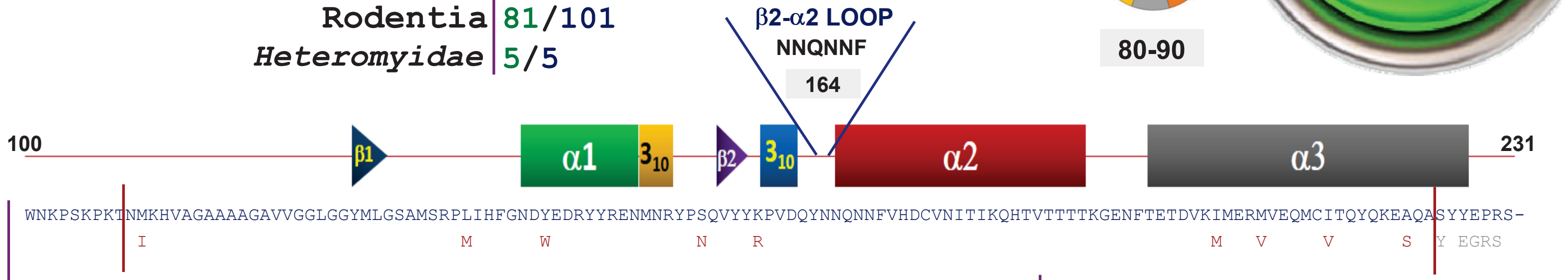
GenBank: XM_013010955

Dipodomys ordii

Rodentia	81/101
Heteromyidae	5/5

P85%

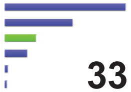


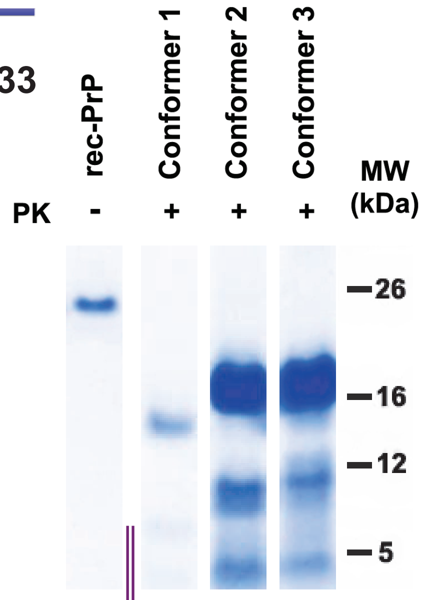


```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPSQVYYKPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKIMERMVEQMCITQYQKEAQASYYEPRS-
          I                           M      W              N    R                                         M    V      V      S  Y EGRS
```

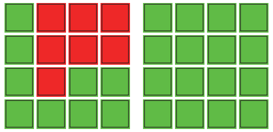
PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found





219 AA



3
Conformers

Tm^{Exp}: ND

ΔΔG: 2.83

***In vitro* studies**

TgVole (1x) — Not tested

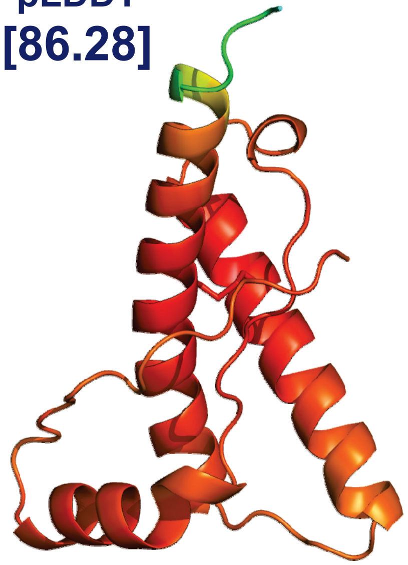
Ord's kangaroo rat — Not tested

***In vivo* studies**

TgVole (1x) — Not tested

Ord's kangaroo rat — Not tested

pLDDT
[86.28]



Protein code: 2568

Banner-tailed kangaroo rat

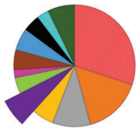
GenBank: BK064155

Dipodomys spectabilis

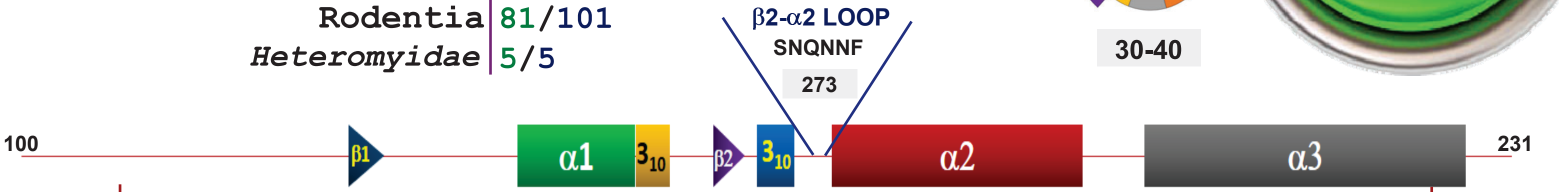
Rodentia	81/101
Heteromyidae	5/5

P67%

39.8



30-40



WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPSQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERMVEQMCITQYQKEAQASYYEPRS-

I V M W N R N I M V V S Y EGRS

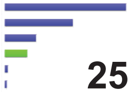
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

Distinct primary sequence across species



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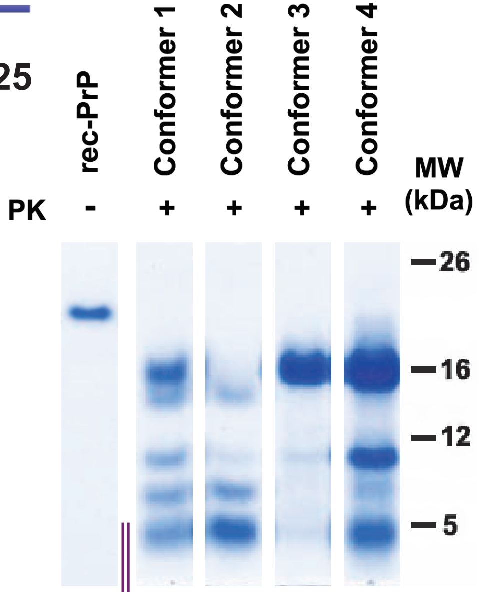
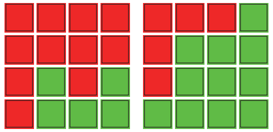


219 AA

4
Conformers



Tm^{Exp}: ND

ΔΔG: -8.72

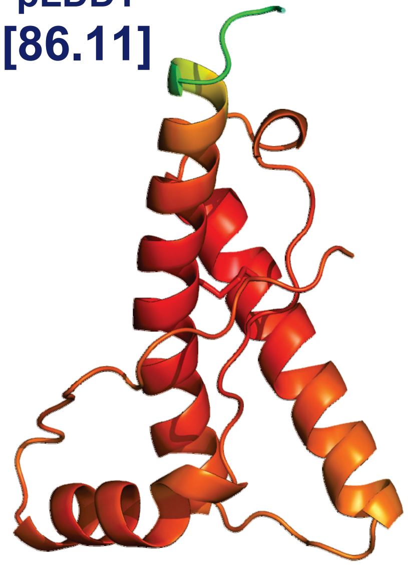
***In vitro* studies**

TgVole (1x)	**Not tested**
Banner-tailed kangaroo rat	**Not tested**

***In vivo* studies**

TgVole (1x)	**Not tested**
Banner-tailed kangaroo rat	**Not tested**

pLDDT
[86.11]



Protein code: 3688

Stephens' kangaroo rat

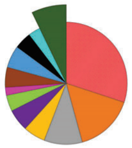
GenBank: BK064064

Dipodomys stephensi

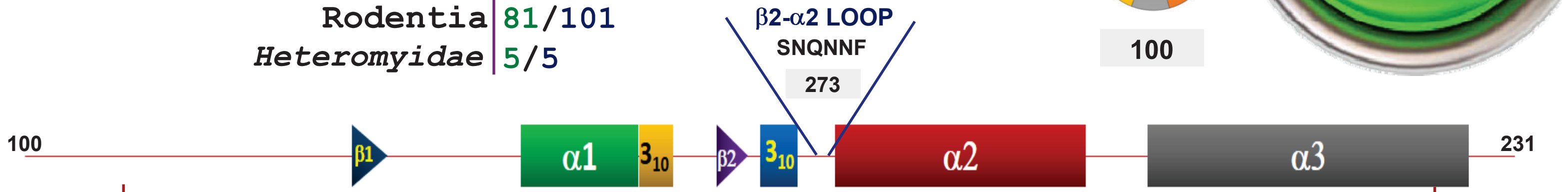
Rodentia	81/101
Heteromyidae	5/5

P100%

100



100



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPSQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERMVEQMCITQYQKEAQAYYEPRS-

I M W N R N I M V V S G S

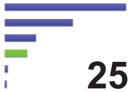
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions

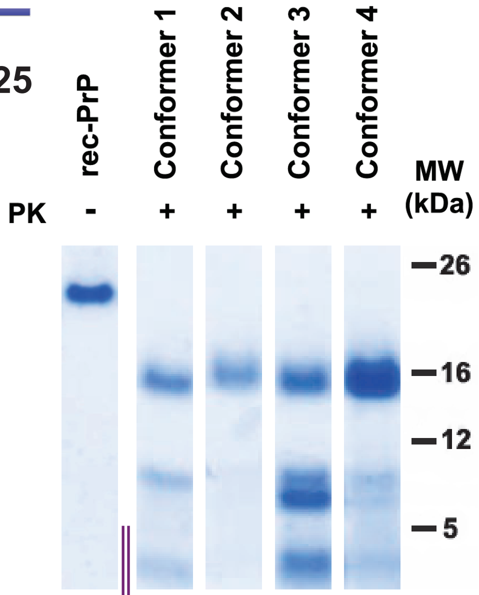
No insertions

No polymorphic variants found

Distinct primary sequence across species



25



218 AA

4
Conformers

Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

Not tested
TgVole (1x)

Not tested
Stephens' kangaroo rat

In vivo studies

Not tested
TgVole (1x)

Not tested
Stephens' kangaroo rat

pLDDT
[86.16]

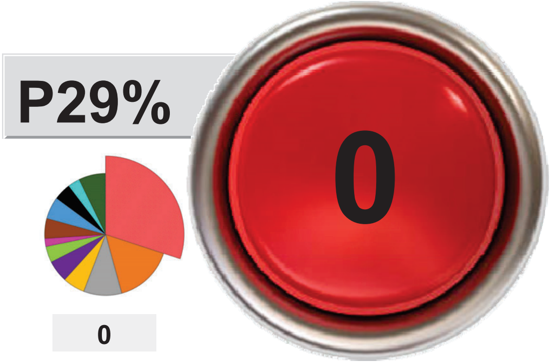
Protein code: 3240

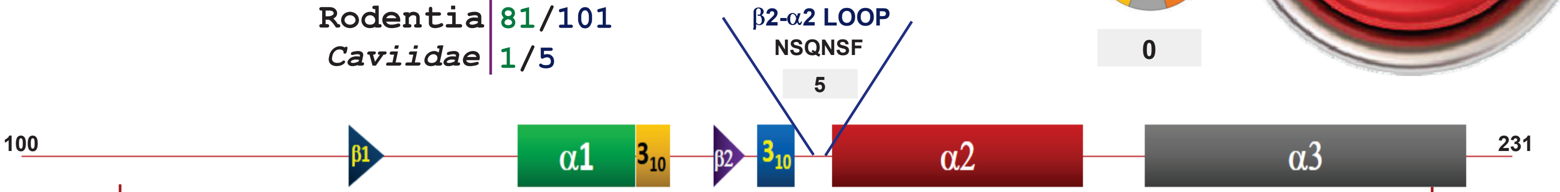
Patagonian mara

GenBank: KM357833

Dolichotis patagonum

Rodentia	81/101
Caviidae	1/5





WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYKPVDQYNSQNSFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAYYYHGRAG-

I V M N W N R N N H M V V EGRSS

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions

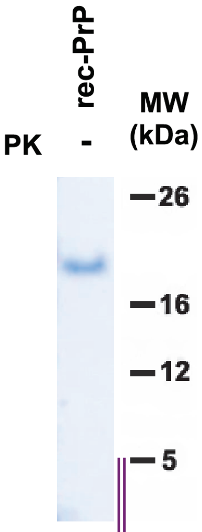
No insertions

No polymorphic variants found

Distinct primary sequence across species

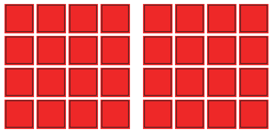
Tm^{Exp}: ND

ΔΔG: ND



202 AA

NO MISFOLDING



0 Conformers

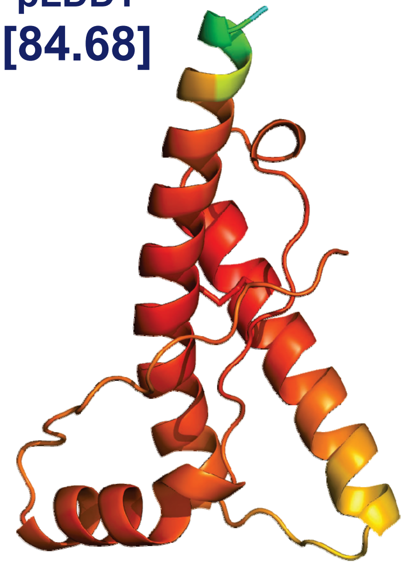
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [84.68]



Protein code: 1087

Transcaucasian mole vole

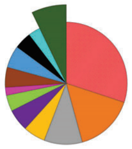
GenBank: BK064014

Ellobius lutescens

Rodentia	81/101
Cricetidae	25/27

Distinct primary sequence across species

P100%



100

100

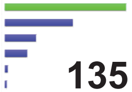
β2-α2 LOOP
NNQNNF
164

`WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRSS-`

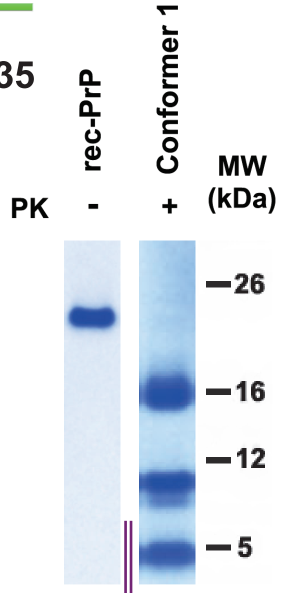
`I`

PrP sequence differs by 1 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

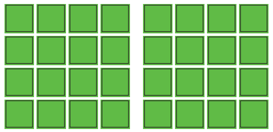


135



202 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: 6.65

In vitro studies

TgVole (1x) Not tested

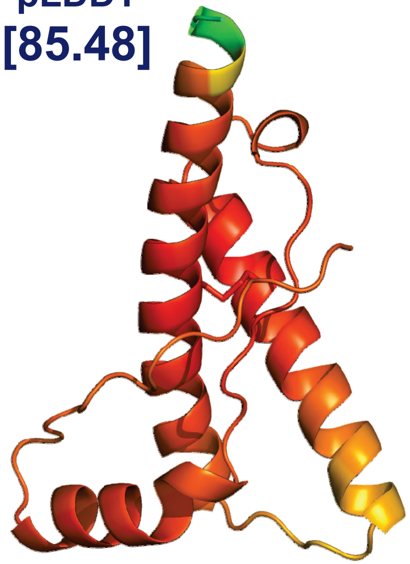
Transcaucasian mole vole Not tested

In vivo studies

TgVole (1x) Not tested

Transcaucasian mole vole Not tested

pLDDT
[85.48]

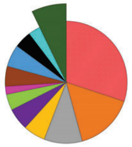


Protein code: 3175

Northern mole vole

GenBank: BK064040

P100%

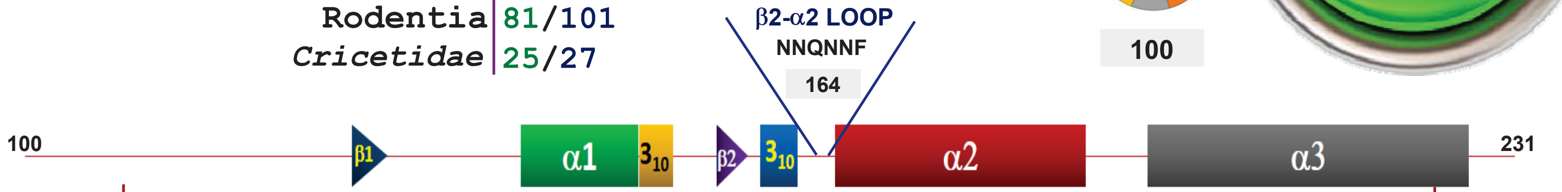


100

100

Ellobius talpinus

Rodentia	81/101
Cricetidae	25/27



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRSS-

I

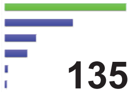
PrP sequence differs by 1 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

Distinct primary sequence across species



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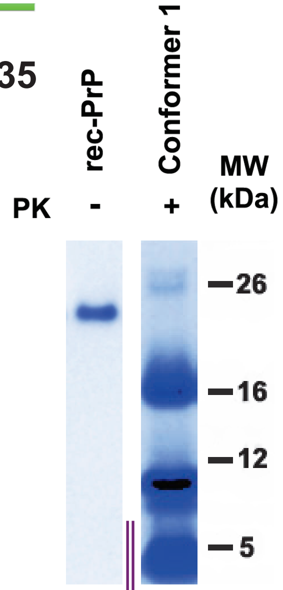


210 AA

1

Conformers

Tm^{Exp}: ND

ΔΔG: 3.73

In vitro studies

Not tested
TgVole (1x)

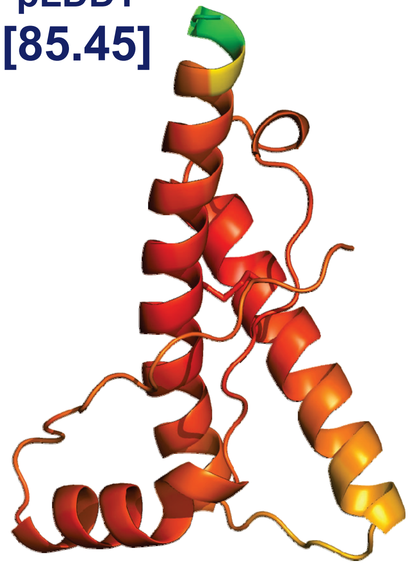
Not tested
Northern mole vole

In vivo studies

Not tested
TgVole (1x)

Not tested
Northern mole vole

pLDDT
[85.45]



Protein code: 3206

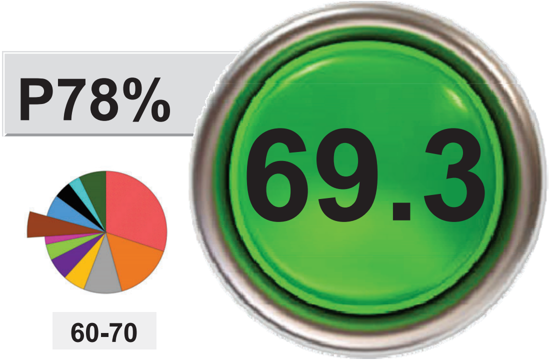
Chinese zokor

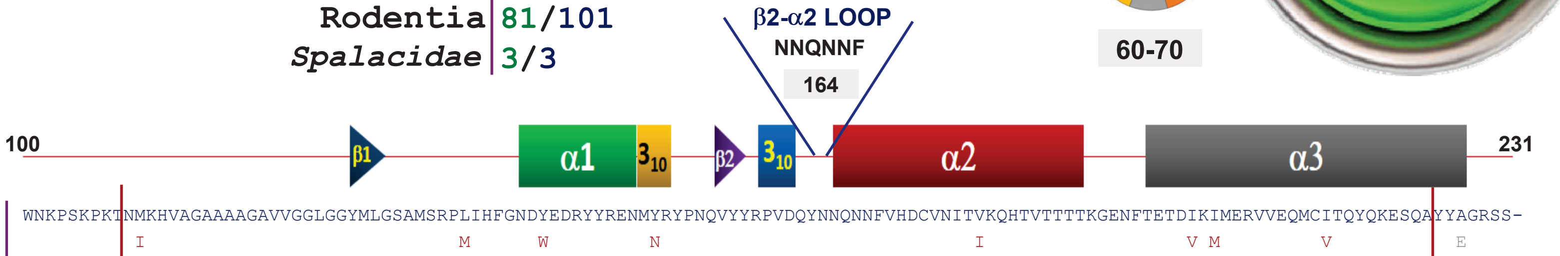
GenBank: BK064949

Eospalax fontanierii

Rodentia	81/101
Spalacidae	3/3

P78%





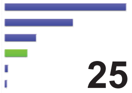
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQKESQAYYAGRSS-
          I                           M      W         N                                I                   V M       V         E
```

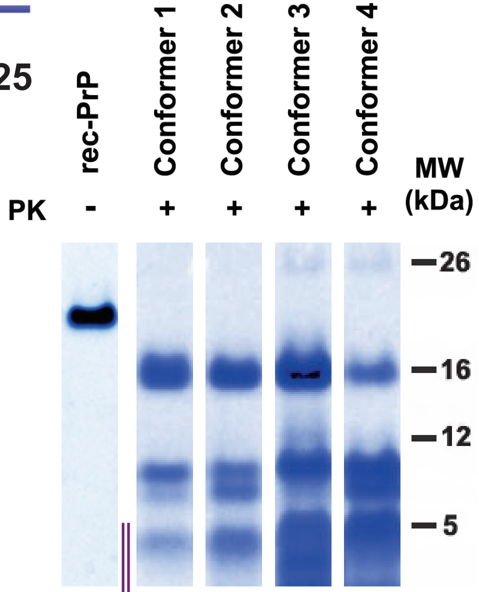
PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions

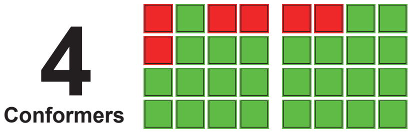
No insertions

No polymorphic variants found





203 AA



Tm^{Exp}: ND

ΔΔG: -3.33

***In vitro* studies**

TgVole (1x) Not tested

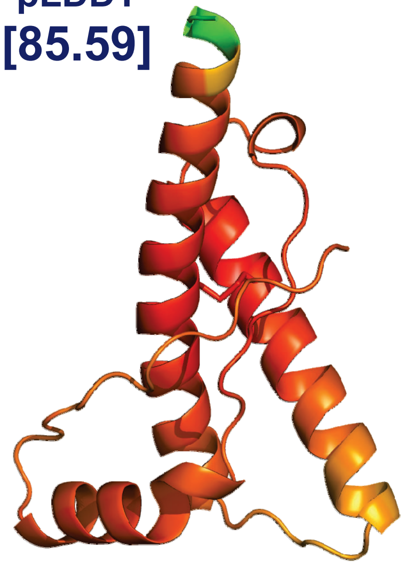
Chinese zokor Not tested

***In vivo* studies**

TgVole (1x) Not tested

Chinese zokor Not tested

pLDDT
[85.59]



Distinct primary sequence across species

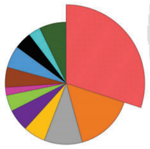
North American porcupine

GenBank: BK063957

Erethizon dorsata

Rodentia 81/101
Erethizontidae 0/2

P29%



0

0

β2-α2 LOOP
SGQKSF
2

`WNKPSKPKTNLKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPDQVYYRPVGQYSGQKSFVQDCVNITIKQHTVTATTKGENFTETDVKIMERVLEQMCTTQYQKESQAYYYRGRAG-`

`I V M N W N N D NN NN H T M V V EGRSS`

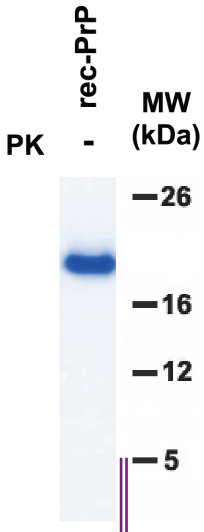
PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

Tm^{Exp}: ND

ΔΔG: ND

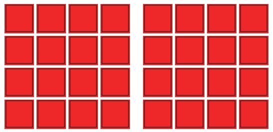


202 AA

NO MISFOLDING

0

Conformers



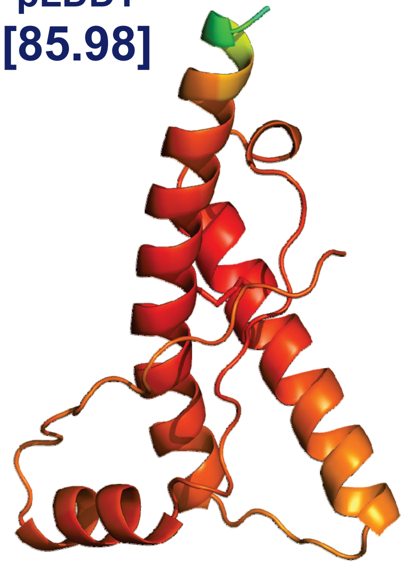
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[85.98]



Protein code: 3085

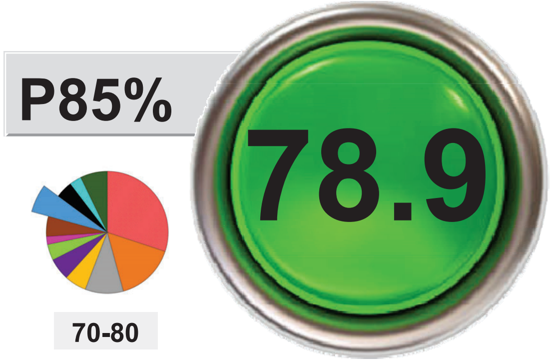
Southern flying squirrel

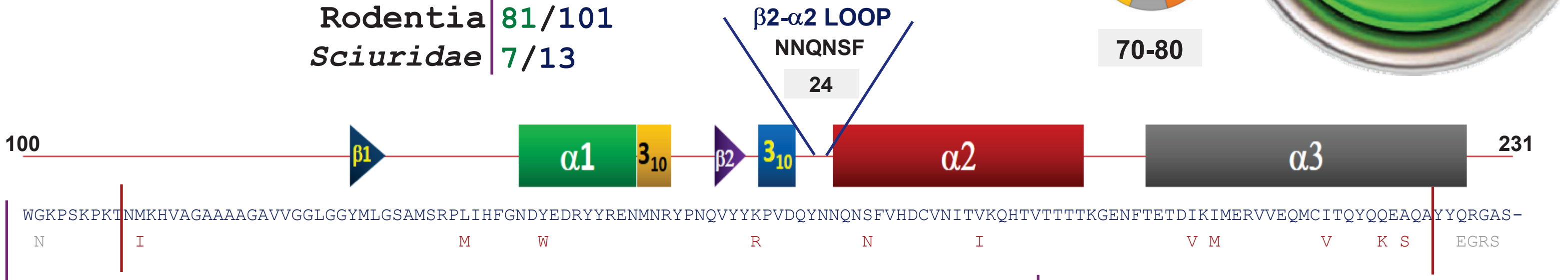
GenBank: BK064183

Glaucomys volans

Rodentia	81/101
Sciuridae	7/13

Distinct primary sequence across species





WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPNQVYYKPVDQYNNQNSFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQEAQAYYQRGAS-

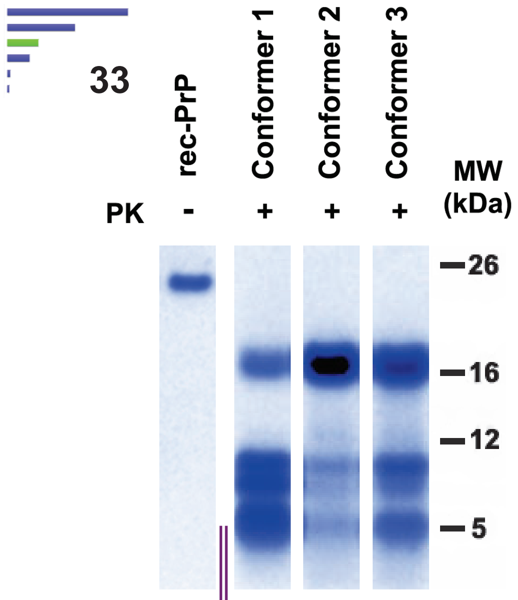
N I M W R N I V M V K S EGRS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

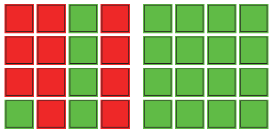
No deletions

No insertions

No polymorphic variants found



221 AA



Tm^{Exp}: ND

ΔΔG: -8.59

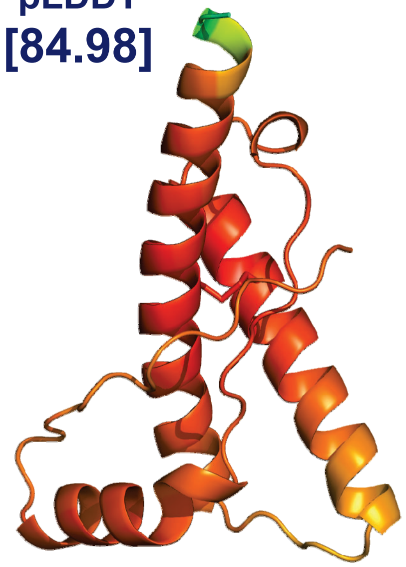
In vitro studies

TgVole (1x)	Not tested
Southern flying squirrel	Not tested

In vivo studies

TgVole (1x)	Not tested
Southern flying squirrel	Not tested

pLDDT [84.98]



Protein code: 4022

Distinct primary sequence across species

Edible dormouse

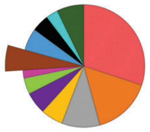
GenBank: BK064048

Glis glis

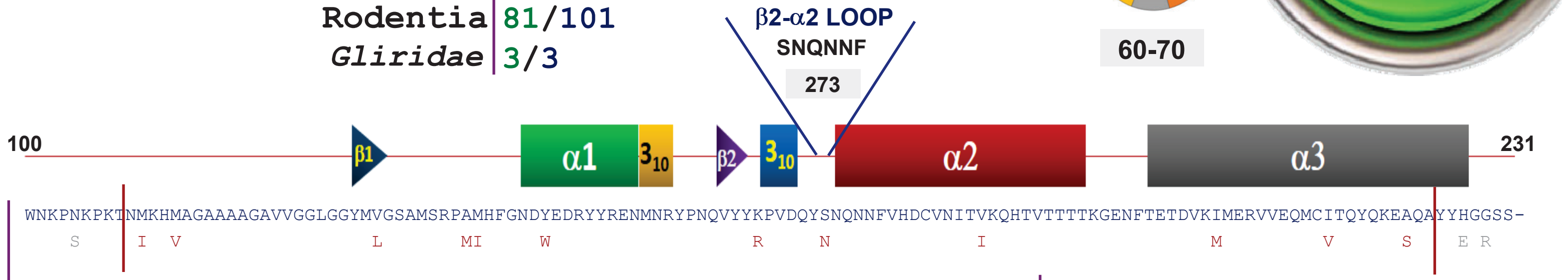
Rodentia 81/101
Gliridae 3/3

P76%

64.3



60-70



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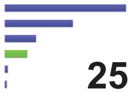
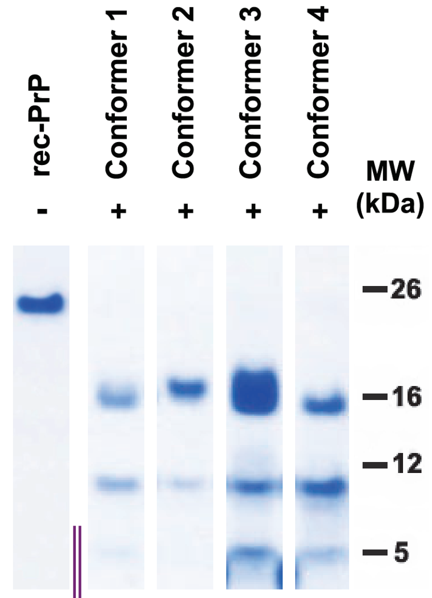
WNKPNKPKTNMKHMAGAAAAGAVVGGLGGYMVGSAMSRPAMHFGNDYEDRYYRENMNRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQKEAQAYYHGGSS-
     S    I  V              L       MI     W                      R     N          I                   M         V       S     E R
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

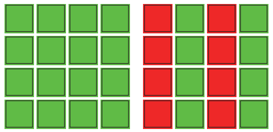


25



218 AA

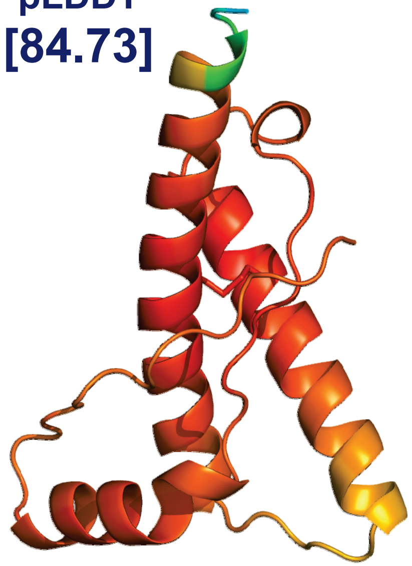
4
Conformers



Tm^{Exp}: ND

ΔΔG: -2.93

pLDDT
[84.73]



In vitro studies

TgVole (1x)	Not tested
Edible dormouse	Not tested

In vivo studies

TgVole (1x)	Not tested
Edible dormouse	Not tested

Protein code: 3217

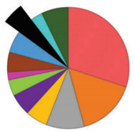
African woodland thicket rat

GenBank: XM_028757107

Grammomys surdaster

Rodentia	81/101
Muridae	16/18

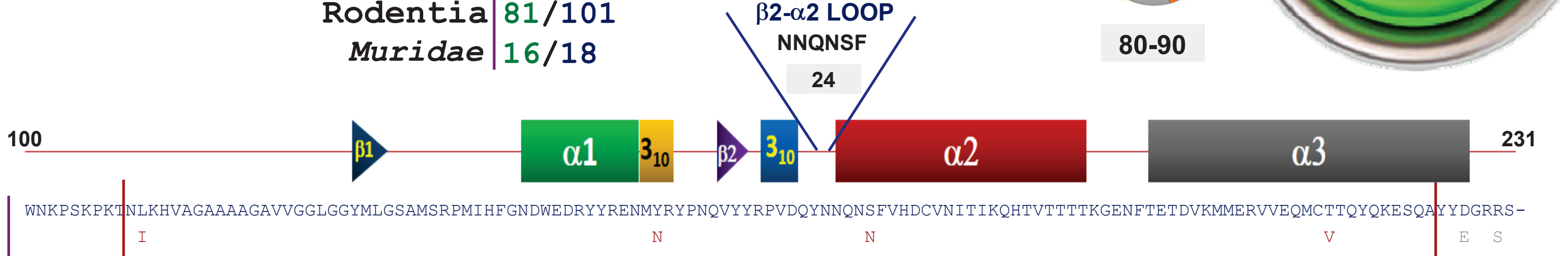
P86%



80-90

83

Distinct primary sequence across species



WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYYRPVDQYNNQNSFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCTTQYQKESQAYYDGRRS-

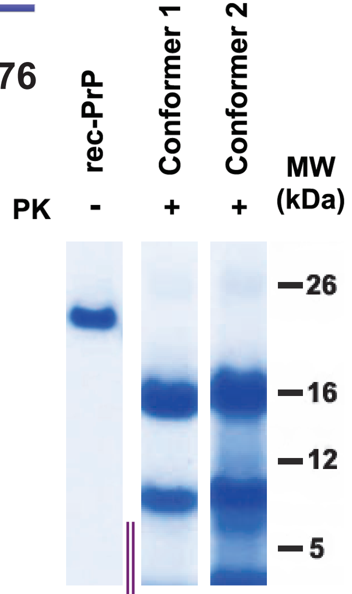
PrP sequence differs by 4 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

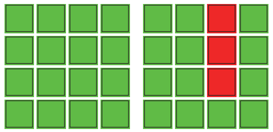
No polymorphic variants found

76



211 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -3.65

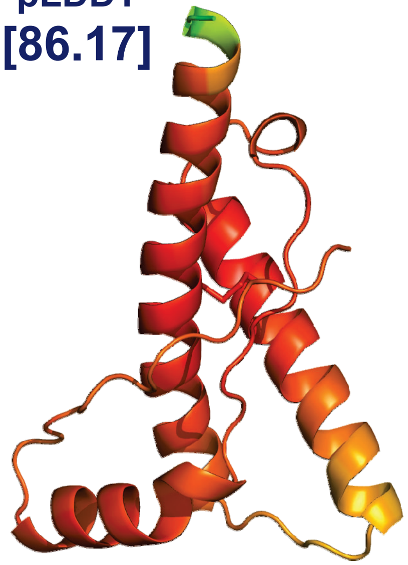
In vitro studies

TgVole (1x)	Not tested
African woodland thicket rat	Not tested

In vivo studies

TgVole (1x)	Not tested
African woodland thicket rat	Not tested

pLDDT [86.17]



Protein code: 1001

Woodland dormouse

GenBank: BK064049

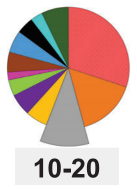
Graphiurus murinus

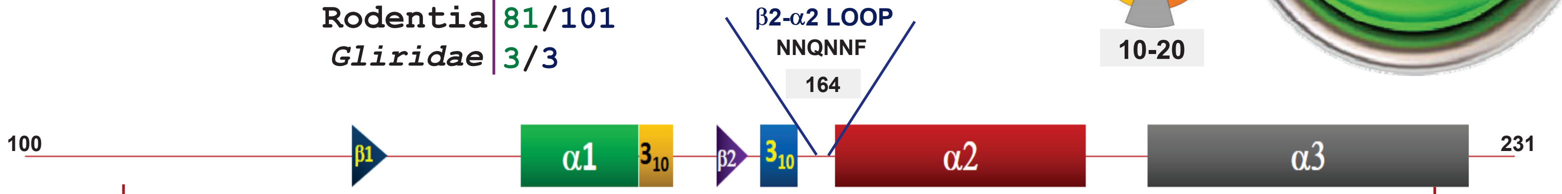
Distinct primary sequence across species

`Rodentia` 81/101
`Gliridae` 3/3

P47%

11.4





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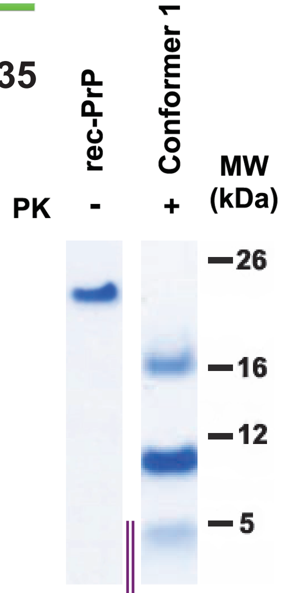
WNKPNKPKTNMKQMAGAAAAGAVVGGVGGFLVGSAMSRPPMHFGNEYEDRYYRENMNRYPNQVYYKPVDQYNNQNNFVRDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYEKEAQAYYQRGAS-
     S     I HV             L  YML         MI     DW                  R           H      I                 M         V   Q  S    EGRS
```

PrP sequence differs by 18 amino acids from the bank vole PrP (see in red)

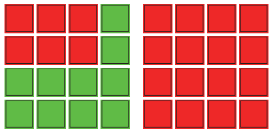
No deletions
No insertions
No polymorphic variants found

135



223 AA

1
Conformers



Tm^{Exp}: ND

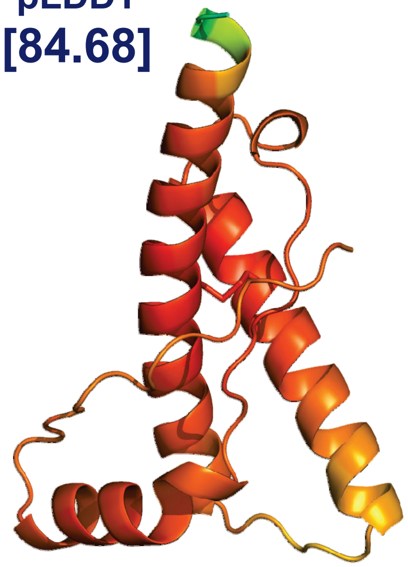
ΔΔG: -7.47

In vitro studies

Not tested
TgVole (1x)

Not tested
Woodland dormouse

pLDDT
[84.68]



In vivo studies

Not tested
TgVole (1x)

Not tested
Woodland dormouse

Protein code: 3218

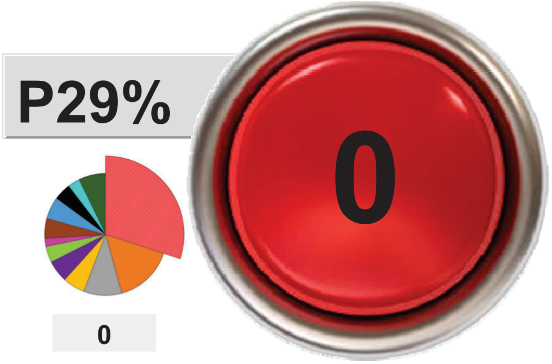
Naked mole-rat

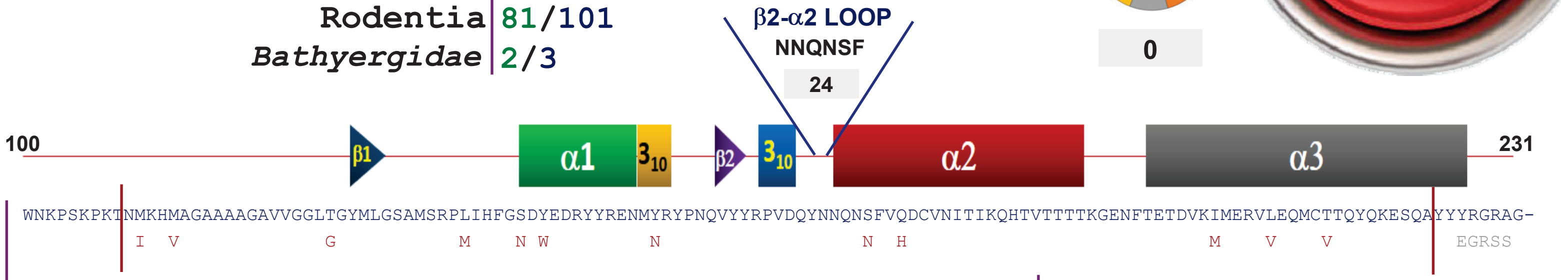
GenBank: XM_004840771

Heterocephalus glaber

Rodentia	81/101
Bathyergidae	2/3

Distinct primary sequence across species





WNKPSKPKTNMKHMAGAAAAGAVVGGLTGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYNNQNSFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAYYYRGRAG-

I V G M N W N N H M V V EGRSS

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

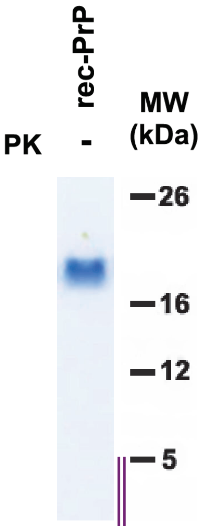
No deletions

No insertions

No polymorphic variants found

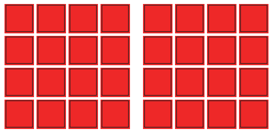
Tm^{Exp}: ND

ΔΔG: ND



202 AA

NO MISFOLDING



0 Conformers

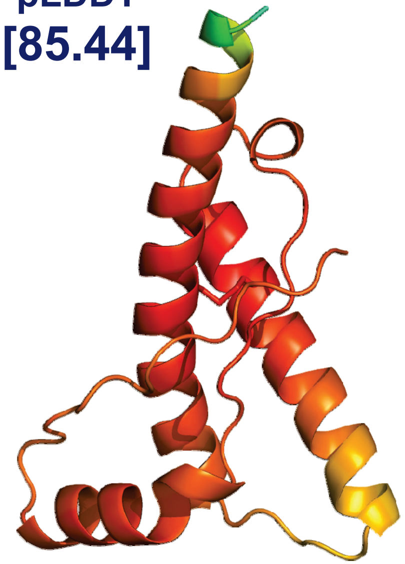
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [85.44]



Protein code: 0978

Capybara

GenBank: KM357831

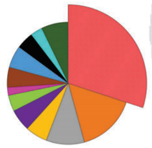
Hydrochoerus hydrochaeris

1 species sharing the same primary sequence

Rock cavy
Kerodon rupestris

Rodentia 81/101
Caviidae 1/5

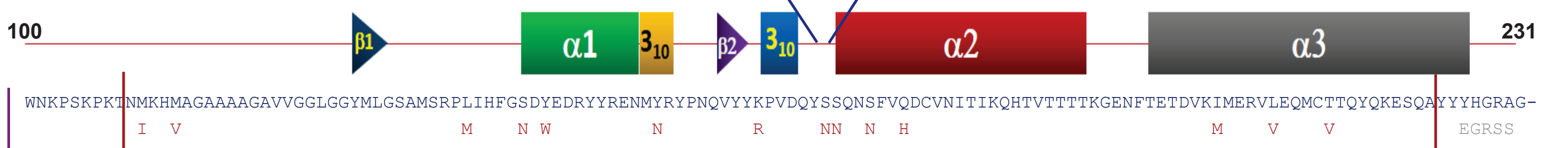
P29%



0

0

β2-α2 LOOP
SSQNSF
6



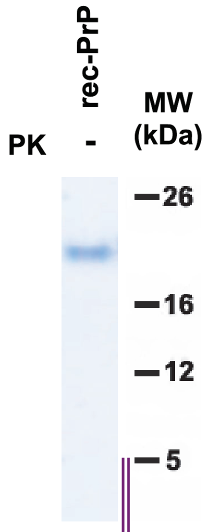
```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYKPVDQYSSQNSFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAYYYHGRAG-
           I  V                            M    N W         N        R      NN  N  H                                M    V    V           EGRSS
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

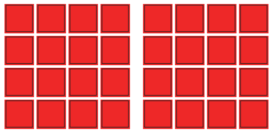
Tm^{Exp}: ND

ΔΔG: ND



202 AA

NO MISFOLDING



0
Conformers

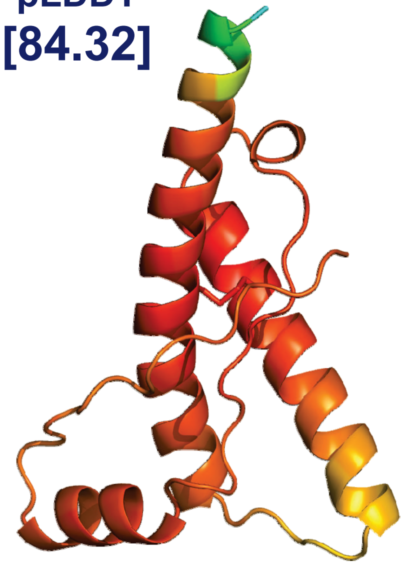
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[84.32]



Protein code: 1435

Allen's wood mouse

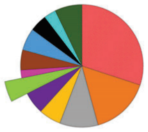
GenBank: BK064167

Hylomyscus alleni

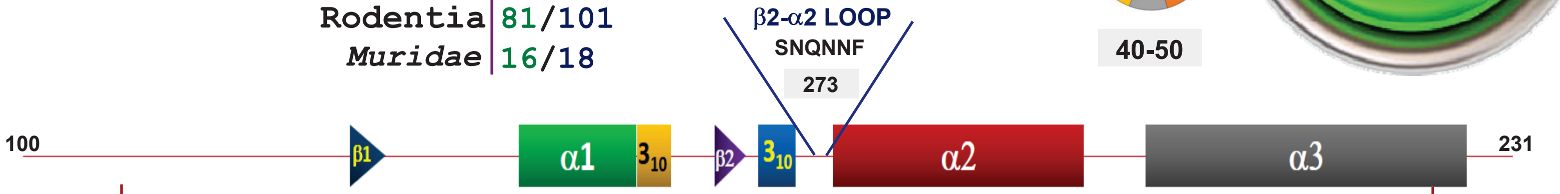
Rodentia 81/101
Muridae 16/18

P67%

40



40-50



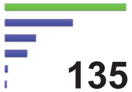
WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGDNFTETDVKMMERVVEQMCVTQYQKESQAYYEGRRS-

I I N N E S

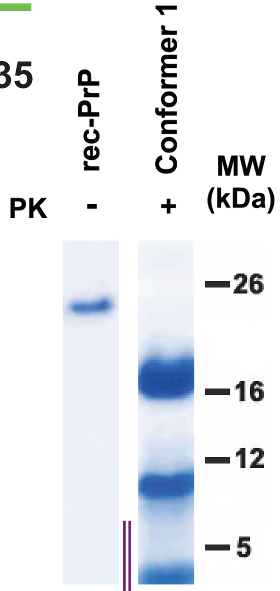
PrP sequence differs by 5 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species

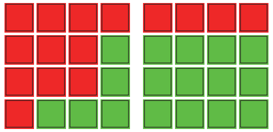


135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -10.63

In vitro studies

TgVole (1x) Not tested

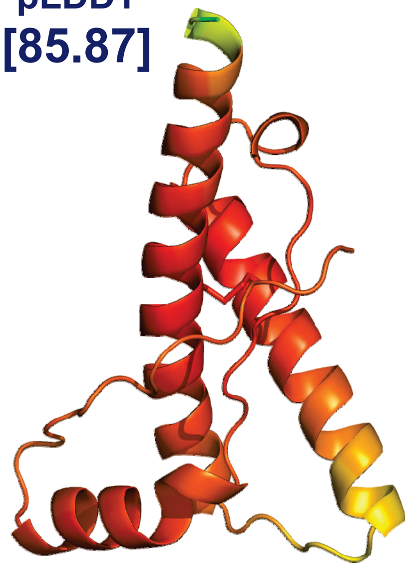
Allen's wood mouse Not tested

In vivo studies

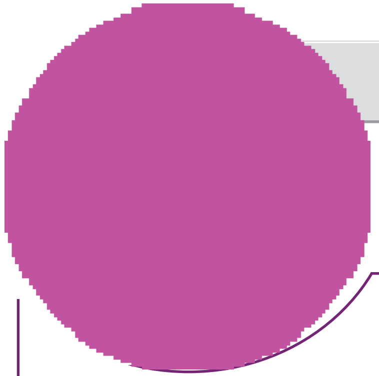
TgVole (1x) Not tested

Allen's wood mouse Not tested

pLDDT
[85.87]



Protein code: 3803



Malayan porcupine

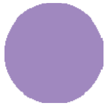
GenBank: BK063933

Hystrix brachyura

`Rodentia` 81/101

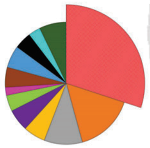
`Hystricidae` 0/1

1 species sharing the same primary sequence



Crested porcupine
Hystrix cristata

P29%



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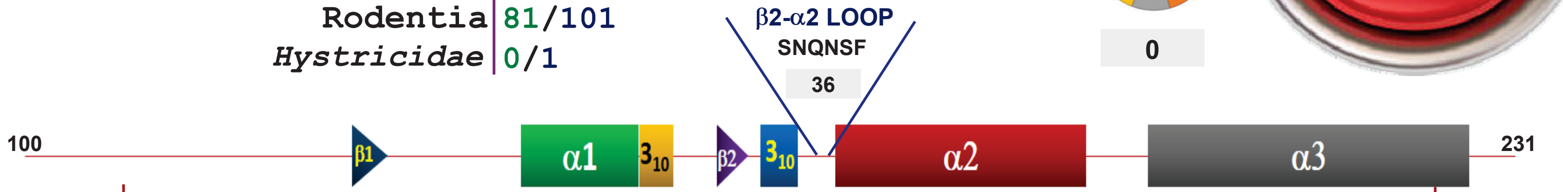


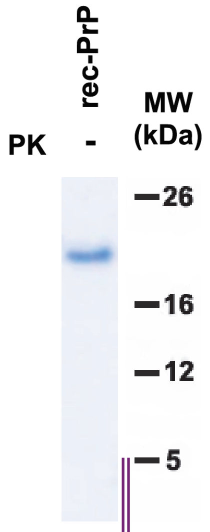
```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESEAYYYRGRAG-
           I  V                           M     N W         N                N   N  H                           M     V     V         Q   EGRSS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

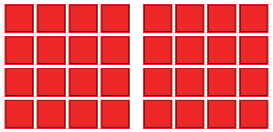
ΔΔG: ND



202 AA

NO MISFOLDING

0
Conformers



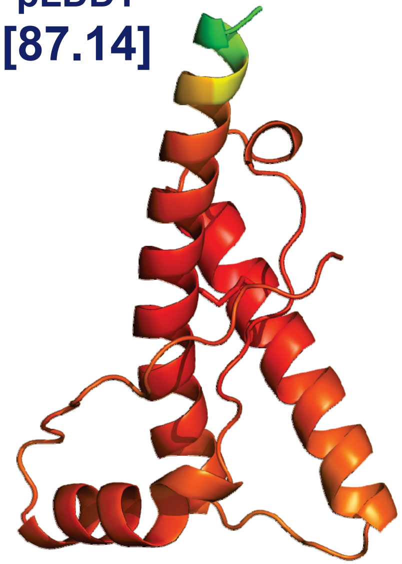
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[87.14]



Protein code: 3056

Lesser Egyptian jerboa

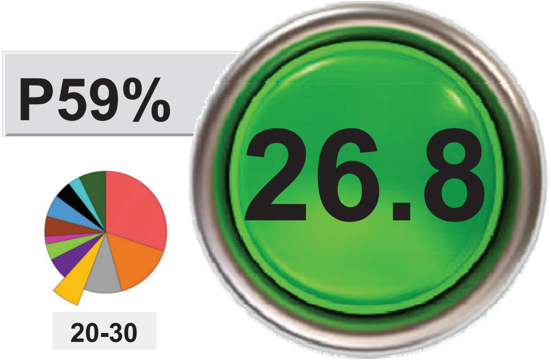
GenBank: BK064939

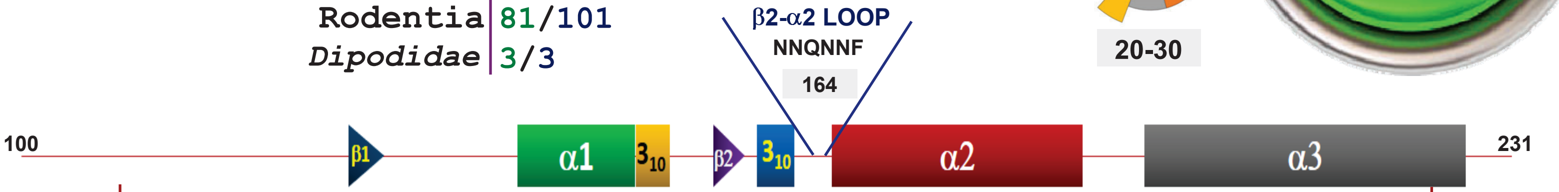
Jaculus jaculus

Rodentia	81/101
Dipodidae	3/3

Distinct primary sequence across species

P59%





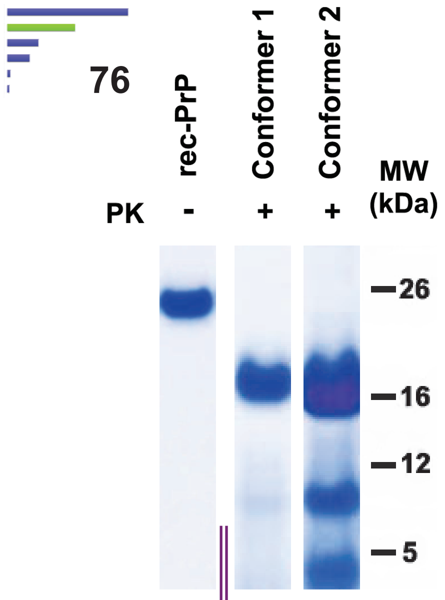
```
WNKPNKPKTSMKHMAGAAAAGAVAGGLGGYMLGSVMSRPSISFGNDYEDRYYRENMNRYPSQVYYKPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQKESQAYLEGRRS-
    S   NI V         V         A    M H   W           N    R                I                  M      V        Y  S
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions

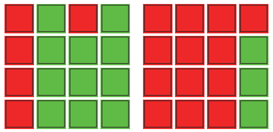
No insertions

No polymorphic variants found



217 AA

2 Conformers



Tm^{Exp}: ND

ΔΔG: -14.88

In vitro studies

TgVole (1x) Not tested

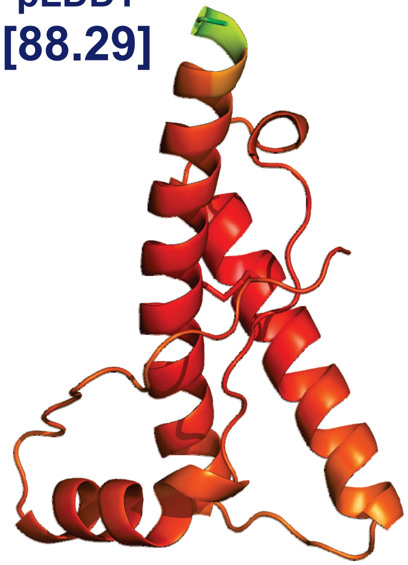
Lesser Egyptian jerboa Not tested

In vivo studies

TgVole (1x) Not tested

Lesser Egyptian jerboa Not tested

pLDDT [88.29]



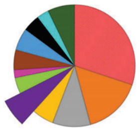
Maned rat

GenBank: BK064153

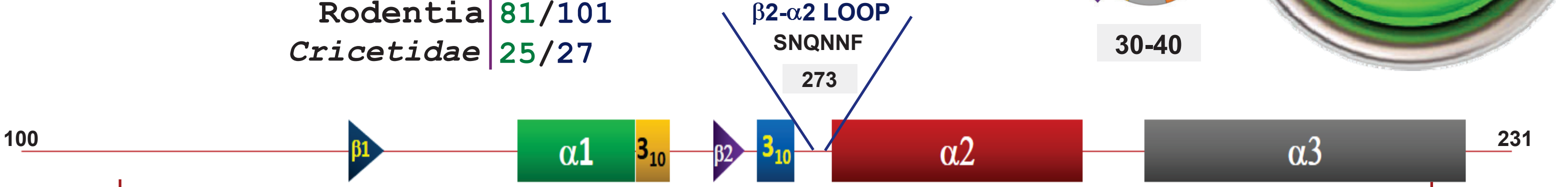
Lophiomys imhausi

Rodentia	81/101
Cricetidae	25/27

P65% **36.6**



30-40



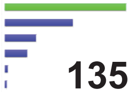
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQRESQAYYDGRRS-

I N N K E S

PrP sequence differs by 4 amino acids from the bank vole PrP (see in red)

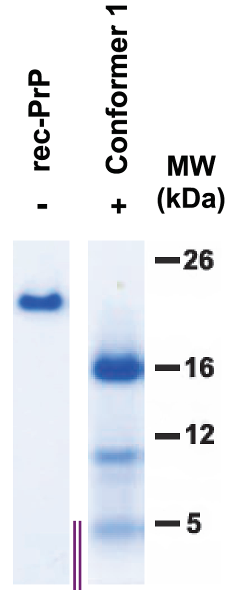
No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species



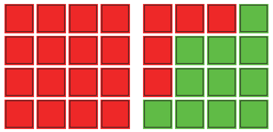
135

PK



217 AA

1 Conformers



Tm^{Exp}: ND

ΔΔG: -2.47

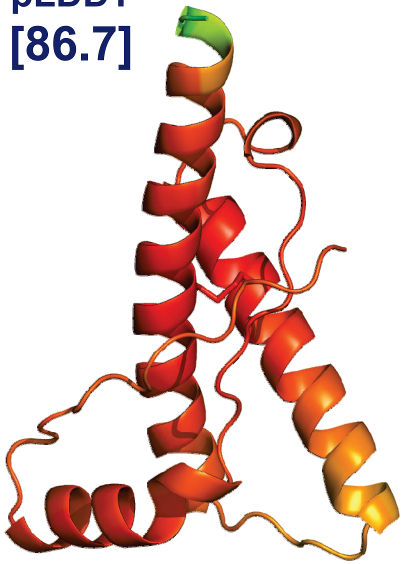
In vitro studies

TgVole (1x)	Not tested
Maned rat	Not tested

In vivo studies

TgVole (1x)	Not tested
Maned rat	Not tested

pLDDT [86.7]



Protein code: 3608

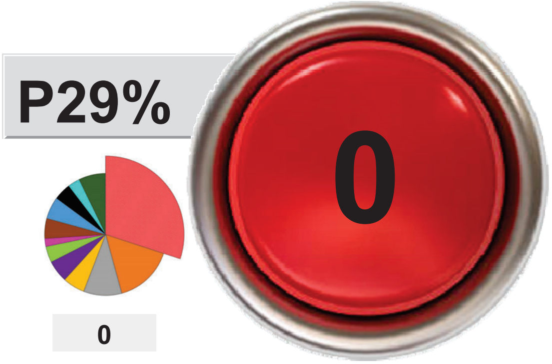
Yellow-bellied marmot

GenBank: XM_027955665

Marmota flaviventris

Rodentia 81/101
Sciuridae 7/13

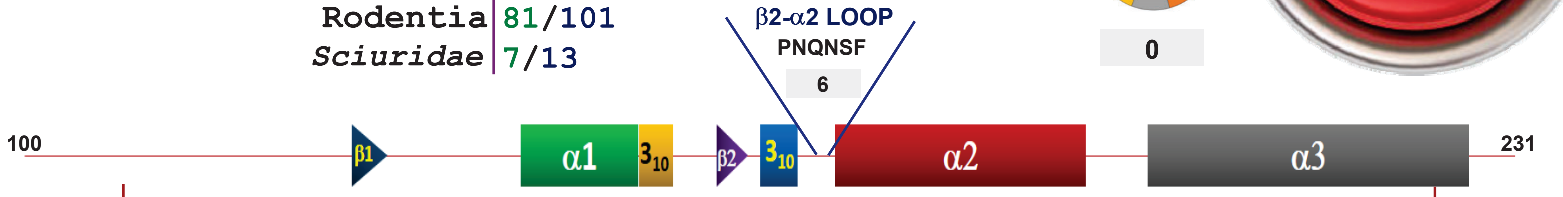
P29%



2 species sharing the same primary sequence

🟩 **Groundhog**
Marmota monax

🟪 **Vancouver Island marmot**
Marmota vancouverensis



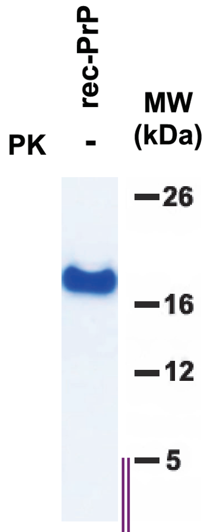
```
WGKPVKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPMMHFGSDYEDRYYRENMNRYPSQVYYKPVDQYPNQNSFVHDCVNITIKQHTVTTTTKGDNFTETDIKIMERVVEQMCTTQYKQEAQAYYQRGSS-
 N  S     I  V                                I   N W            N    R     N  N                E     V M        V   QK S   EGR
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -10.36



195 AA

NO MISFOLDING

0
Conformers

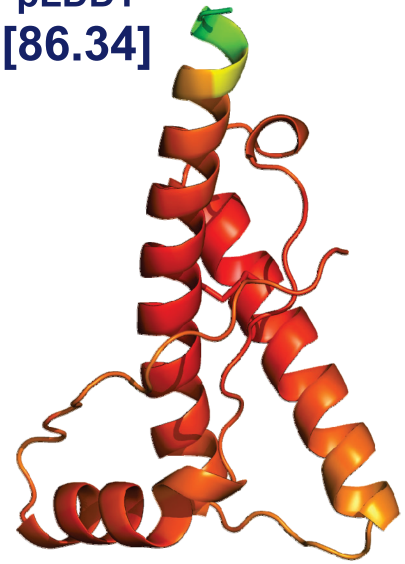
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.34]



Protein code: 1099

Alpine marmot

GenBank: XM_015482632

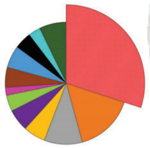
Marmota marmota

Rodentia 81/101
Sciuridae 7/13

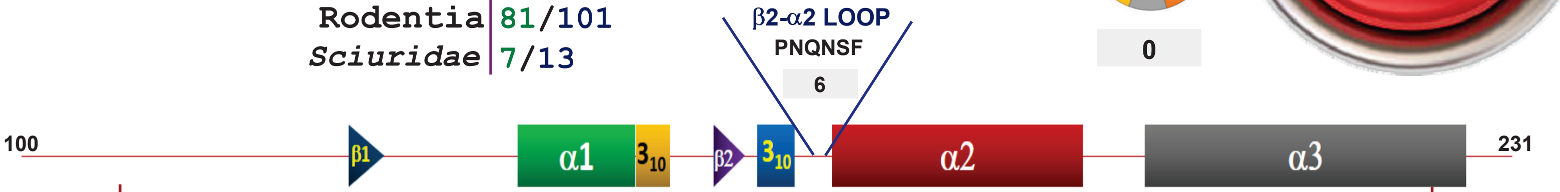
1 species sharing the same primary sequence

🟥 **Himalayan marmot**
Marmota himalayana

P29%



0



WGKPVKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPMMHFGSDYEDRYYRENMNRYPSQVYYKPMDQYPNQNSFVHDCVNITIKQHTVTTTTKGDNFTETDIKIMERVVEQMCTTQYKQEAQAYYQRGSS-

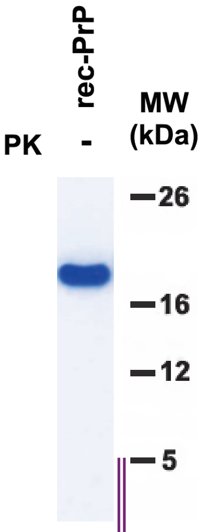
N S I V I N W N R V N N E V M V QK S EGR

PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

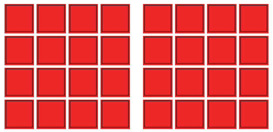
ΔΔG: -8.03



195 AA

NO MISFOLDING

0
Conformers



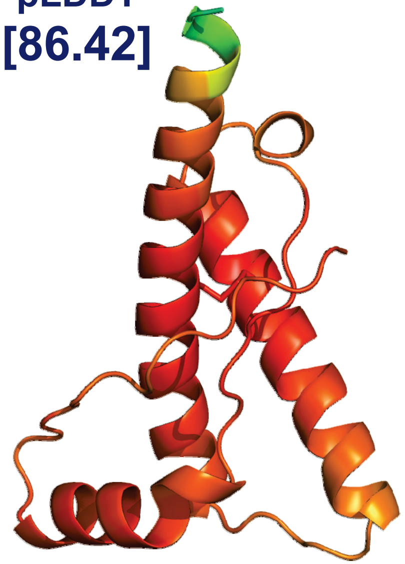
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.42]



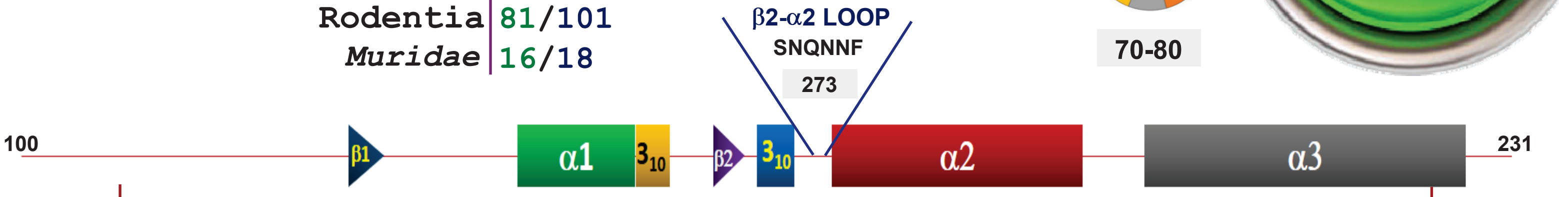
Protein code: 2667

Southern multimammate mouse

GenBank: XM_031371966

Mastomys coucha

Rodentia 81/101
Muridae 16/18

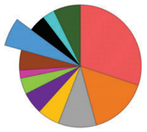


WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRRS-
I N N S

PrP sequence differs by 3 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

P82%



70-80

74.6

Tm^{Exp}: ND

ΔΔG: -6.17

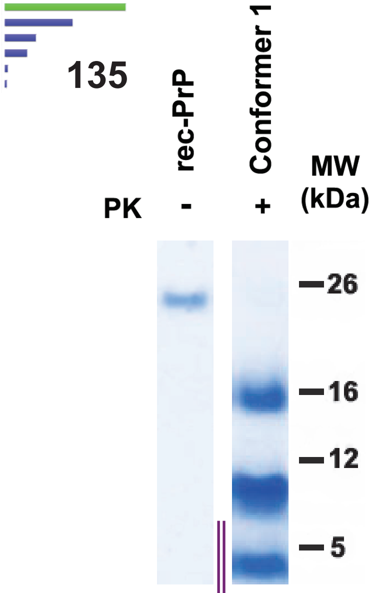
4 species sharing the same primary sequence

Natal multimammate mouse
Mastomys natalensis

Muennink's spiny rat
Tokudaia muenninki

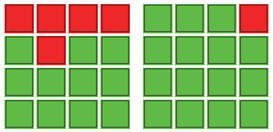
Ryukyu spiny rat
Tokudaia osimensis

Tokunoshima spiny rat
Tokudaia tokunoshimensis



211 AA

1
Conformers



In vitro studies

TgVole (1x) Not tested

Southern multimammate mouse Not tested

In vivo studies

TgVole (1x) Not tested

Southern multimammate mouse Not tested

pLDDT
[86.01]

Protein code: 1098

Red spiny rat

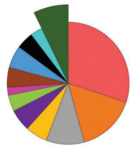
GenBank: KF466947

Maxomys surifer

Rodentia	81/101
Muridae	16/18

P100%

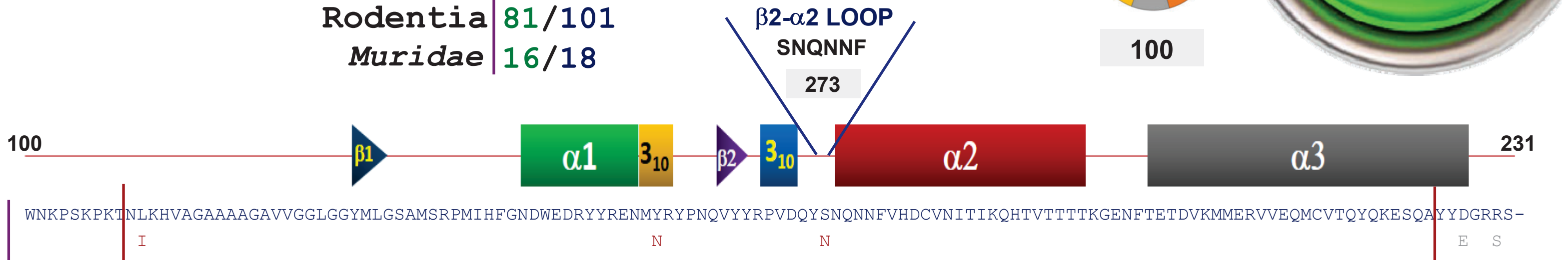
100



100

1 species sharing the same primary sequence

Gairdner's shrewmouse
Mus pahari

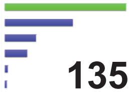


PrP sequence differs by 3 amino acids from the bank vole PrP (see in red)

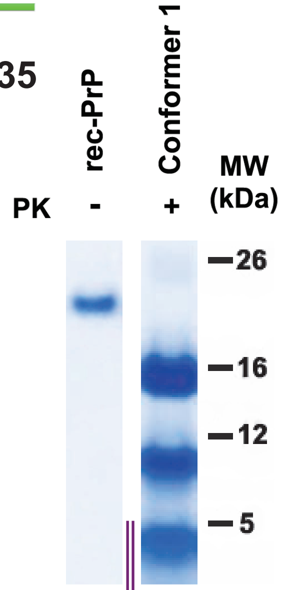
No deletions

No insertions

No polymorphic variants found



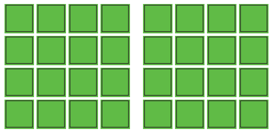
135



211 AA

1

Conformers



Tm^{Exp}: 67.6 ºC

ΔΔG: -0.97

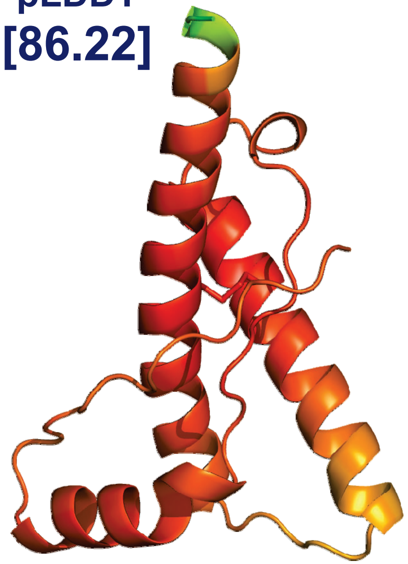
In vitro studies

TgVole (1x)	Not tested
Red spiny rat	Not tested

In vivo studies

TgVole (1x)	Not tested
Red spiny rat	Not tested

pLDDT
[86.22]



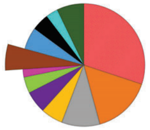
Protein code: 1440

Libyan jird

GenBank: BK064826

P74%

62.5

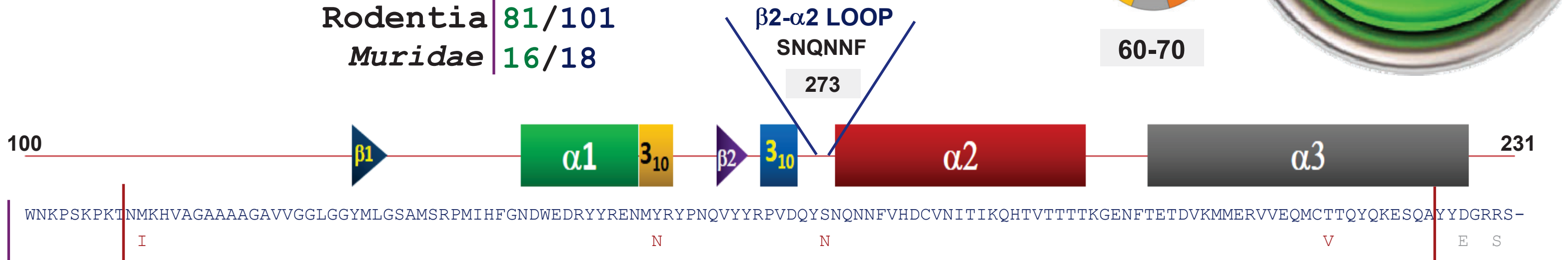


60-70

Meriones libycus

Rodentia	81/101
Muridae	16/18

Distinct primary sequence across species



```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCTTQYQKESQAYYDGRRS-
           I                                          N              N                                         V                E  S
```

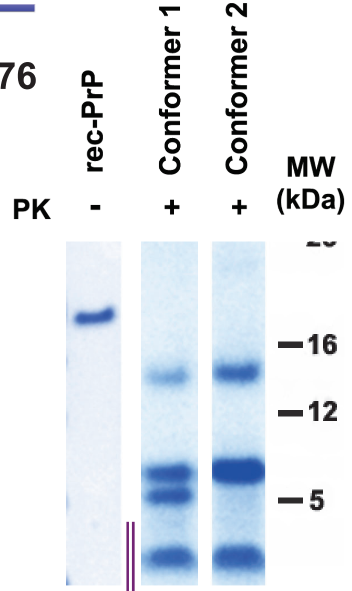
PrP sequence differs by 4 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

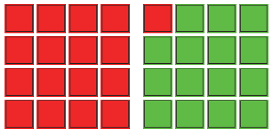
76



210 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: -15.45

In vitro studies

TgVole (1x)	Not tested
Libyan jird	Not tested

In vivo studies

TgVole (1x)	Not tested
Libyan jird	Not tested

pLDDT [93.88]

Protein code: 4640

Mongolian gerbil

GenBank: XM_021651076

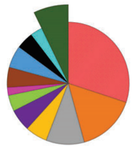
Meriones unguiculatus

Rodentia	81/101
Muridae	16/18

1 species sharing the same primary sequence

Great gerbil
Rhombomys opimus

P100% **100**



100

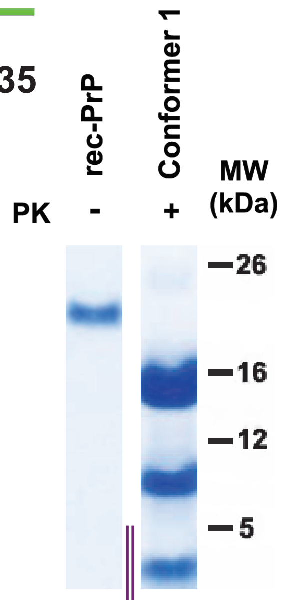
β2-α2 LOOP
SNQNNF
273

```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-
          I                                           N               N                                                        E  S
```

PrP sequence differs by 3 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

135



210 AA

1 Conformers

Tm^{Exp}: ND

ΔΔG: -3.71

In vitro studies

TgVole (1x) — Propagate

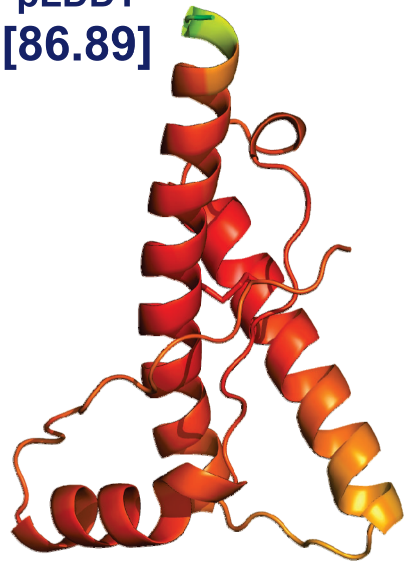
Mongolian gerbil — Propagate

In vivo studies

TgVole (1x) — Infectious

Mongolian gerbil — Ongoing

pLDDT [86.89]



Protein code: 1111

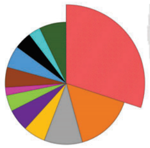
Syrian hamster

GenBank: AH001830

Mesocricetus auratus

Rodentia	81/101
Cricetidae	25/27

P29%

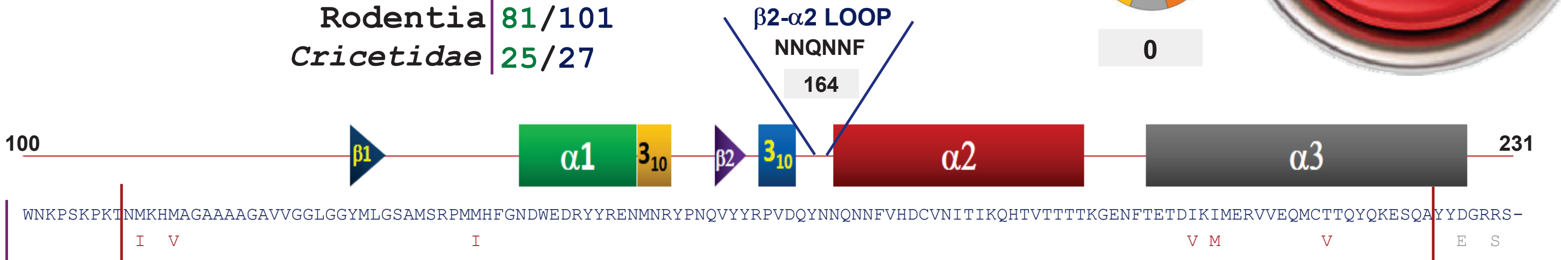


0

0

1 species sharing the same primary sequence

Turkish hamster
Mesocricetus brandti



WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPMMHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDIKIMERVVEQMCTTQYQKESQAYYDGRRS-

I V I V M V E S

PrP sequence differs by 6 amino acids from the bank vole PrP (see in red)

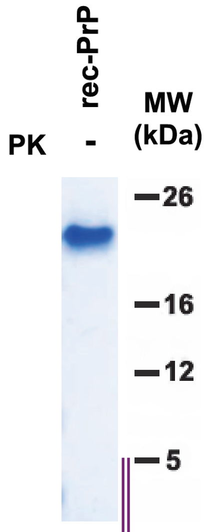
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -0.58



211 AA

NO MISFOLDING

0

Conformers

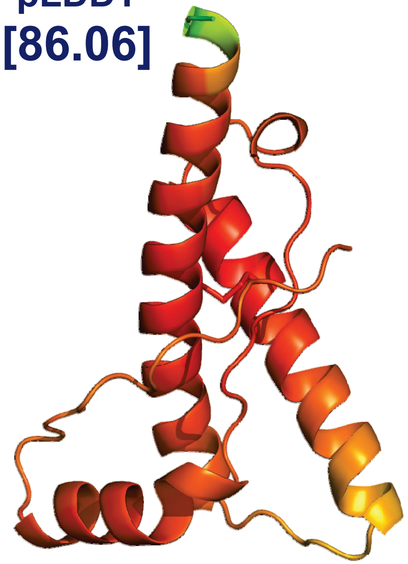
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.06]



Protein code: 0133

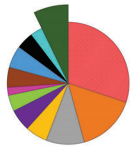
Field vole

GenBank: AF367625

Distinct primary sequence across species

P100%

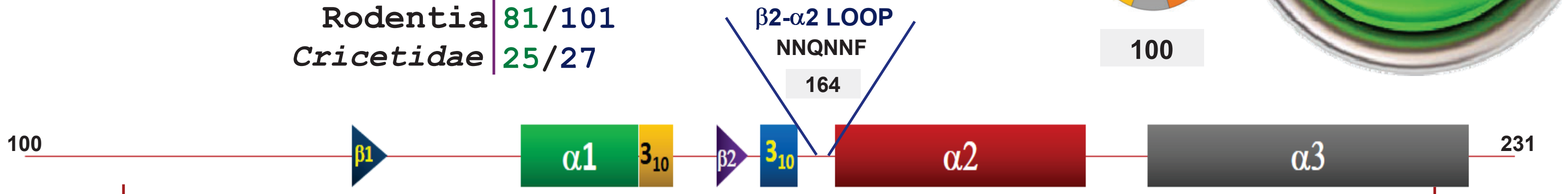
100



100

Microtus agrestis

Rodentia	81/101
Cricetidae	25/27



```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRHS-
          I                                                                                                                           S
```

PrP sequence differs by 1 amino acids from the bank vole PrP (see in red)

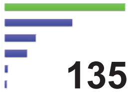
No deletions

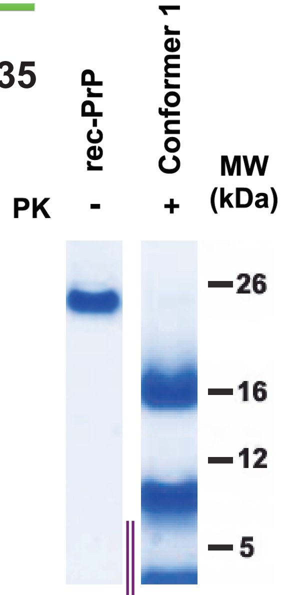
No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -1.99





210 AA

1

Conformers

In vitro studies

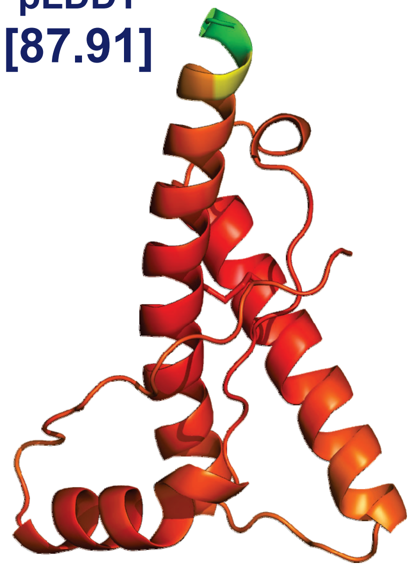
TgVole (1x)	Not tested
Field vole	Not tested

In vivo studies

TgVole (1x)	Not tested
Field vole	Not tested

pLDDT

[87.91]



Protein code: 1423

Common vole

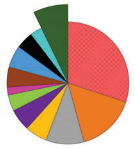
GenBank: BK064089

Microtus arvalis

Rodentia 81/101
Cricetidae 25/27

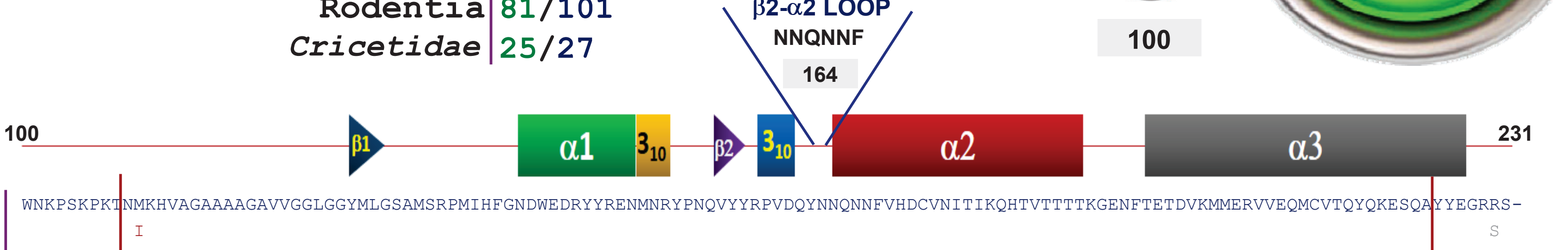
Distinct primary sequence across species

P100%



100

100

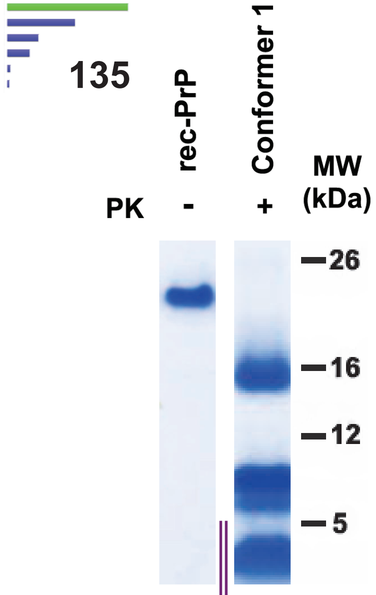


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRRS-

I S

PrP sequence differs by 1 amino acids from the bank vole PrP (see in red)

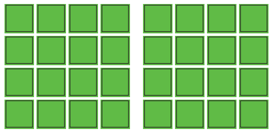
No deletions
No insertions
No polymorphic variants found



210 AA

1

Conformers



Tm^{Exp}: ND

ΔΔG: 2.34

In vitro studies

TgVole (1x) Not tested

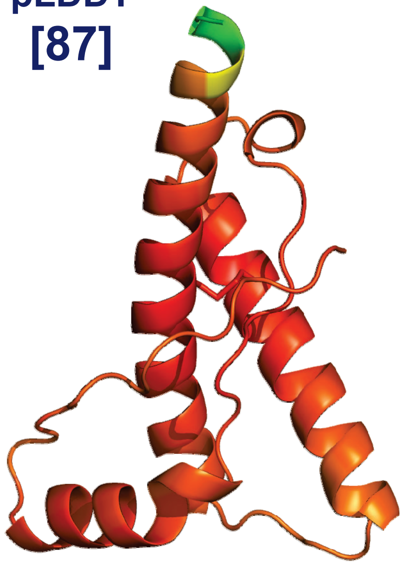
Common vole Not tested

In vivo studies

TgVole (1x) Not tested

Common vole Not tested

pLDDT
[87]



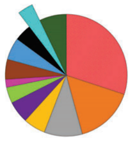
Protein code: 3268

Reed vole

GenBank: BK064090

P92%

94.3

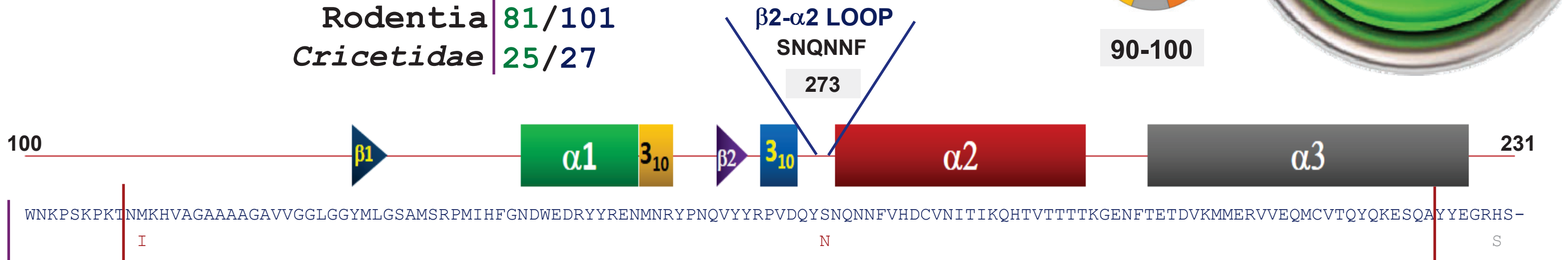


90-100

Microtus fortis

Rodentia	81/101
Cricetidae	25/27

Distinct primary sequence across species



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRHS-

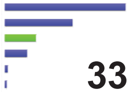
I N S

PrP sequence differs by 2 amino acids from the bank vole PrP (see in red)

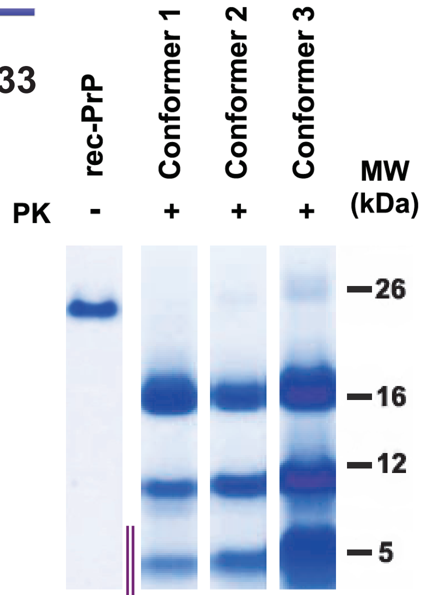
No deletions

No insertions

No polymorphic variants found



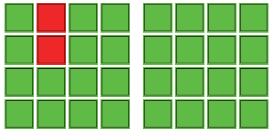
33



210 AA

3

Conformers



Tm^{Exp}: ND

ΔΔG: -3.21

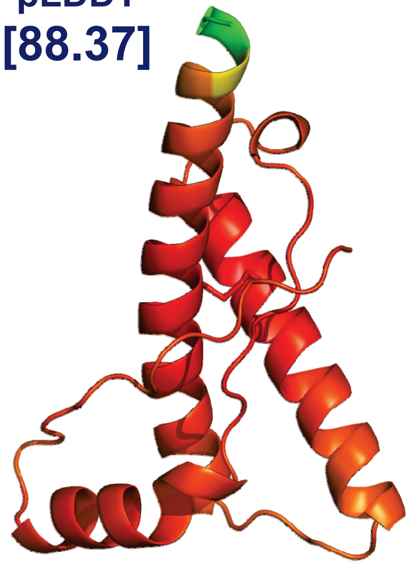
In vitro studies

TgVole (1x)	Not tested
Reed vole	Not tested

In vivo studies

TgVole (1x)	Not tested
Reed vole	Not tested

pLDDT [88.37]



Protein code: 3269

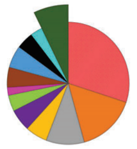
Prairie vole

GenBank: XM_005365568

Microtus ochrogaster

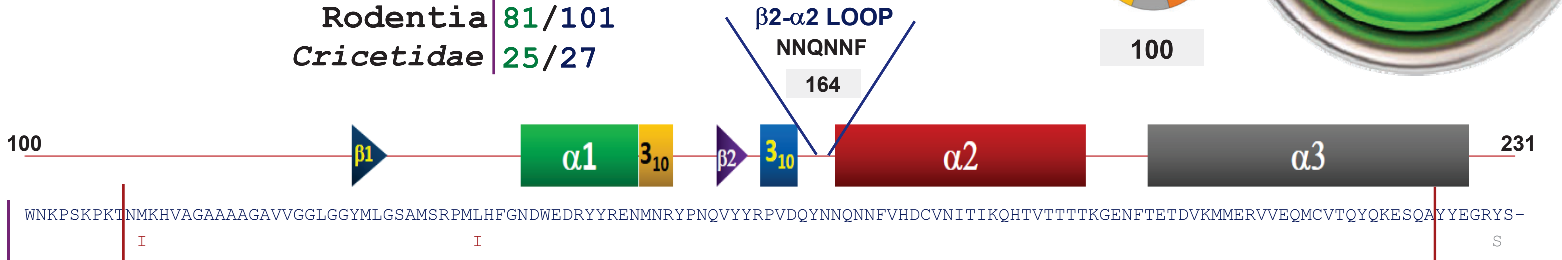
Rodentia	81/101
Cricetidae	25/27

P100%



100

100

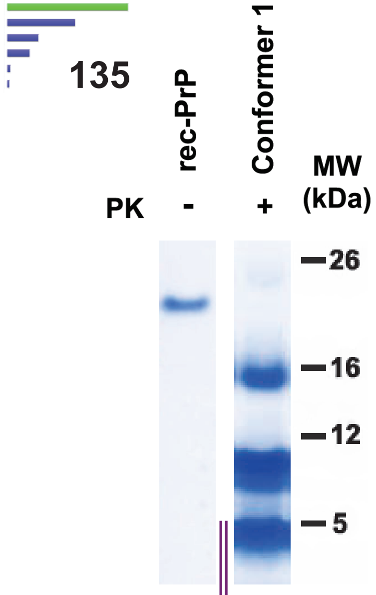


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRYS-

PrP sequence differs by 2 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Distinct primary sequence across species



210 AA

1
Conformers

Tm^{Exp}: ND

ΔΔG: -13.33

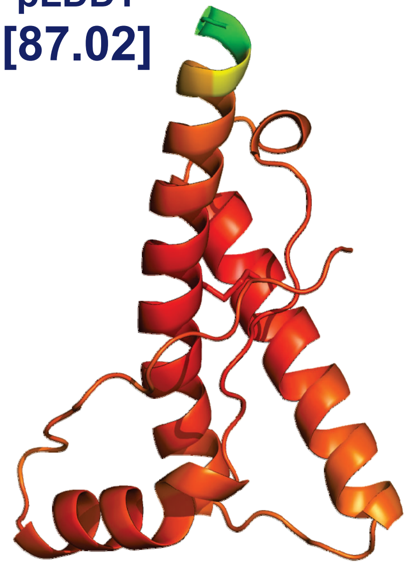
pLDDT
[87.02]

In vitro studies

TgVole (1x)	Not tested
Prairie vole	Not tested

In vivo studies

TgVole (1x)	Not tested
Prairie vole	Not tested



Protein code: 1094

Tundra vole

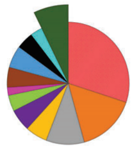
GenBank: BK064091

Microtus oeconomus

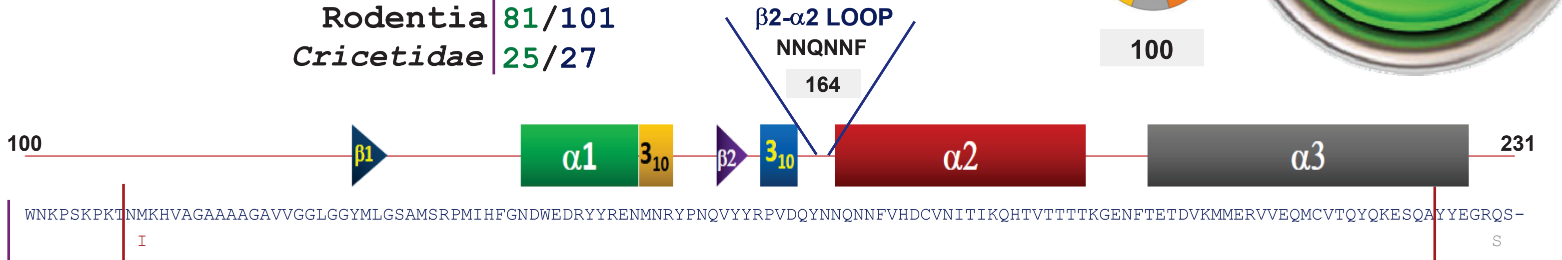
Rodentia	81/101
Cricetidae	25/27

Distinct primary sequence across species

P100% **100**



100



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRQS-

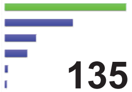
I S

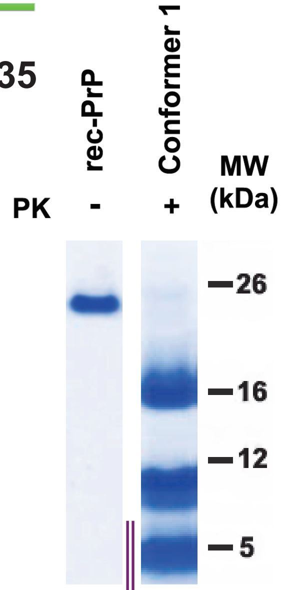
PrP sequence differs by 1 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

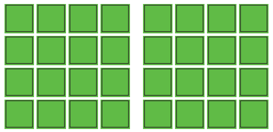
No polymorphic variants found





210 AA

1 Conformers



Tm^{Exp}: ND

ΔΔG: -3.36

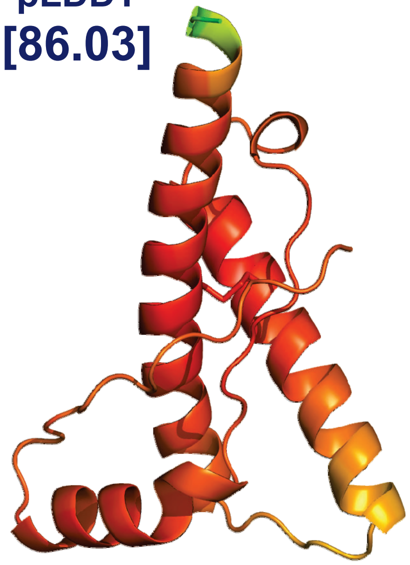
***In vitro* studies**

TgVole (1x)	Not tested
Tundra vole	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Tundra vole	Not tested

pLDDT [86.03]



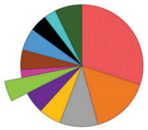
Creeping vole

GenBank: BK064150

Microtus oregoni

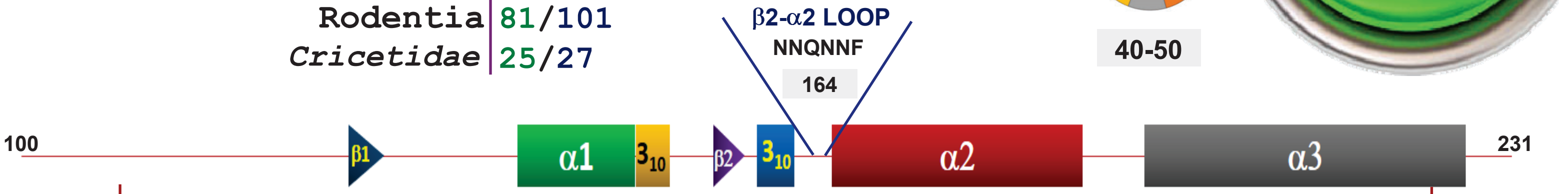
Rodentia	81/101
Cricetidae	25/27

P68%



40-50

42.9



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYQGRYS-

I N E S

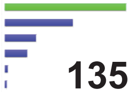
PrP sequence differs by 2 amino acids from the bank vole PrP (see in red)

No deletions

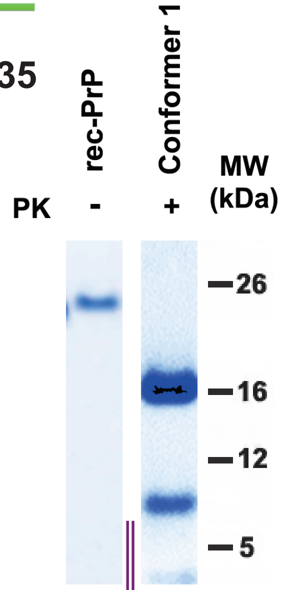
No insertions

No polymorphic variants found

Distinct primary sequence across species



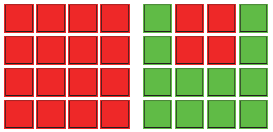
135



210 AA

1

Conformers



Tm^{Exp}: ND

ΔΔG: -4.39

In vitro studies

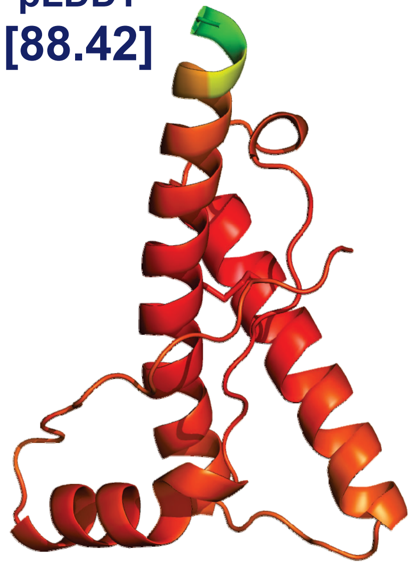
TgVole (1x)	Not tested
Creeping vole	Not tested

In vivo studies

TgVole (1x)	Not tested
Creeping vole	Not tested

pLDDT

[88.42]



Protein code: 3388

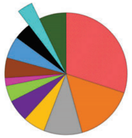
Meadow vole

GenBank: GQ850541

Microtus pennsylvanicus

Rodentia 81/101
Cricetidae 25/27

P92%



90-100

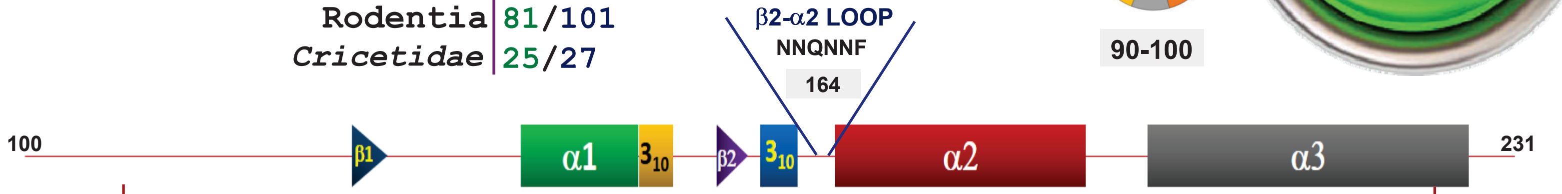
96.4

3 species sharing the same primary sequence

● **California vole** *Microtus californicus*

● **Montane vole** *Microtus montanus*

● **Water vole** *Microtus richardsoni*

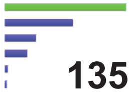


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRYS-

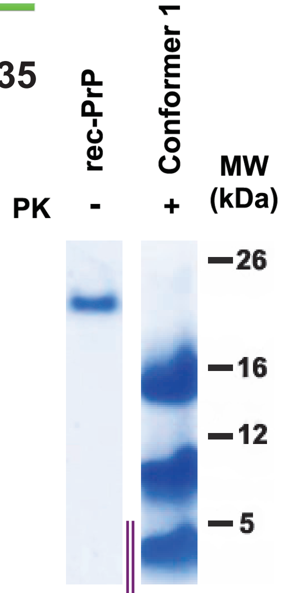
I S

PrP sequence differs by 1 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

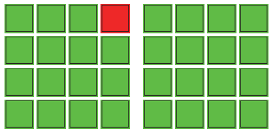


135



210 AA

1 Conformers



Tm^{Exp}: ND

ΔΔG: -3.72

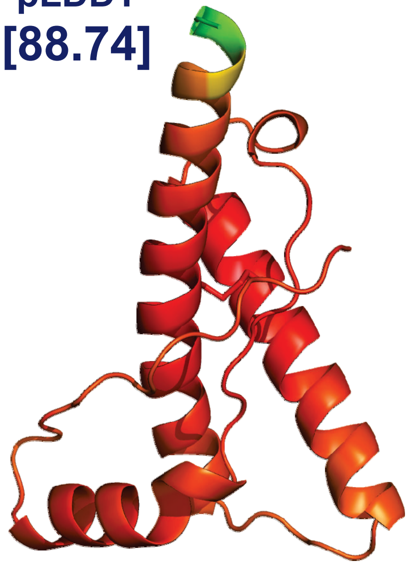
In vitro studies

TgVole (1x)	Not tested
Meadow vole	Not tested

In vivo studies

TgVole (1x)	Not tested
Meadow vole	Not tested

pLDDT [88.74]



Protein code: 1422

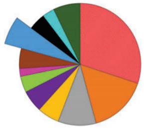
Mouse

GenBank: NM_011170

Mus musculus

Rodentia 81/101
Muridae 16/18

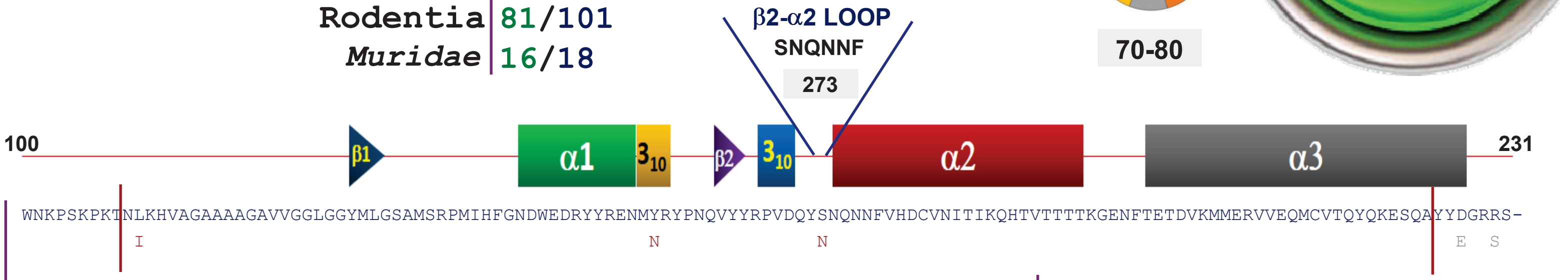
P85% 79.6



70-80

16 species sharing the same primary sequence

- ● **Ryukyu mouse** *Mus caroli*
- ● **Cook's mouse** *Mus cookii*
- ● **Fawn-colored mouse** *Mus cervicolor*
- ● **Sheath-tailed mouse** *Mus fragilicauda*
- ● **Wood mouse** *Apodemus sylvaticus*
- ● **Indo pencil-tailed tree mouse** *Chiropodomys gliroides*
- ● **Steppe mouse** *Mus spicilegus*
- ● **E broad-toothed field mouse** *Apodemus mystacinus*
- ● **African pygmy mouse** *Mus minutoides*
- ● **Algerian mouse** *Mus spretus*
- ● **Large Japanese field mouse** *Apodemus speciosus*
- ● **Delectable soft-furred mouse** *Praomys delectorum*
- ● **Desert mouse** *Pseudomys desertor*
- ● **Broad-toothed mouse** *Mastacomys fuscus*
- ● **Smoky mouse** *Pseudomys fumeus*
- ● **Rakali** *Hydromys chrysogaster*

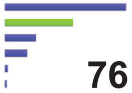


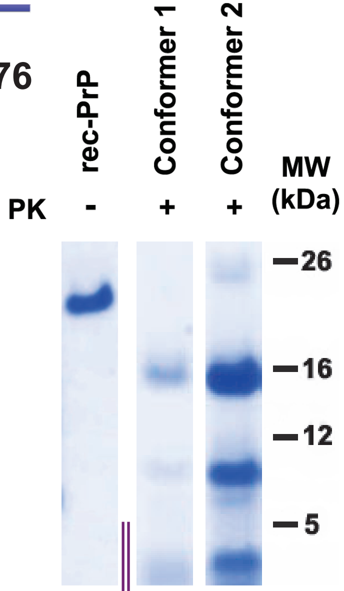
WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-

I N N E S

PrP sequence differs by 3 amino acids from the bank vole PrP (see in red)

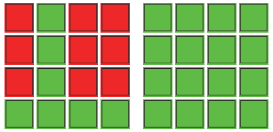
No deletions
No insertions
It shows polymorphic variants





210 AA

2
Conformers



Tm^{Exp}: 68.3 ºC

ΔΔG: -3.3

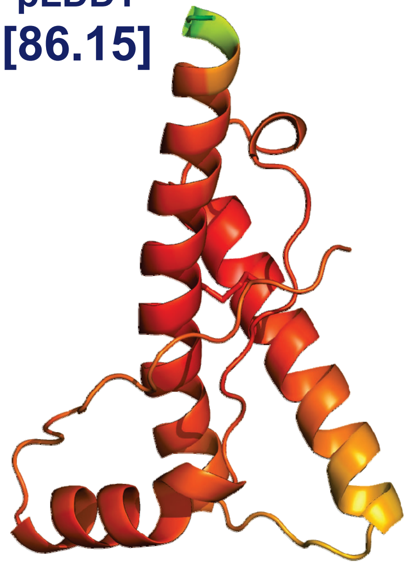
In vitro studies

TgVole (1x)	Propagate
Mouse	Propagate

In vivo studies

TgVole (1x)	Infectious
Mouse	Infectious

pLDDT
[86.15]



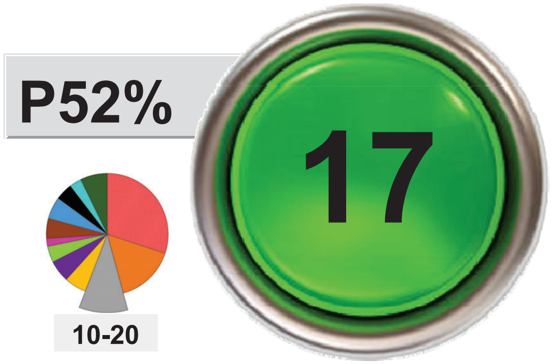
Protein code: 0113

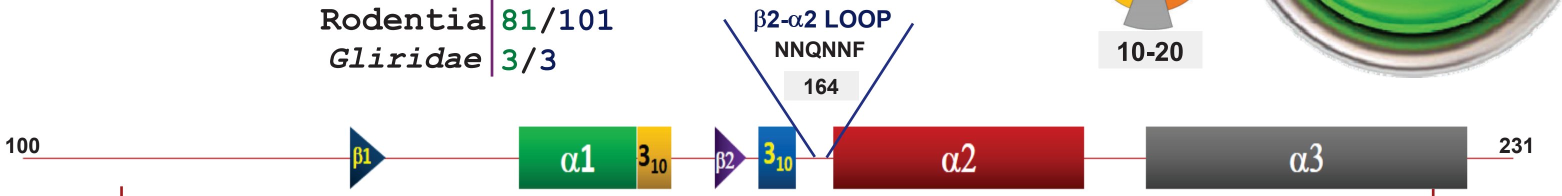
Hazel dormouse

GenBank: BK064106

Muscardinus avellanarius

Rodentia	81/101
Gliridae	3/3





WNKPNKPKTNMKHMAGAAAAGAVVGGLGGYMVGSAMSRPPMHFGNDYEDRYYRENMNRYPNQVYYKPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQKEAQAYYQRGAS-

S I V L MI W R I M V S EGRS

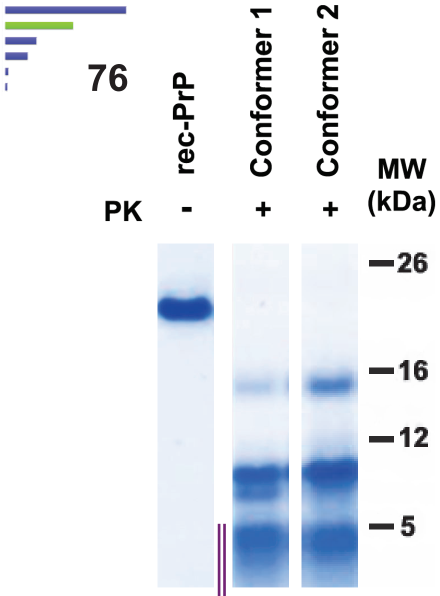
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions

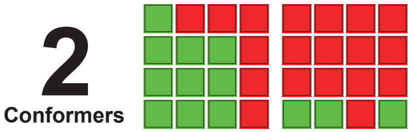
No insertions

No polymorphic variants found

Distinct primary sequence across species



214 AA



Tm^{Exp}: ND

ΔΔG: -5.66

In vitro studies

TgVole (1x) Not tested

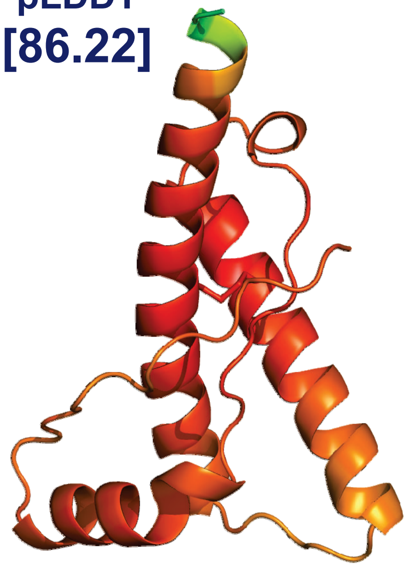
Hazel dormouse Not tested

In vivo studies

TgVole (1x) Not tested

Hazel dormouse Not tested

pLDDT [86.22]



Protein code: 3285

Distinct primary sequence across species

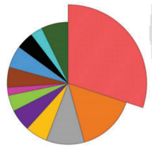
Coypu

GenBank: BK064010

Myocastor coypus

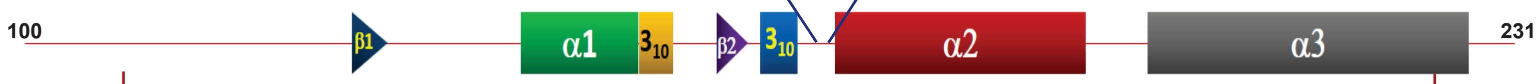
Rodentia	81/101
Echimyidae	0/1

P29%


0

0

β2-α2 LOOP
SNQNNF
273



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLQQMCTTQYQKESQAYYYHGRAG-

I M W N N H M VE V EGRSS

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

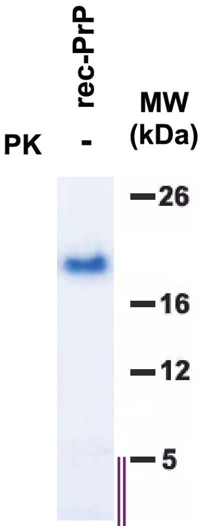
No deletions

No insertions

No polymorphic variants found

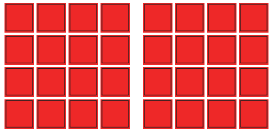
Tm^{Exp}: ND

ΔΔG: ND



202 AA

NO MISFOLDING


0
Conformers

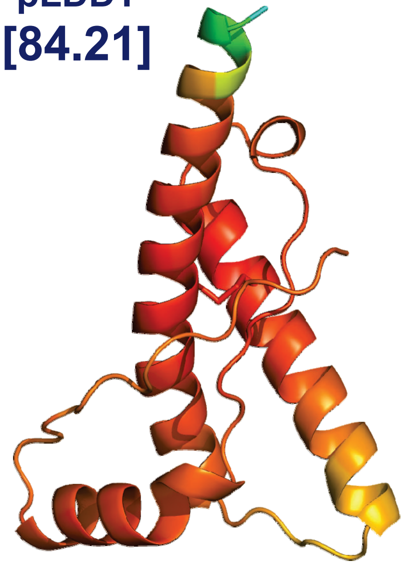
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[84.21]



Protein code: 3171

Southern red-backed vole

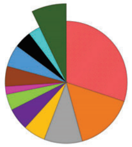
GenBank: GQ850538

Myodes gapperi

Rodentia 81/101
Cricetidae 25/27

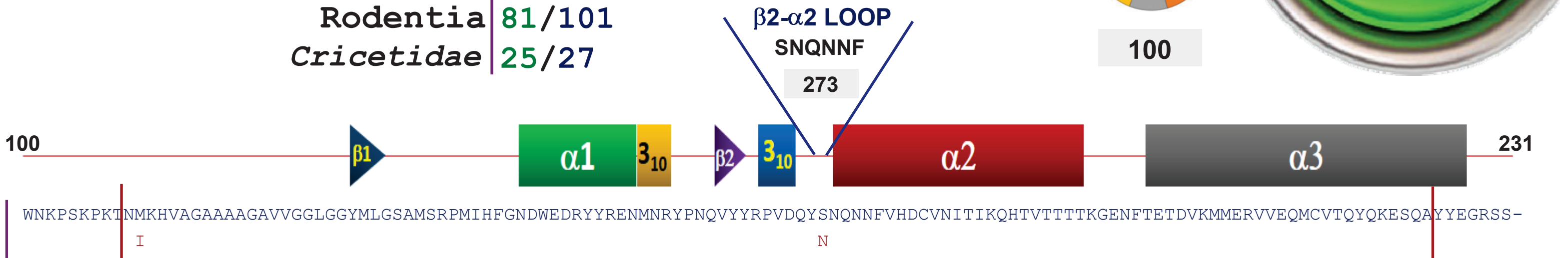
P100%

100



100

Distinct primary sequence across species



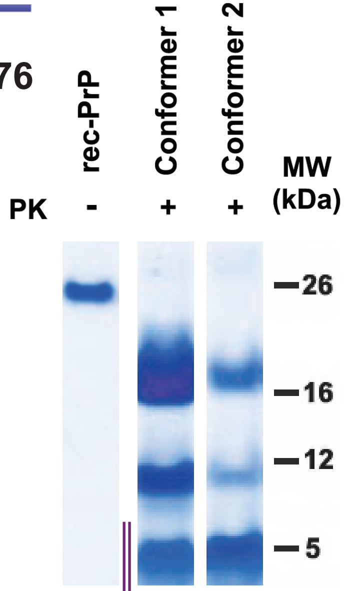
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRSS-

I N

PrP sequence differs by 2 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

76



211 AA

2
Conformers

Tm^{Exp}: ND

ΔΔG: 4.84

In vitro studies

TgVole (1x) Not tested

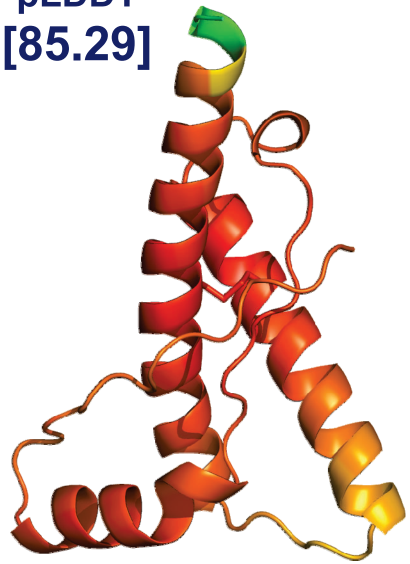
Southern red-backed vole Not tested

In vivo studies

TgVole (1x) Not tested

Southern red-backed vole Not tested

pLDDT [85.29]



Protein code: 1390

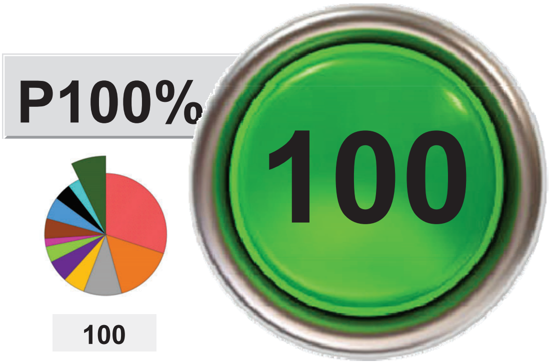
Bank vole

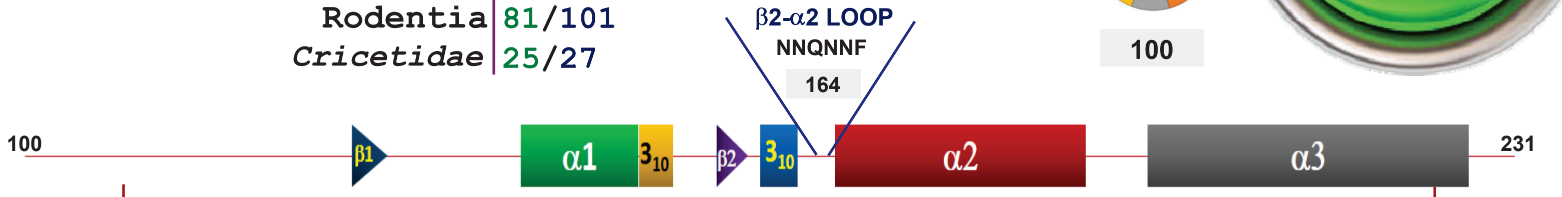
GenBank: AF367624

Myodes glareolus

Rodentia	81/101
Cricetidae	25/27

P100%





`WNKPSKPKTNIKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRSS-`

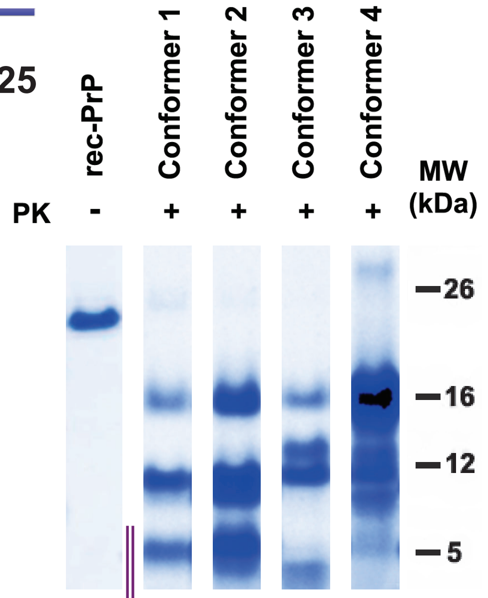
PrP sequence differs by 0 amino acids from the bank vole PrP (see in red)

No deletions

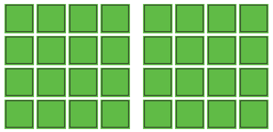
No insertions

It shows polymorphic variants

Distinct primary sequence across species



211 AA



4
Conformers

Tm^{Exp}: 66.5 ºC

ΔΔG: 0

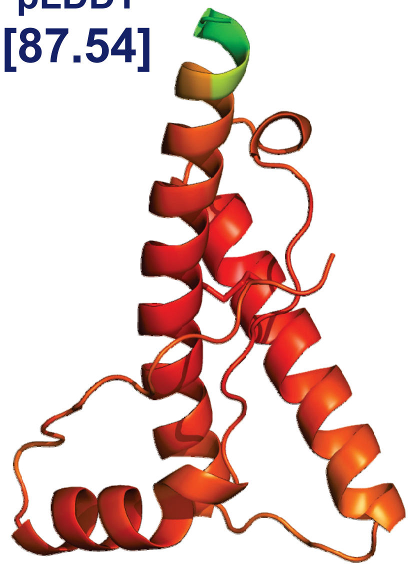
***In vitro* studies**

TgVole (1x)	**Propagate**
Mouse	**Propagate**

***In vivo* studies**

TgVole (1x)	**Infectious**
Mouse	**Infectious**

pLDDT [87.54]



Shergylaensis vole

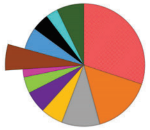
GenBank: BK064207

Neodon shergylaensis

Rodentia 81/101
Cricetidae 25/27

P74%

62.5



60-70

Distinct primary sequence across species

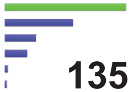
β2-α2 LOOP
NNQNNF
164

WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYEKESQAYYEGRRS-

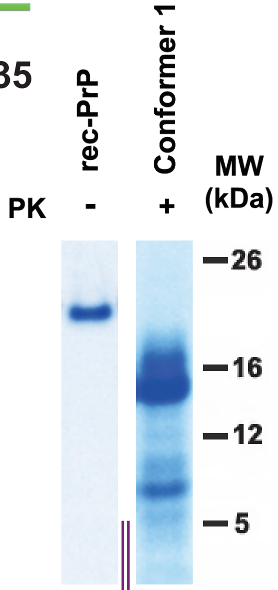
I Q S

PrP sequence differs by 2 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



135



209 AA

Tm^{Exp}: ND

ΔΔG: -15.47

In vitro studies

TgVole (1x) Not tested

Shergylaensis vole Not tested

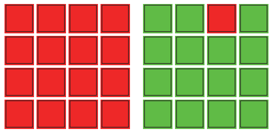
In vivo studies

TgVole (1x) Not tested

Shergylaensis vole Not tested

pLDDT
[92.02]

1
Conformers



Protein code: 4584

Desert woodrat

GenBank: BK064110

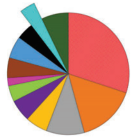
Neotoma lepida

Rodentia 81/101

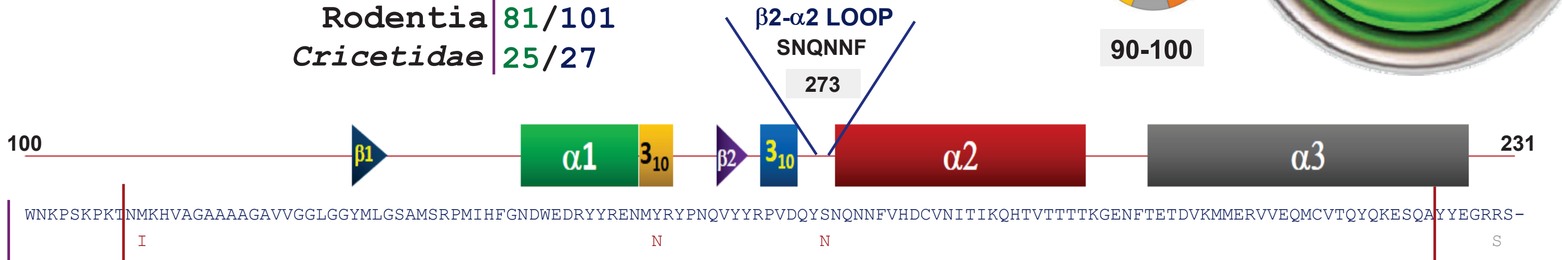
Cricetidae 25/27

P91%

92.9



90-100



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRRS-

I N N S

PrP sequence differs by 3 amino acids from the bank vole PrP (see in red)

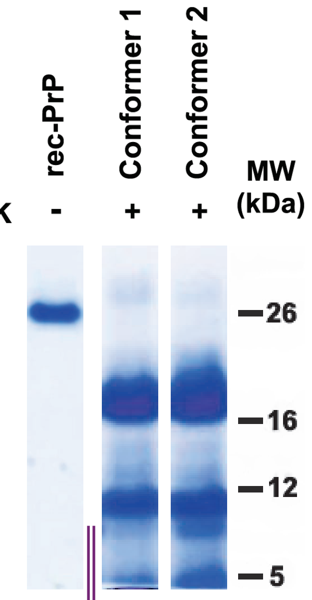
No deletions

No insertions

No polymorphic variants found

Distinct primary sequence across species

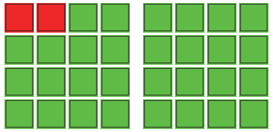
76



210 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: -3.66

In vitro studies

TgVole (1x) Not tested

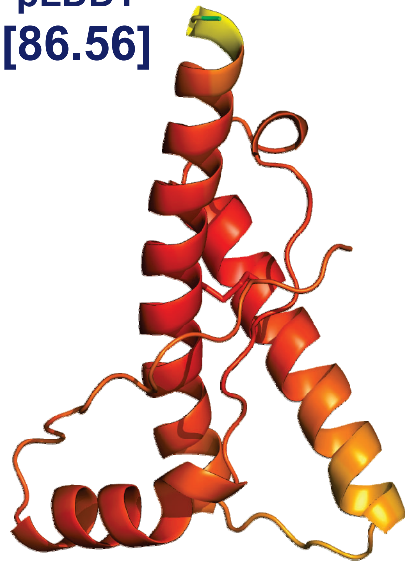
Desert woodrat Not tested

In vivo studies

TgVole (1x) Not tested

Desert woodrat Not tested

pLDDT [86.56]



Protein code: 3290

Distinct primary sequence across species

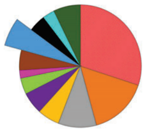
Common degu

GenBank: XM_023718589

Octodon degus

Rodentia	81/101
Octodontidae	3/3

P81%



70-80

71.4

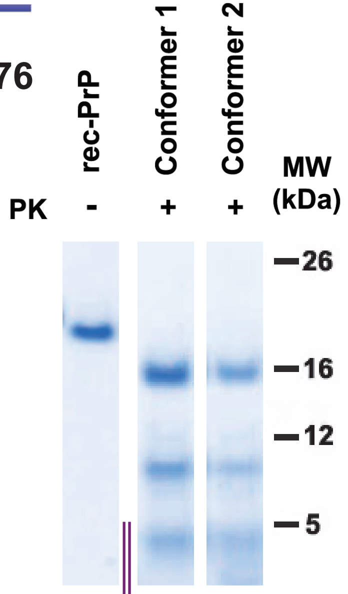
β2-α2 LOOP
SNQNNF
273

```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLQQMCTTQYQKESQAYYYHGRAG-
           I                           M      W        N       R     N     H                                 M    VE   V            EGRSS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

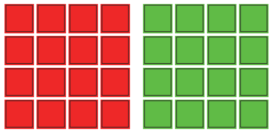
No deletions
No insertions
No polymorphic variants found

76



202 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

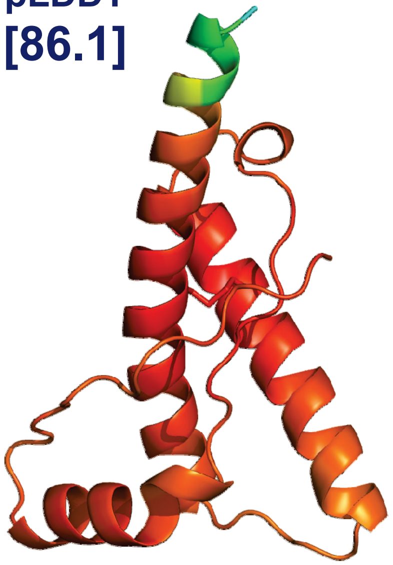
Common degu Not tested

In vivo studies

TgVole (1x) Not tested

Common degu Not tested

pLDDT
[86.1]



Protein code: 1003

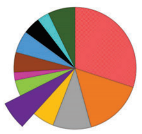
Mountain viscacha rat

GenBank: BK064011

Octomys mimax

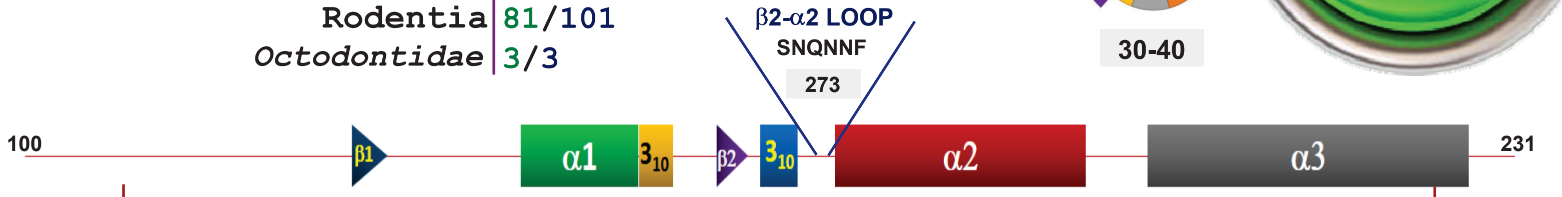
Rodentia 81/101
Octodontidae 3/3

P64%



30-40

Distinct primary sequence across species

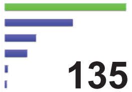


`WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLQQMCTTQYQKESQAYYYHGMAG-`

`I M W N R N H M VE V EGRSS`

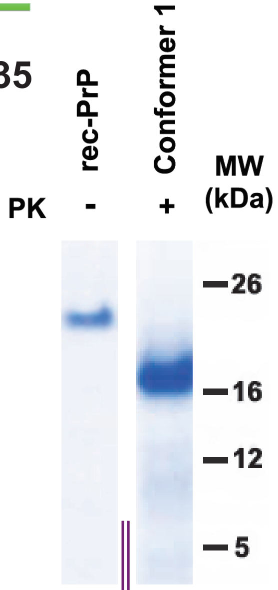
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

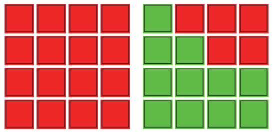
No deletions
No insertions
No polymorphic variants found



135

202 AA





1
Conformers

Tm^{Exp}: ND

ΔΔG: ND

***In vitro* studies**

TgVole (1x) Not tested

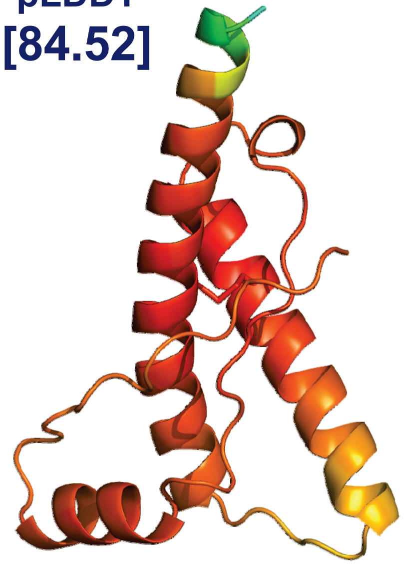
Mountain viscacha rat Not tested

***In vivo* studies**

TgVole (1x) Not tested

Mountain viscacha rat Not tested

pLDDT
[84.52]



Protein code: 3172

Muskrat

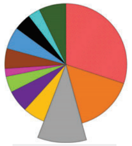
GenBank: BK064026

Ondatra zibethicus

Rodentia 81/101
Cricetidae 25/27

P51%

16.1



1 species sharing the same primary sequence

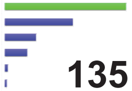
Arctic lemming
Dicrostonyx torquatus

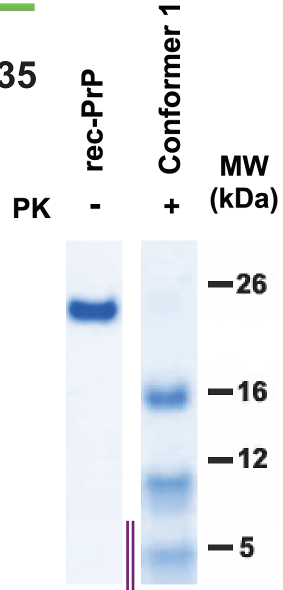
β2-α2 LOOP
NNQNNF
164

WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRSS-
I

PrP sequence differs by 1 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found





211 AA

1
Conformers

Tm^{Exp}: ND

ΔΔG: 0.61

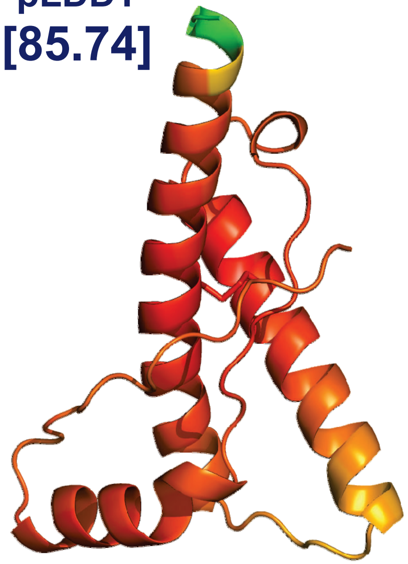
In vitro studies

TgVole (1x)	Not tested
Muskrat	Not tested

In vivo studies

TgVole (1x)	Not tested
Muskrat	Not tested

pLDDT
[85.74]



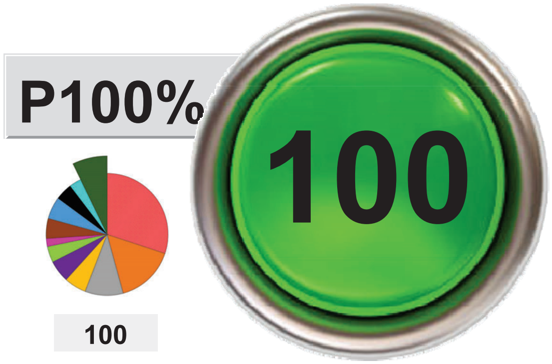
Protein code: 3191

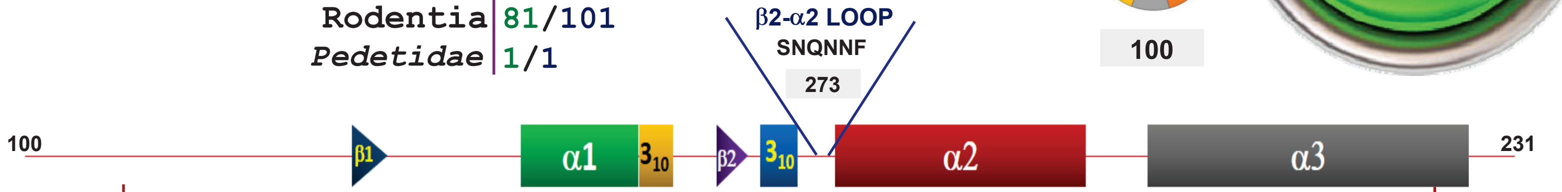
South African springhare

GenBank: BK064021

Pedetes capensis

Rodentia 81/101
Pedetidae 1/1

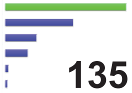


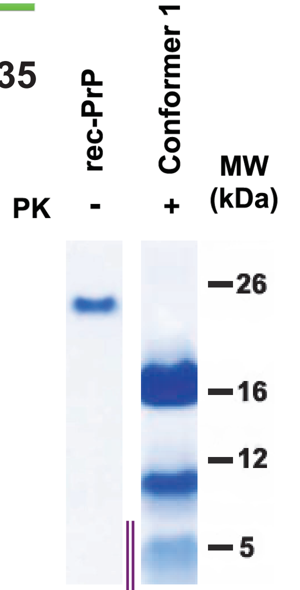


WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRDNMYRYPNQVYYKPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQKESQAYYEGRS-
N I M W E N R N V S

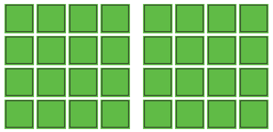
PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found





212 AA



1
Conformers

Tm^{Exp}: ND
ΔΔG: ND

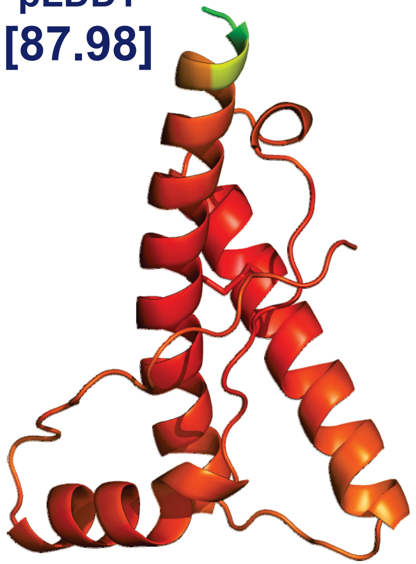
In vitro studies

TgVole (1x) Not tested
South African springhare Not tested

In vivo studies

TgVole (1x) Not tested
South African springhare Not tested

pLDDT
[87.98]



Distinct primary sequence across species

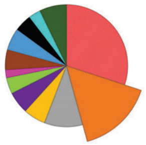
Protein code: 3186

Little pocket mouse

GenBank: BK064022

P34%

0.9



0-10

Perognathus longimembris

Rodentia	81/101
Heteromyidae	5/5

Distinct primary sequence across species

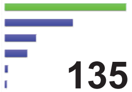
β2-α2 LOOP
NNQNNF
164

WNKPNKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNDYEDRYYRENMNRYPSQVYYKPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGDNFTETDVKIMERMVEQMCITQYQKESRAYYEPRS-

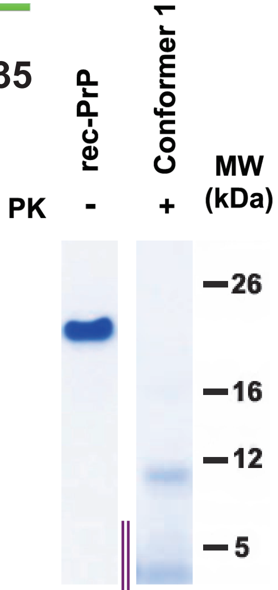
S NI V MI W N R I E M V V Q G S

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



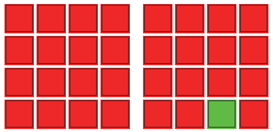
135



203 AA

1

Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

Not tested
TgVole (1x)

Not tested
Little pocket mouse

In vivo studies

Not tested
TgVole (1x)

Not tested
Little pocket mouse

pLDDT
[84.21]

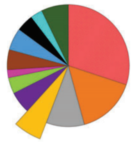
Protein code: 3187

Texas mouse

GenBank: BK064023

P59%

26.8



20-30

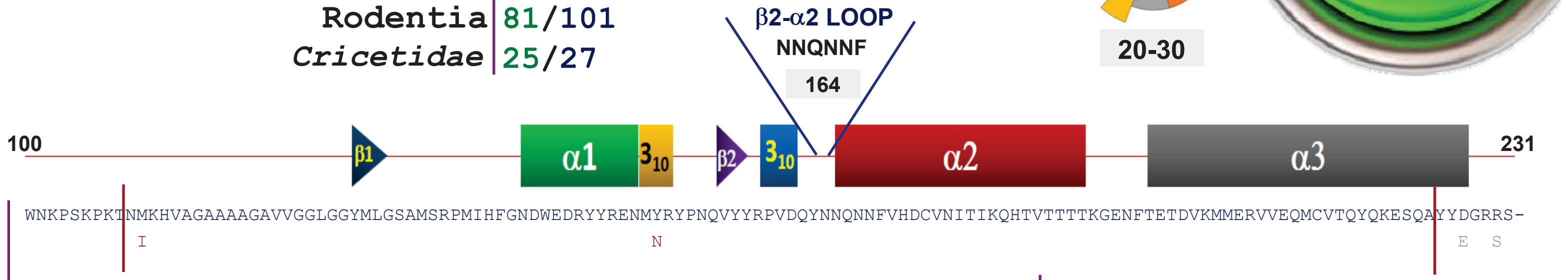
Peromyscus attwateri

`Rodentia` 81/101

`Cricetidae` 25/27

1 species sharing the same primary sequence

Northern rock mouse
Peromyscus nasutus

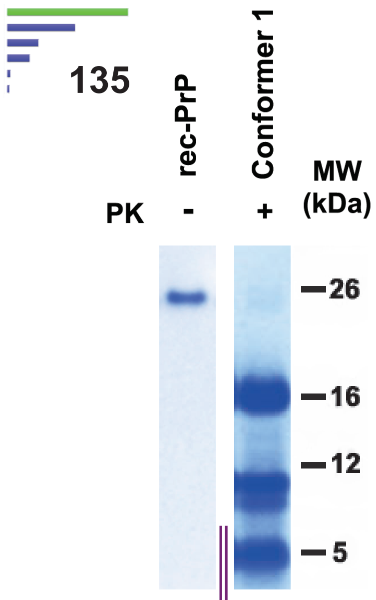


`WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-`

PrP sequence differs by 2 amino acids from the bank vole PrP (see in red)

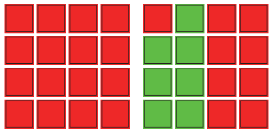
No deletions
No insertions
No polymorphic variants found

135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: 1.56

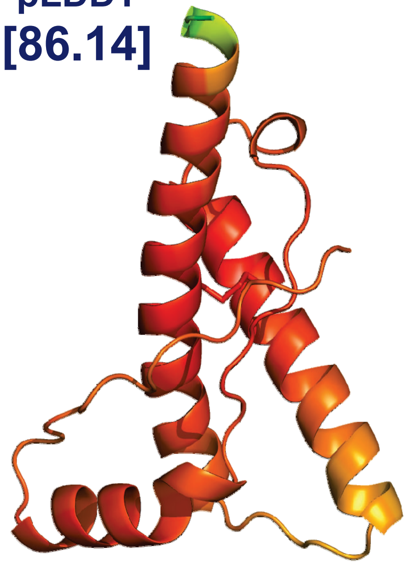
***In vitro* studies**

TgVole (1x)	Not tested
Texas mouse	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Texas mouse	Not tested

pLDDT
[86.14]



Protein code: 3188

California mouse

GenBank: BK064122

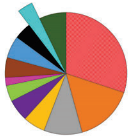
Peromyscus californicus insignis

1 species sharing the same primary sequence

Cactus mouse
Peromyscus eremicus

Rodentia	81/101
Cricetidae	25/27

P90%



90-100

β2-α2 LOOP
NNQNNF
164

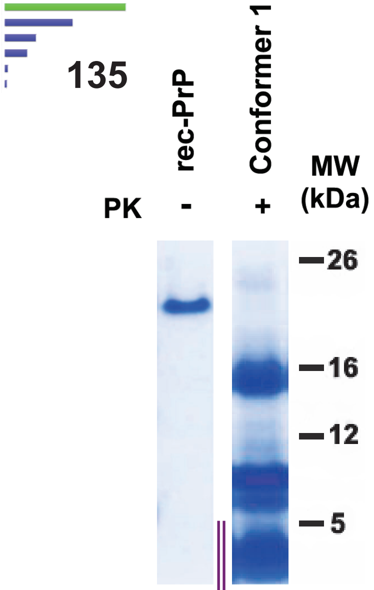
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDWEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-
          I                               I             N                                                                          E  S
```

PrP sequence differs by 3 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

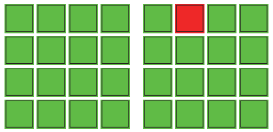
Tm^{Exp}: ND

ΔΔG: -8.01



211 AA

1
Conformers



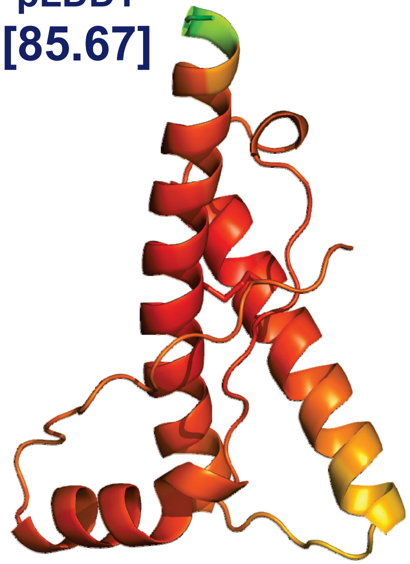
In vitro studies

TgVole (1x)	Not tested
California mouse	Not tested

In vivo studies

TgVole (1x)	Not tested
California mouse	Not tested

pLDDT
[85.67]



Protein code: 3303

Canyon mouse

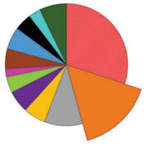
GenBank: BK064807

Peromyscus crinitus

Rodentia 81/101
Cricetidae 25/27

Distinct primary sequence across species

P34%



0-10

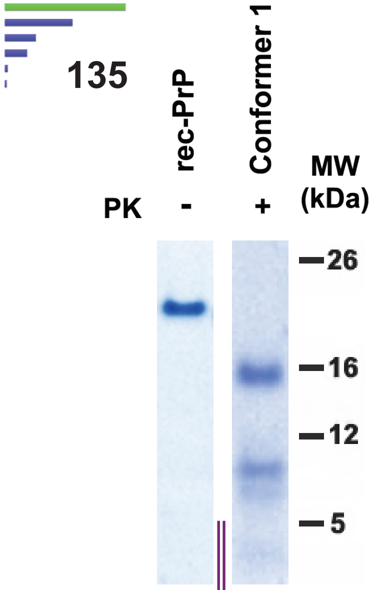
0.9

β2-α2 LOOP
NNQNNF
164

```
WNKPSKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-
           I  V                                          N                                                                        E  S
```

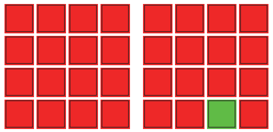
PrP sequence differs by 3 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -1.39

In vitro studies

TgVole (1x) Not tested

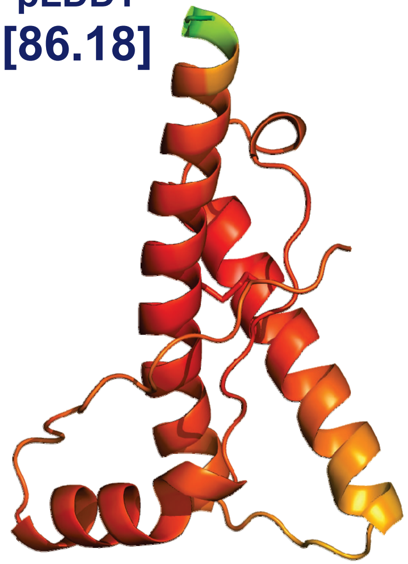
Canyon mouse Not tested

In vivo studies

TgVole (1x) Not tested

Canyon mouse Not tested

pLDDT
[86.18]



Protein code: 3975

White-footed mouse

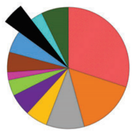
GenBank: XM_028878611

Peromyscus leucopus

Rodentia 81/101
Cricetidae 25/27

P86%

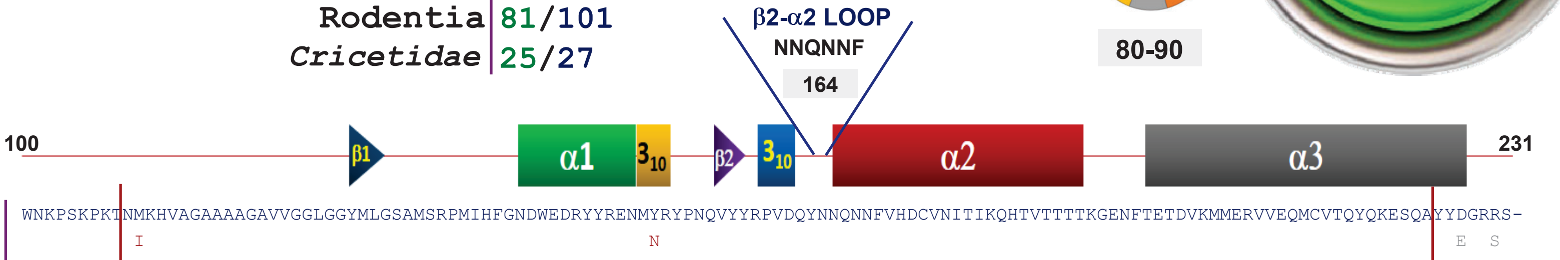
82.1



80-90

6 species sharing the same primary sequence

- **Long-haired grass mouse** *Abrothrix hirta*
- **Long-haired akodont** *Abrothrix longipilis hirtus*
- **Southern grasshopper mouse** *Onychomys torridus*
- **Aztec mouse** *Peromyscus aztecus*
- **Plateau mouse** *Peromyscus melanophrys*
- **Mexican deer mouse** *Peromyscus mexicanus*

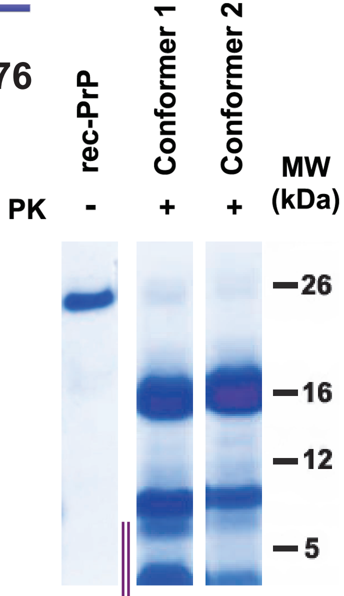


```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-
          I                                            N                                                                             E  S
```

PrP sequence differs by 2 amino acids from the bank vole PrP (see in red)

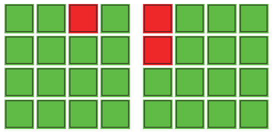
No deletions
No insertions
No polymorphic variants found

76



211 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -1.47

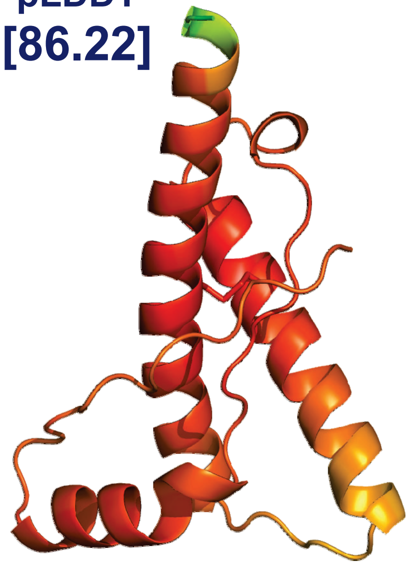
In vitro studies

TgVole (1x)	Not tested
White-footed mouse	Not tested

In vivo studies

TgVole (1x)	Not tested
White-footed mouse	Not tested

pLDDT
[86.22]



Protein code: 1011

Oldfield mouse

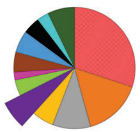
GenBank: EF467170

Peromyscus polionotus subgriseus

Rodentia	81/101
Cricetidae	25/27

P62%

32.5



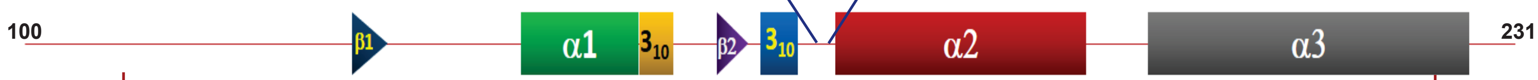
30-40

2 species sharing the same primary sequence

Deer mouse
Peromyscus maniculatus bairdii

Roborovski hamster
Phodopus roborovskii

β2-α2 LOOP
NNQNNF
164



```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-
           I                                                                                                                       E  S
```

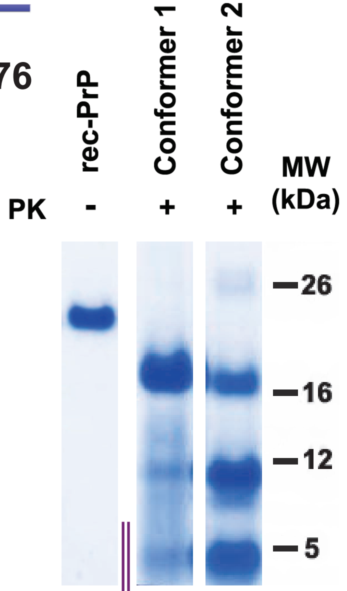
PrP sequence differs by 1 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

76

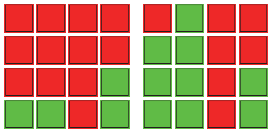


211 AA

Tm^{Exp}: ND

ΔΔG: 1.23

2
Conformers



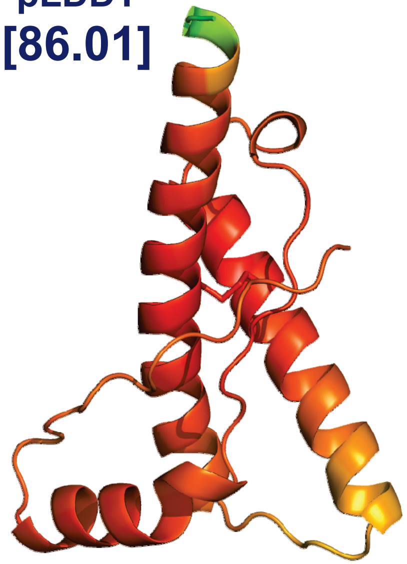
***In vitro* studies**

TgVole (1x)	Not tested
Oldfield mouse	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Oldfield mouse	Not tested

pLDDT
[86.01]



Protein code: 0941

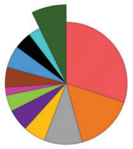
Red and white giant flying squirrel

GenBank: KM357835

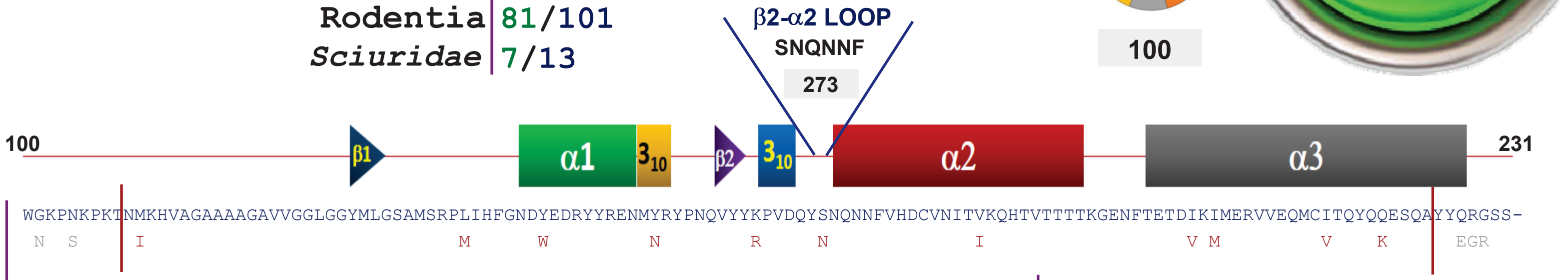
Petaurista alborufus

Rodentia 81/101
Sciuridae 7/13

P100%

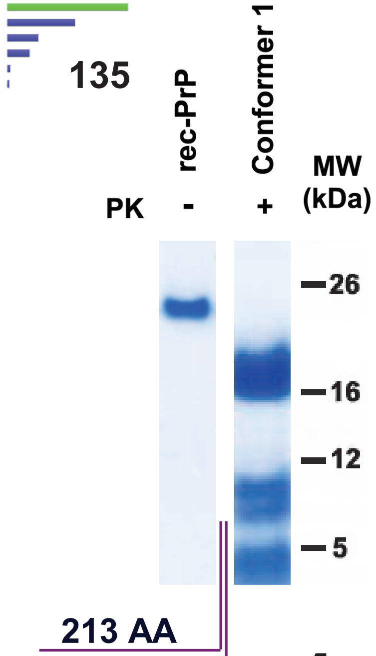


100



PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



213 AA

1 Conformers

Tm^{Exp}: ND

ΔΔG: -12.03

***In vitro* studies**

TgVole (1x) Not tested

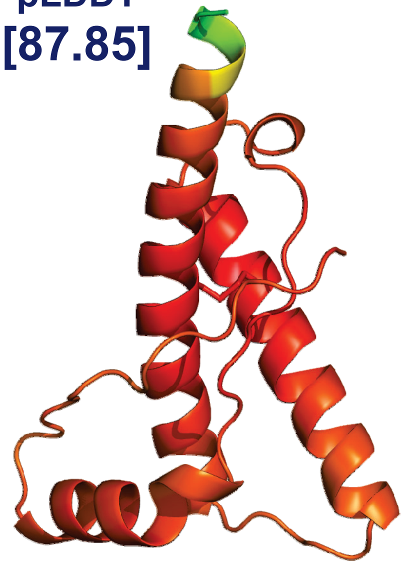
Red and white giant flying Not tested

***In vivo* studies**

TgVole (1x) Not tested

Red and white giant flying Not tested

pLDDT [87.85]



Distinct primary sequence across species

Protein code: 1454

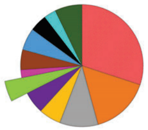
Dassie rat

GenBank: BK063990

Petromus typicus

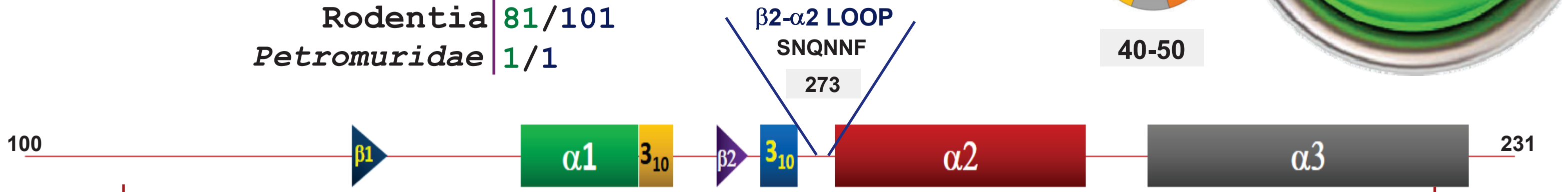
Rodentia 81/101
Petromuridae 1/1

P71% **48.2**



40-50

Distinct primary sequence across species

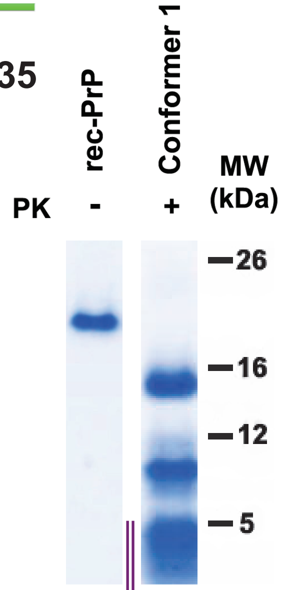


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAYYYRGRAG-
I M N W N R N H M V V EGRSS

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

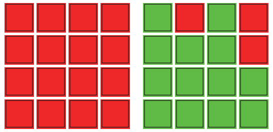
No deletions
No insertions
No polymorphic variants found

135



202 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

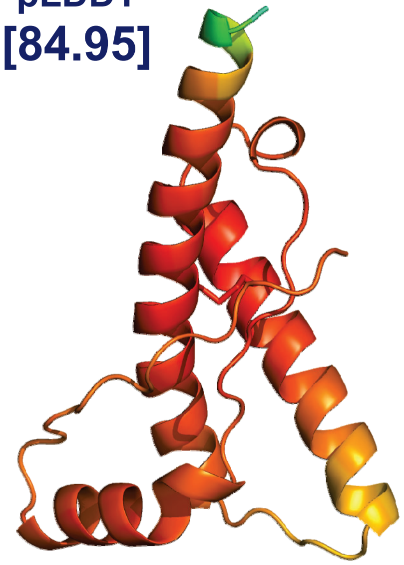
In vitro studies

TgVole (1x)	Not tested
Dassie rat	Not tested

In vivo studies

TgVole (1x)	Not tested
Dassie rat	Not tested

pLDDT
[84.95]



Protein code: 3148

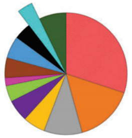
Campbell's dwarf hamster

GenBank: EU886367

Phodopus campbelli

Rodentia 81/101
Cricetidae 25/27

P90% **91.1**



90-100

Distinct primary sequence across species

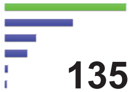
β2-α2 LOOP
NNQNNF
164

WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQRESQAYYDGRRS-

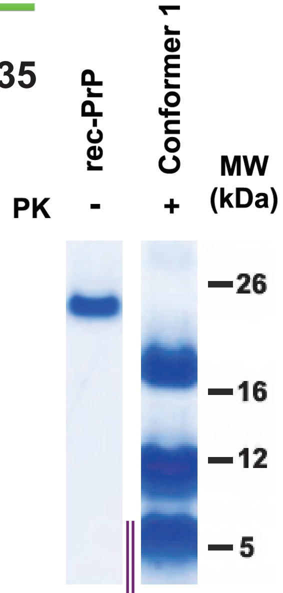
I K E S

PrP sequence differs by 2 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

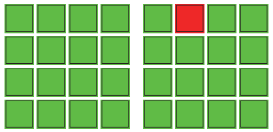


135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -0.53

In vitro studies

TgVole (1x) Not tested

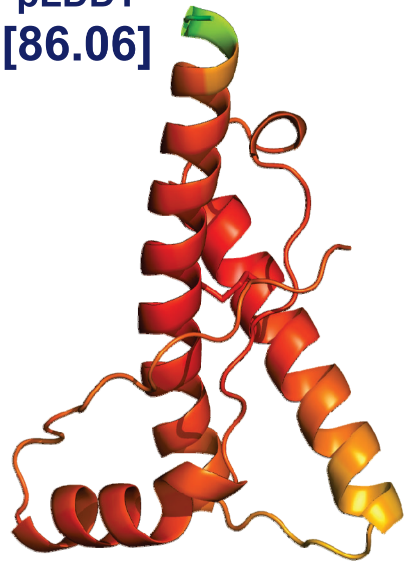
Campbell's dwarf hamster Not tested

In vivo studies

TgVole (1x) Not tested

Campbell's dwarf hamster Not tested

pLDDT
[86.06]



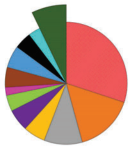
Protein code: 1433

Distinct primary sequence across species

Russian hamster

GenBank: EU886368

P100%

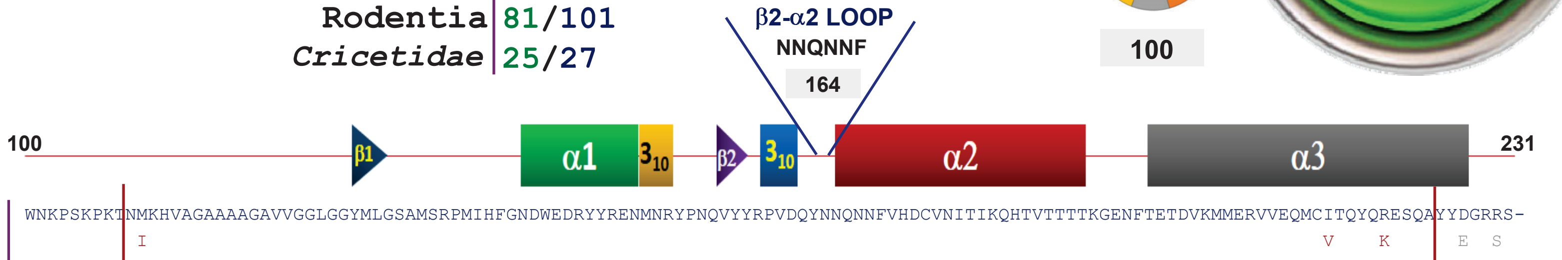


100

100

Phodopus sungorus

Rodentia 81/101
Cricetidae 25/27



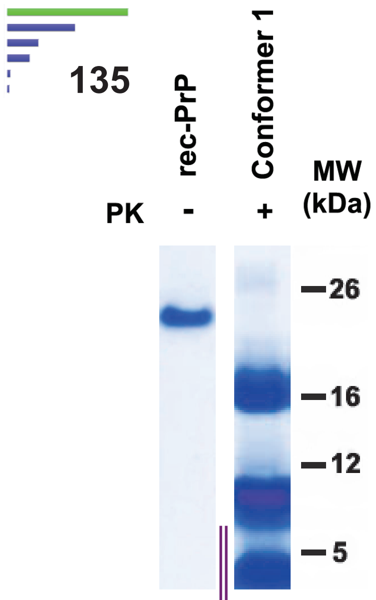
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQRESQAYYDGRRS-

I V K E S

PrP sequence differs by 3 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

135



211 AA

1

Conformers

Tm^{Exp}: ND

ΔΔG: -1.18

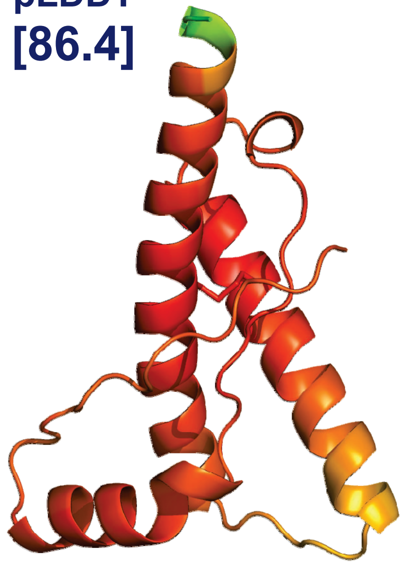
***In vitro* studies**

TgVole (1x)	Propagate
Russian hamster	Propagate

***In vivo* studies**

TgVole (1x)	Infectious
Russian hamster	Not tested

pLDDT
[86.4]



Protein code: 0822

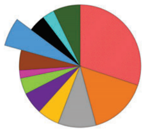
Fat sand rat

GenBank: BK063966

Psammomys obesus

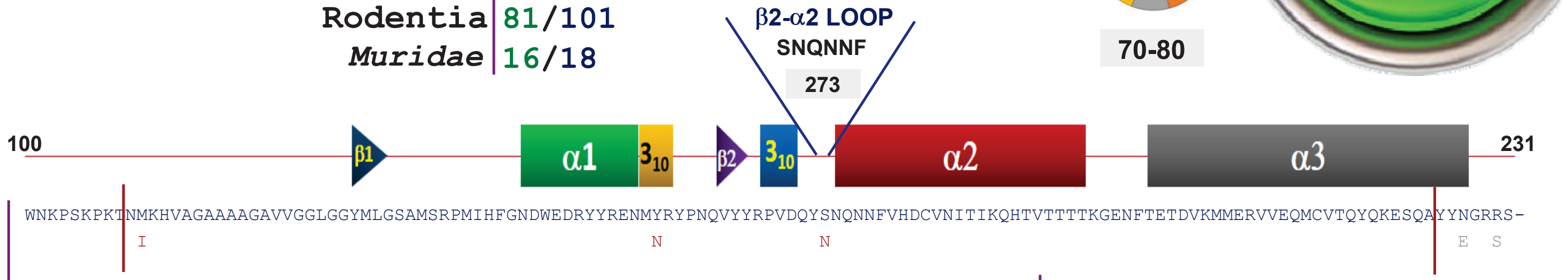
Rodentia	81/101
Muridae	16/18

P83%



70-80

75



PrP sequence differs by 3 amino acids from the bank vole PrP (see in red)

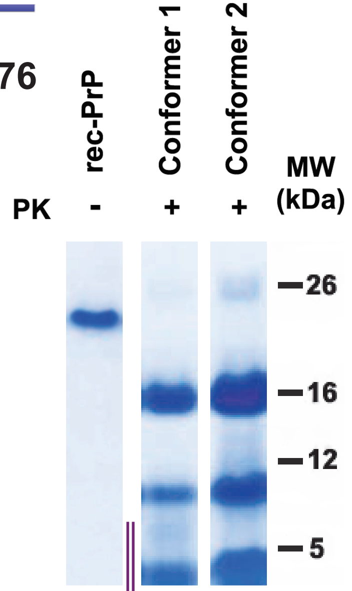
No deletions

No insertions

No polymorphic variants found

Distinct primary sequence across species

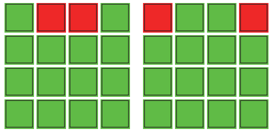
76



210 AA

2

Conformers



Tm^{Exp}: ND

ΔΔG: 1.23

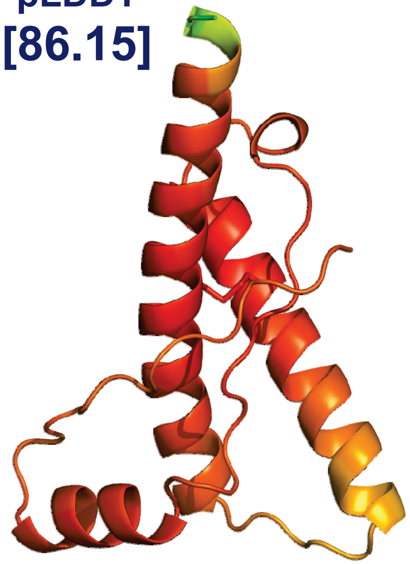
In vitro studies

TgVole (1x)	Not tested
Fat sand rat	Not tested

In vivo studies

TgVole (1x)	Not tested
Fat sand rat	Not tested

pLDDT [86.15]

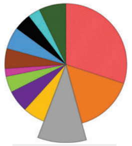


Protein code: 3096

Ricefield rat

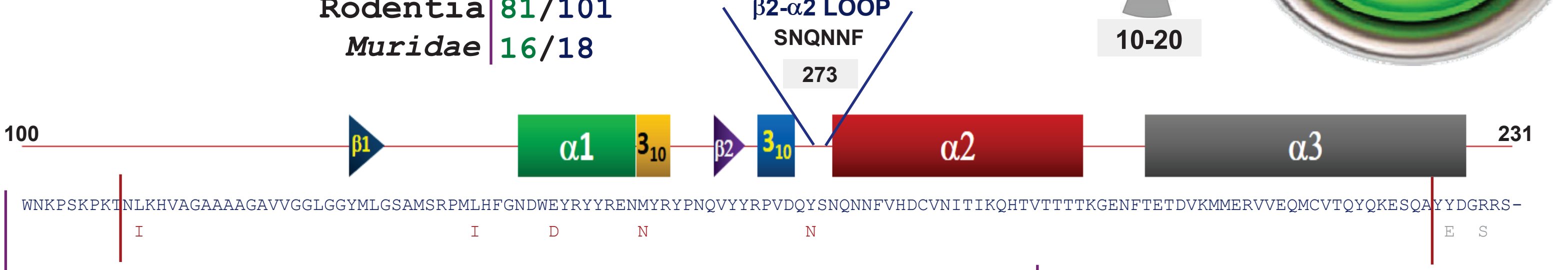
GenBank: KF466955

P50% **16.1**



Rattus argentiventer

Rodentia	81/101
Muridae	16/18



WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDWEYRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-

I I D N N E S

PrP sequence differs by 5 amino acids from the bank vole PrP (see in red)

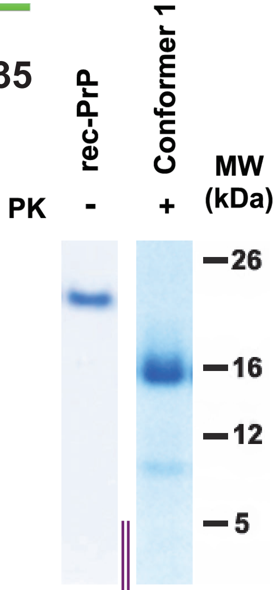
No deletions

No insertions

No polymorphic variants found

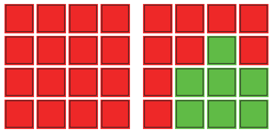
Distinct primary sequence across species

135



211 AA

1 Conformers



Tm^{Exp}: ND

ΔΔG: -12.39

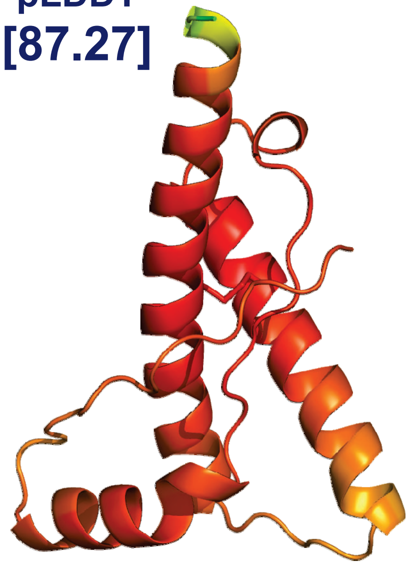
In vitro studies

TgVole (1x)	Not tested
Ricefield rat	Not tested

In vivo studies

TgVole (1x)	Not tested
Ricefield rat	Not tested

pLDDT [87.27]



Protein code: 1341

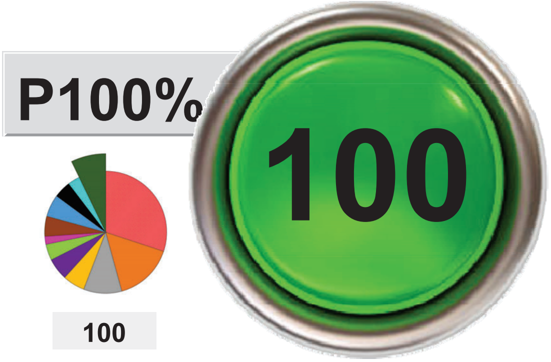
Brown rat

GenBank: BK063913

Rattus norvegicus

Rodentia	81/101
Muridae	16/18

P100%



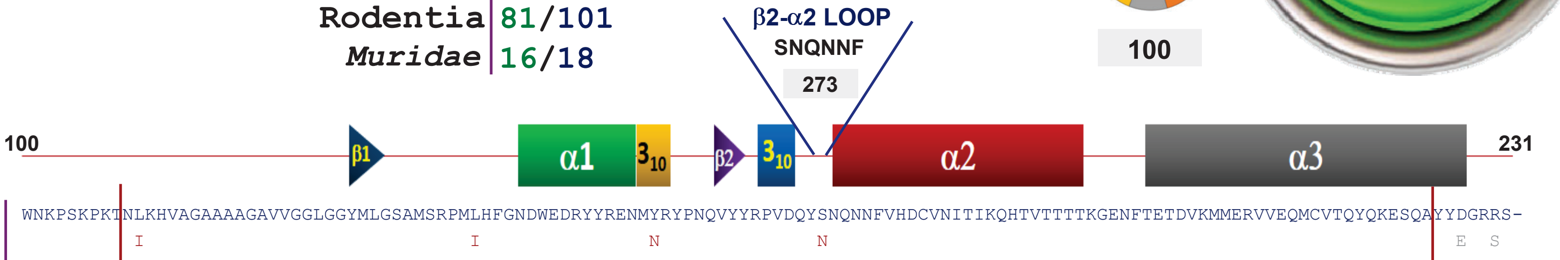
4 species sharing the same primary sequence

Lesser ricefield rat
Rattus losea

Himalayan field rat
Rattus nitidus

Rat
Rattus rattus

Tanezumi rat
Rattus tanezumi

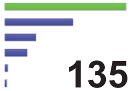


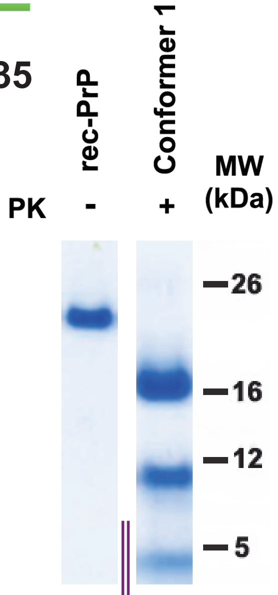
PrP sequence differs by 4 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

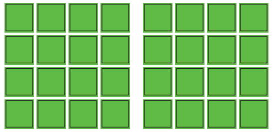
No polymorphic variants found





211 AA

1
Conformers



Tm^{Exp}: 68.1 °C

ΔΔG: -6.76

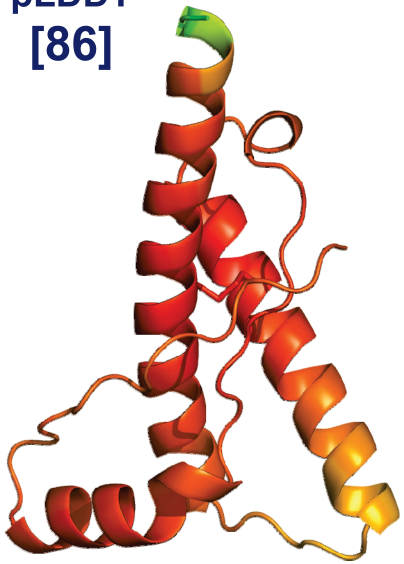
***In vitro* studies**

TgVole (1x)	**Propagate**
Rat	**Propagate**

***In vivo* studies**

TgVole (1x)	**Infectious**
Rat	**Not tested**

pLDDT
[86]



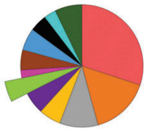
Protein code: 0825

Mesic four-striped grass rat

GenBank: BK064164

P67%

40.4



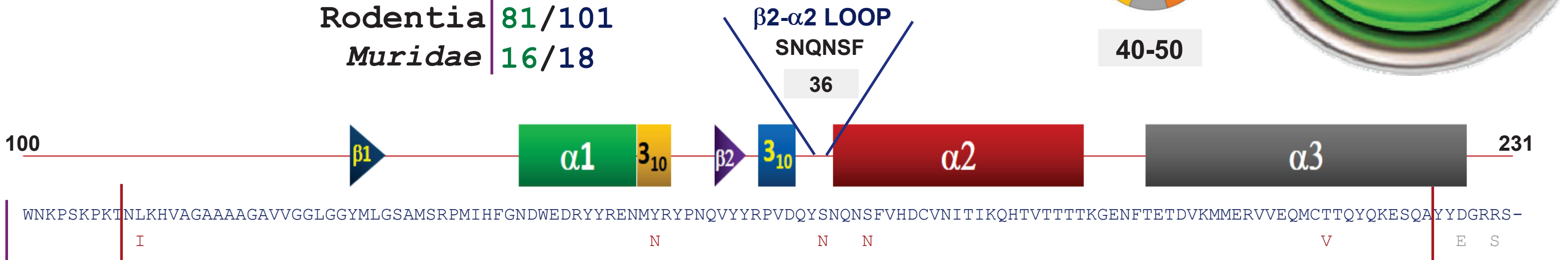
40-50

Rhabdomys dilectus

Rodentia	81/101
Muridae	16/18

1 species sharing the same primary sequence

Four-striped grass mouse
Rhabdomys pumilio



WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNSFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCTTQYQKESQAYYDGRRS-

I N N N V E S

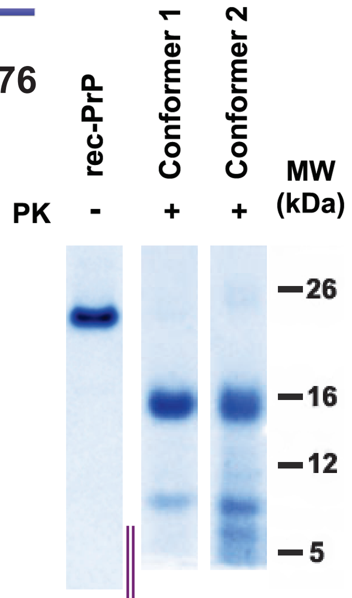
PrP sequence differs by 5 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

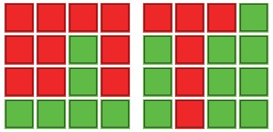
No polymorphic variants found

76



211 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -4.89

In vitro studies

TgVole (1x) Not tested

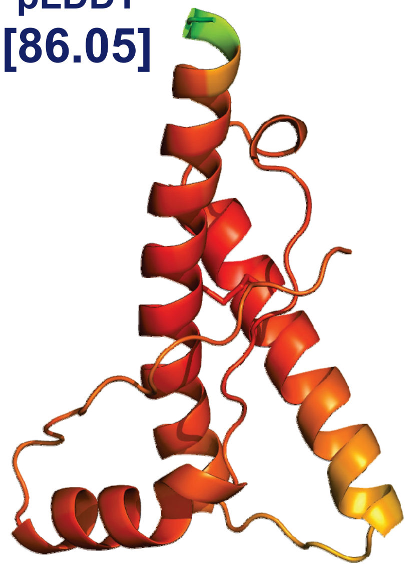
Mesic four-striped grass rat Not tested

In vivo studies

TgVole (1x) Not tested

Mesic four-striped grass rat Not tested

pLDDT
[86.05]



Protein code: 3800

Hoary bamboo rat

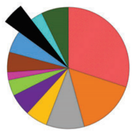
GenBank: BK063999

Rhizomys pruinosus

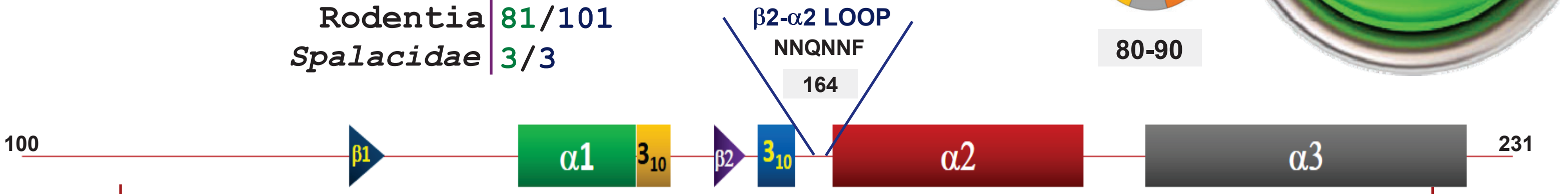
Rodentia	81/101
Spalacidae	3/3

P89%

87.5



80-90

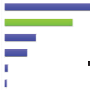


```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFPSDYENRYYQENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITVKQHTITTTTKGENFTETDIKMMERVVEQMCITQYQKESQAYYDGRRS-
```

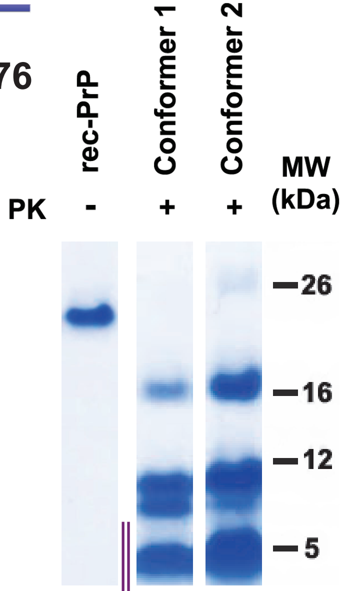
Differences (in red): I, M, GN, WD, R, N, I, V, V, V; (grey) E, S

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

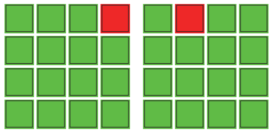


76



212 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -9.79

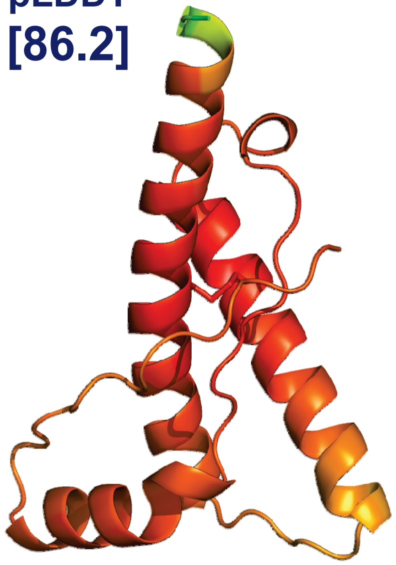
***In vitro* studies**

TgVole (1x)	Not tested
Hoary bamboo rat	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Hoary bamboo rat	Not tested

pLDDT
[86.2]



Protein code: 3159

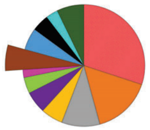
Distinct primary sequence across species

Mount Data shrew-rat

GenBank: BK064163

P77%

67.5



60-70

Rhynchomys soricoides

Rodentia	81/101
Muridae	16/18

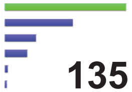
Distinct primary sequence across species

β2-α2 LOOP
SNQNNF
273

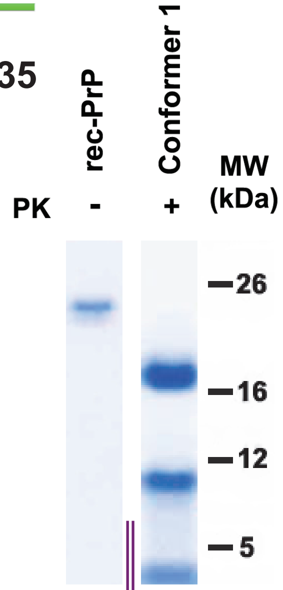
WNKPSKPKTNLKQMAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYEGRRS-
I HV N N S

PrP sequence differs by 5 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

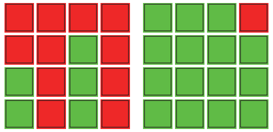


135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -6.81

In vitro studies

TgVole (1x) Not tested

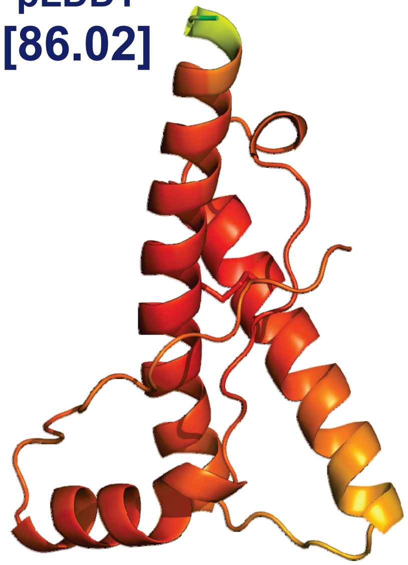
Mount Data shrew-rat Not tested

In vivo studies

TgVole (1x) Not tested

Mount Data shrew-rat Not tested

pLDDT
[86.02]



Protein code: 3799

Paulina’s limestone rat

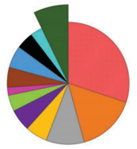
GenBank: KF466958

Saxatilomys paulinae

Rodentia	81/101
Muridae	16/18

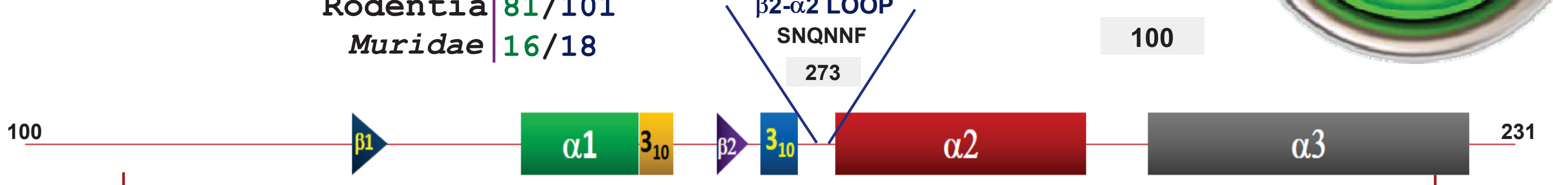
P100%

100



100

Distinct primary sequence across species



`WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-`

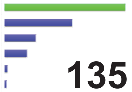
`I I N N E S`

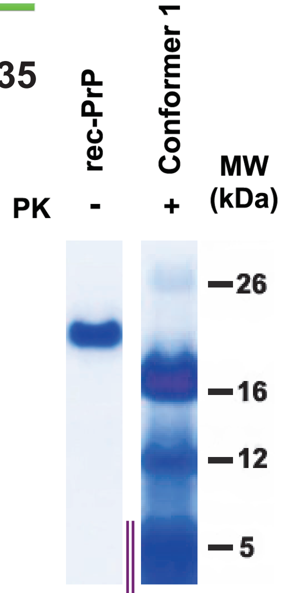
PrP sequence differs by 4 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found

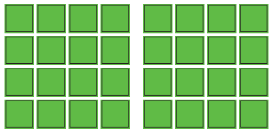




201 AA

1

Conformers



Tm^{Exp}: ND

$\Delta\Delta G$: -10.57

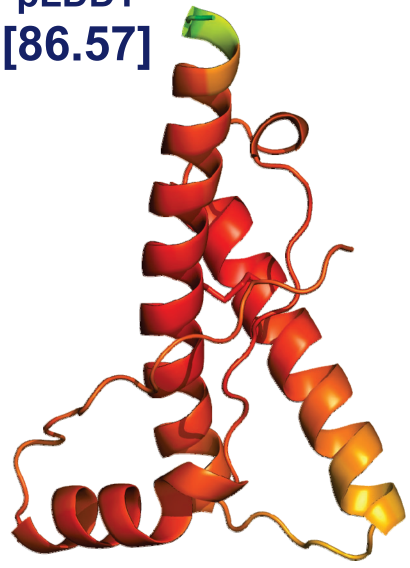
***In vitro* studies**

TgVole (1x)	Not tested
Paulina’s limestone rat	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Paulina’s limestone rat	Not tested

pLDDT
[86.57]



Eastern gray squirrel

GenBank: BK064159

Sciurus carolinensis

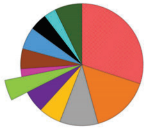
Rodentia 81/101
Sciuridae 7/13

1 species sharing the same primary sequence

Fox squirrel
Sciurus niger

P69%

44.6



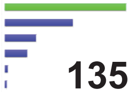
40-50

β2-α2 LOOP
SNQNNF
273

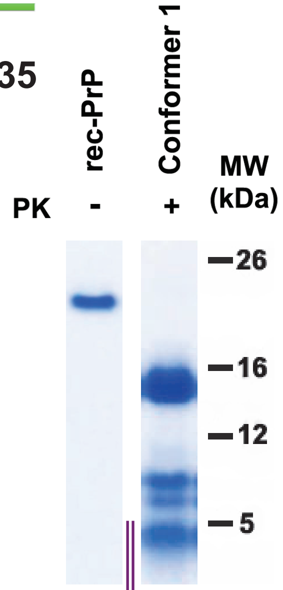
```
WGKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQEAQAYYQRGSS-
 N        I                         M      W          N        R      N              I                        V M         V     K S    EGR
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

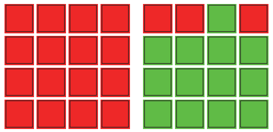


135



213 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -14.31

In vitro studies

TgVole (1x) Not tested

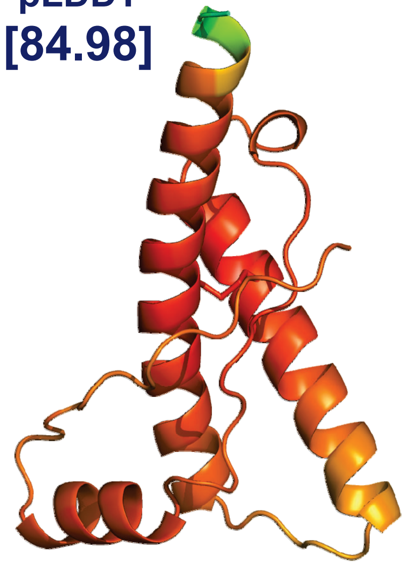
Eastern gray squirrel Not tested

In vivo studies

TgVole (1x) Not tested

Eastern gray squirrel Not tested

pLDDT
[84.98]



Protein code: 3708

Guayaquil squirrel

GenBank: KM357836

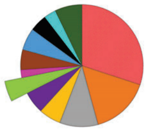
Sciurus stramineus

Rodentia	81/101
Sciuridae	7/13

Distinct primary sequence across species

P71%

48.2



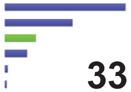
40-50

β2-α2 LOOP
SNQNNF
273

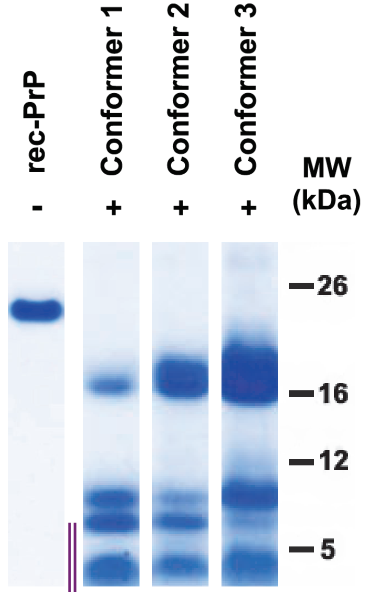
```
WSKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMNRYPNQVYYKPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQEAQAYYQRGAS-
  N  S     I                                  M    N W                          R     N                                 V M          V    K S    EGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

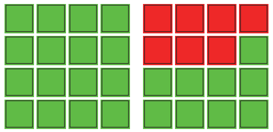


33



213 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: -7.89

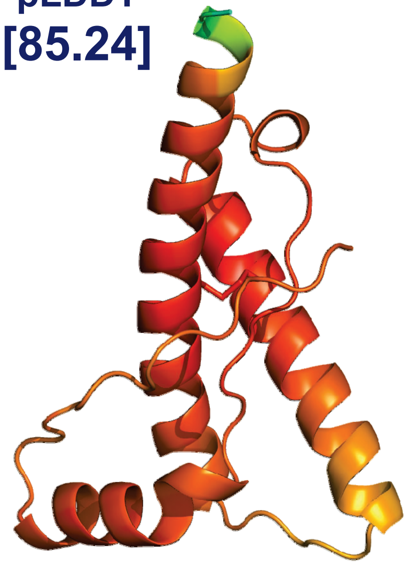
***In vitro* studies**

TgVole (1x)	**Not tested**
Guayaquil squirrel	**Not tested**

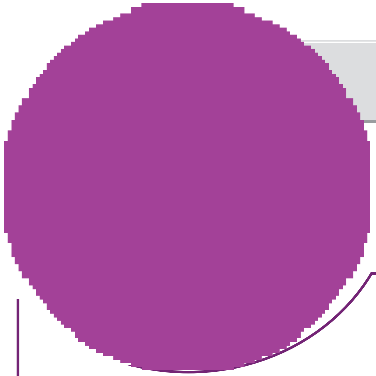
***In vivo* studies**

TgVole (1x)	**Not tested**
Guayaquil squirrel	**Not tested**

pLDDT
[85.24]



Protein code: 1091



Red squirrel

GenBank: AY133037

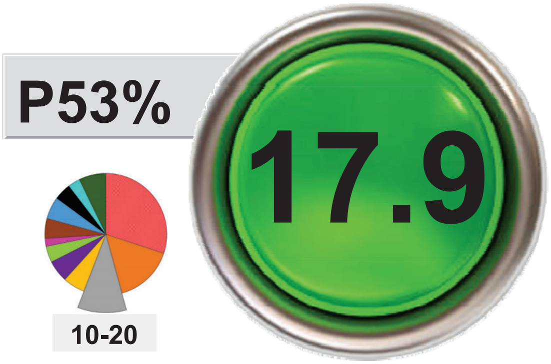
Sciurus vulgaris

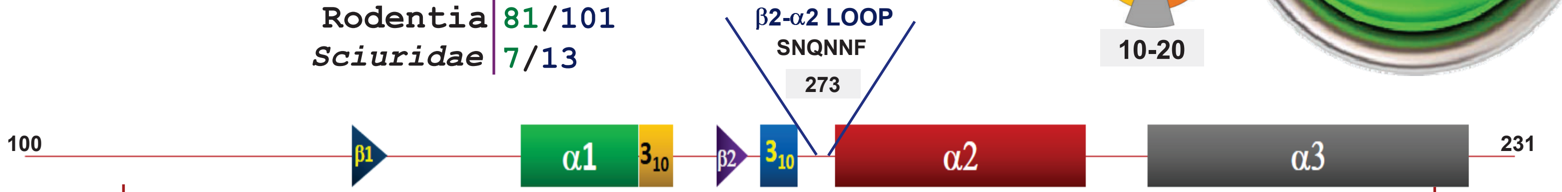
Rodentia	81/101
Sciuridae	7/13

2 species sharing the same primary sequence

● **Japanese squirrel**
Sciurus lis

● **Cape ground squirrel**
Xerus inauris





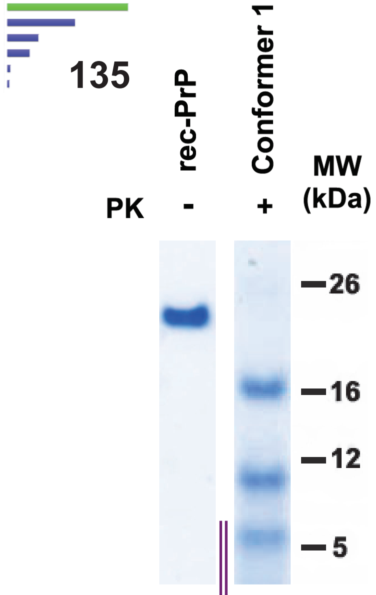
```
WGKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQEAQAYYQRGSS-
 N  S    I                            M     W        N       R     N        I                        V M         V    K S   EGR
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

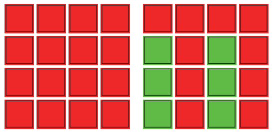
No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -15.13



213 AA



1
Conformers

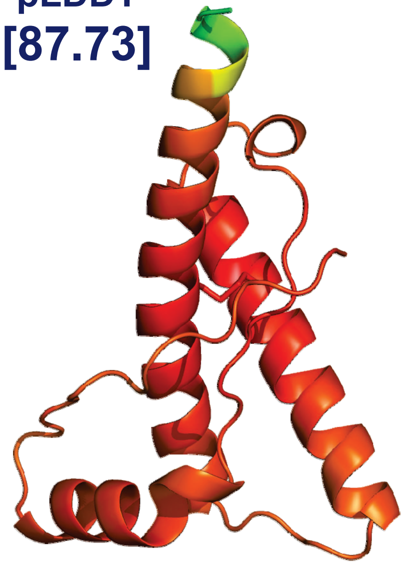
In vitro studies

TgVole (1x)	Not tested
Red squirrel	Not tested

In vivo studies

TgVole (1x)	Not tested
Red squirrel	Not tested

pLDDT
[87.73]



Protein code: 0949

Tawny-bellied cotton rat

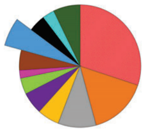
GenBank: AF117324

Sigmodon fulviventer

Rodentia 81/101
Cricetidae 25/27

P83%

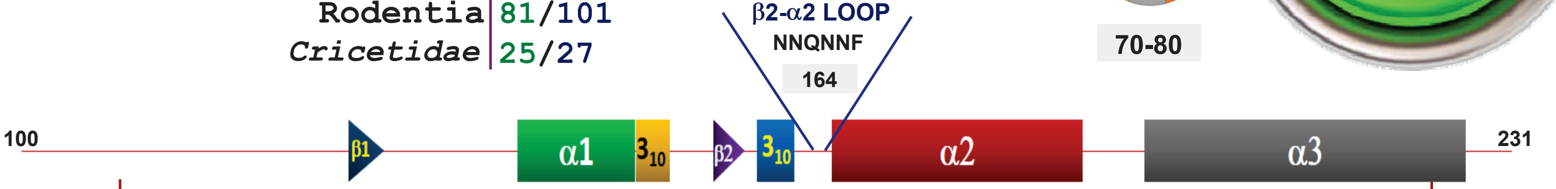
75



70-80

1 species sharing the same primary sequence

Hispid cotton rat
Sigmodon hispidus

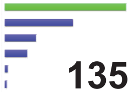


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-

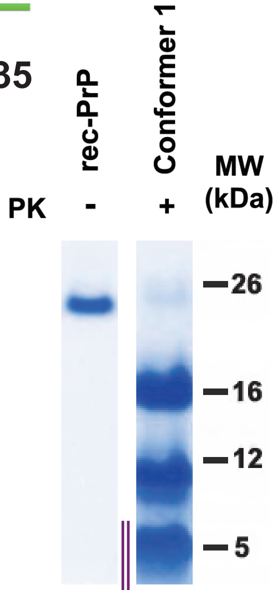
I N E S

PrP sequence differs by 2 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

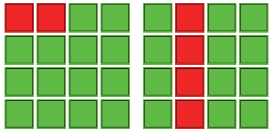


135



211 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -0.82

In vitro studies

TgVole (1x) **Not tested**

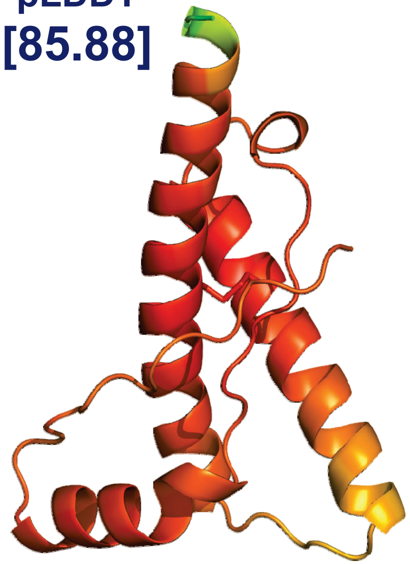
Tawny-bellied cotton rat **Not tested**

In vivo studies

TgVole (1x) **Not tested**

Tawny-bellied cotton rat **Not tested**

pLDDT
[85.88]



Protein code: 1349

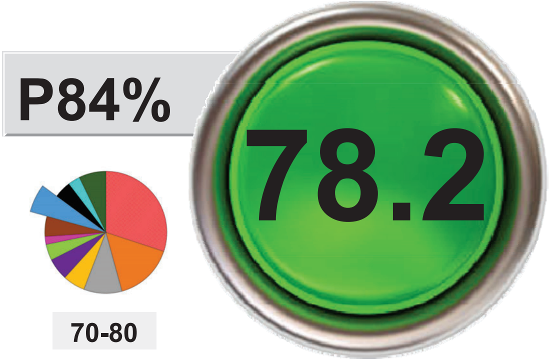
Distinct primary sequence across species

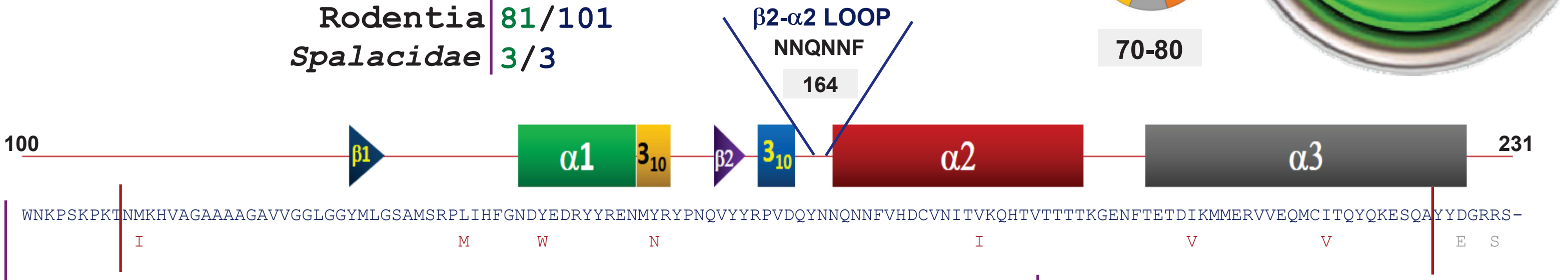
Upper Galilee Mountains blind mole-rat

GenBank: XM_008835893

Spalax galili

Rodentia	81/101
Spalacidae	3/3

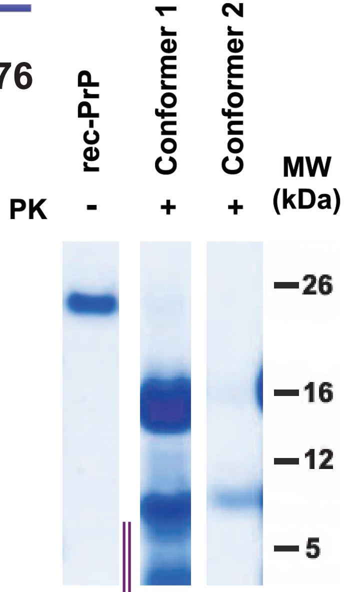




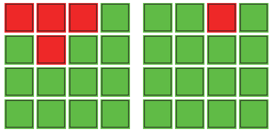
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKMMERVVEQMCITQYQKESQAYYDGRRS-

PrP sequence differs by 7 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



213 AA



Tm^{Exp}: ND

ΔΔG: -10.9

***In vitro* studies**

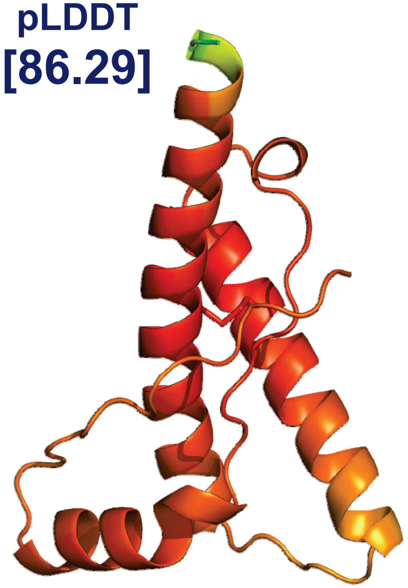
TgVole (1x) — Not tested

Upper Galilee Mountains blind — Not tested

***In vivo* studies**

TgVole (1x) — Not tested

Upper Galilee Mountains blind — Not tested



Protein code: 1088

Distinct primary sequence across species

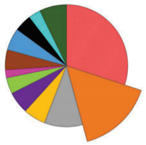
California ground squirrel

GenBank: BK064192

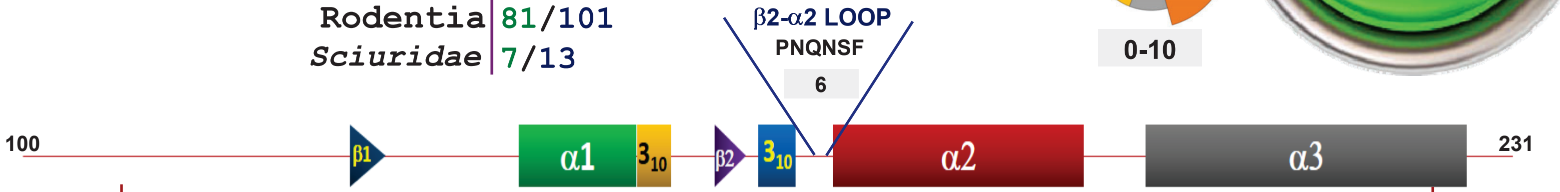
Spermophilus beecheyi

Rodentia	81/101
Sciuridae	7/13

P31%


0-10

0.4



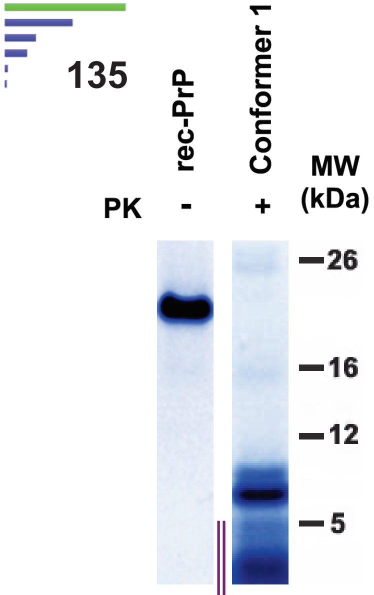
```
WGKPVKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMMHFGSDYEDRYYRENMNRYPNQVYYKPVDQYPNQNSFVHDCVNITIKQHTVTTTTKGDNFTETDIKIMERVVEQMCTTQYKQEAQAYYQRGSS-
 N  S    NI                           I   N W                   R      N   N                        E     V M         V   QK S     EGR
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions

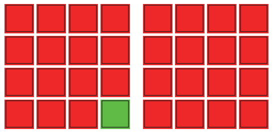
No insertions

No polymorphic variants found



204 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -11.31

***In vitro* studies**

TgVole (1x) — Not tested

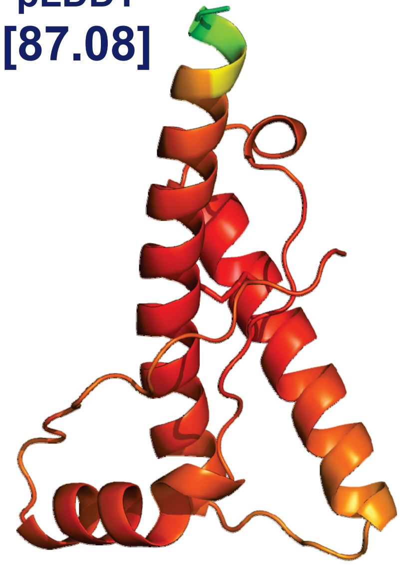
California ground squirrel — Not tested

***In vivo* studies**

TgVole (1x) — Not tested

California ground squirrel — Not tested

pLDDT
[87.08]



Distinct primary sequence across species

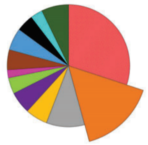
Daurian ground squirrel

GenBank: BK063919

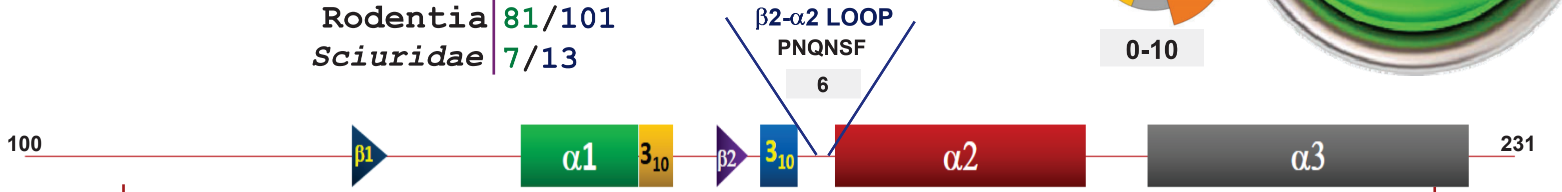
Spermophilus dauricus

Rodentia	81/101
Sciuridae	7/13

P29%



0-10

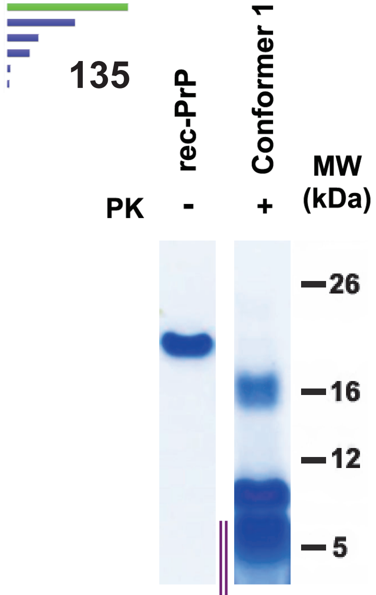


WGKPVKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPMMHFGSDYEDRYYRENMNRYPSQVYYKPVDQYPNQNSFVHDCVNITIKQHTTTTTTKGDNFTETDIKIMERVVEQMCTTQYKQEAQQAYYPRGSS-

N S NI V I N W N R N N V E V M V QK S AY EG S

PrP sequence differs by 19 amino acids from the bank vole PrP (see in red)

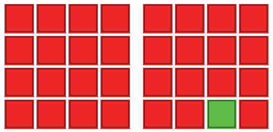
No deletions
No insertions
No polymorphic variants found



197 AA

1

Conformers



Tm^{Exp}: ND

ΔΔG: ND

***In vitro* studies**

Not tested
TgVole (1x)

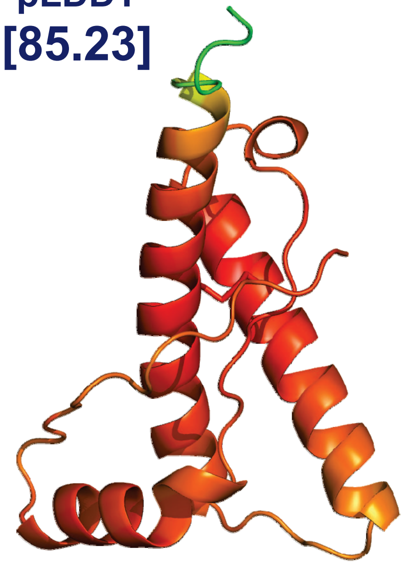
Not tested
Daurian ground squirrel

***In vivo* studies**

Not tested
TgVole (1x)

Not tested
Daurian ground squirrel

pLDDT
[85.23]



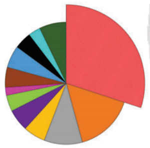
Protein code: 2025

Distinct primary sequence across species

Arctic ground squirrel

GenBank: XM_026385776

P29%



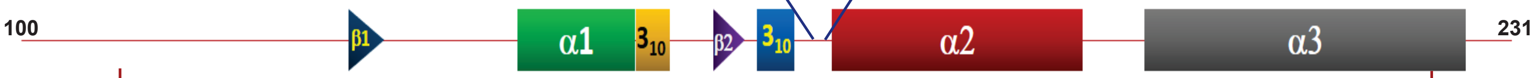
0

0

Spermophilus parryii

Rodentia	81/101
Sciuridae	7/13

β2-α2 LOOP
PNQNSF
6



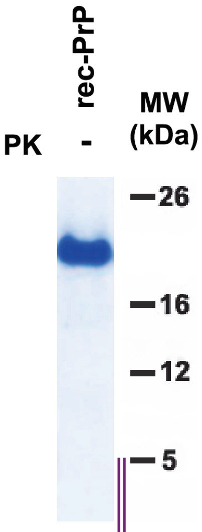
```
GGKPVKPKTSMKHMAGAAAAGAVVGGLGGYMLGSAMSRPMMHFGNDYEDRYYRENMNRYPSQVYYKPVDQYPNQNSFVHDCVNITIKQHTTTTTTKGDNFTETDIKIMERVVEQMCTTQYKQEAQQAYYPRGSS-
WN   S    NI  V                          I     W              N    R     N   N                V       E      V M          V   QK S AY EG S
```

PrP sequence differs by 18 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

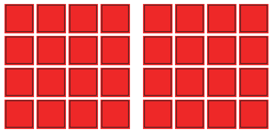
Tm^{Exp}: ND

ΔΔG: ND



207 AA

NO MISFOLDING



0
Conformers

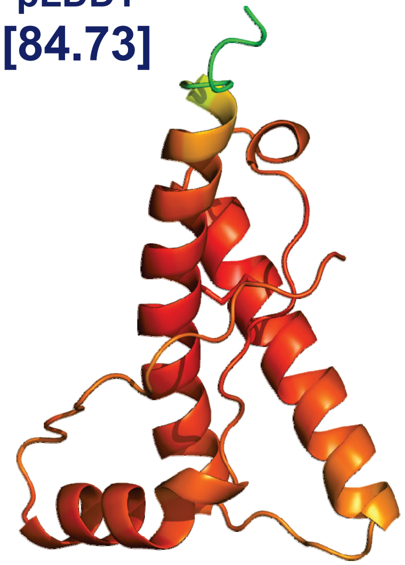
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[84.73]



Protein code: 1119

Thirteen-lined ground squirrel

GenBank: XM_005320503

Spermophilus tridecemlineatus

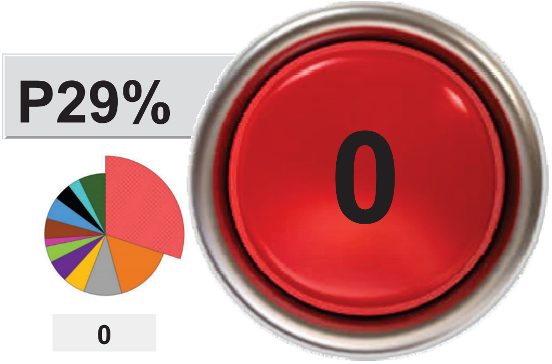
Rodentia 81/101
Sciuridae 7/13

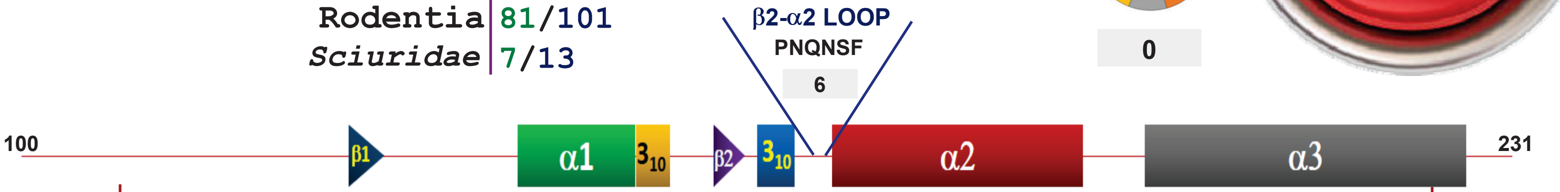
2 species sharing the same primary sequence

Gunnison's prairie dog
Cynomys gunnisoni

Black-tailed prairie dog
Cynomys ludovicianus

P29%





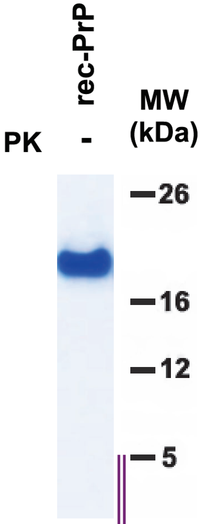
```
WGKPVKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPMMHFGNDYEDRYYRENMNRYPSQVYYKPVDQYPNQNSFVHDCVNITIKQHTTTTTTKGDNFTETDIKIMERVVEQMCTTQYKQEAQQAYYPRGSS-
 N  S    NI                               I     W            N     R      N   N                V      E       V M         V   QK S AY EG S
```

PrP sequence differs by 17 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

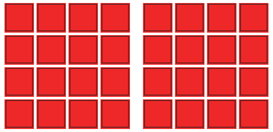
Tm^{Exp}: ND

ΔΔG: ND



205 AA

NO MISFOLDING



0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [83.82]

Protein code: 1106

Siberian chipmunk

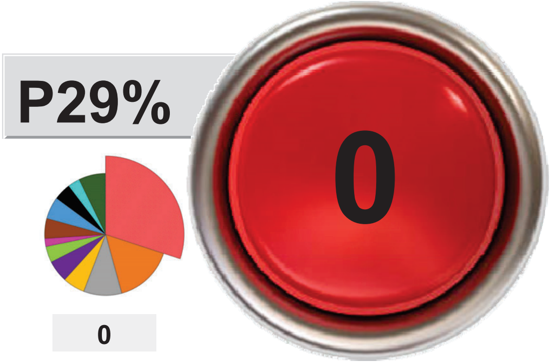
GenBank: BK064209

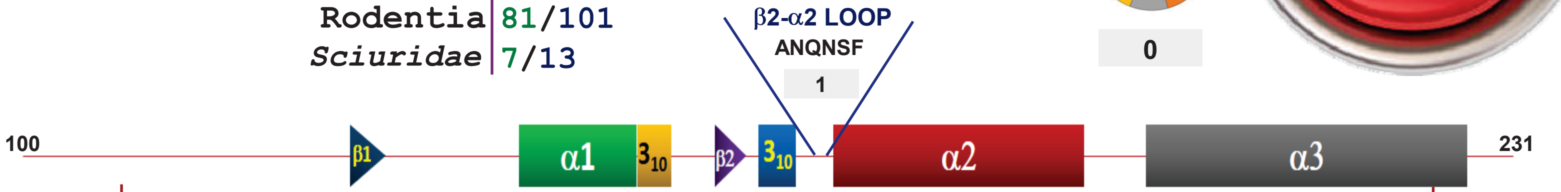
Tamias sibiricus

Rodentia	81/101
Sciuridae	7/13

Distinct primary sequence across species

P29%





WGKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPPMHFGNDYEDRYYRENMNRYPNQVYYKPVDQYANQNSFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCTTKYQQEAQAYYQRGSS-

N S I V MI W R N N I V M V Q K S EGR

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

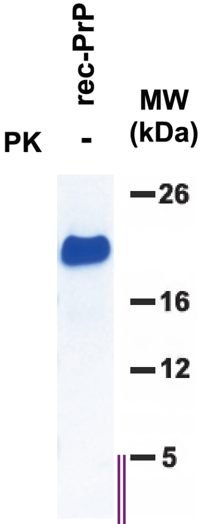
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: -11.42

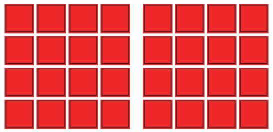


205 AA

NO MISFOLDING

0

Conformers



In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT

[93.27]

Protein code: 4618

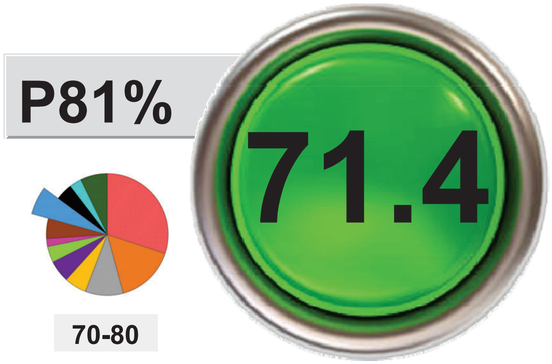
Botta's pocket gopher

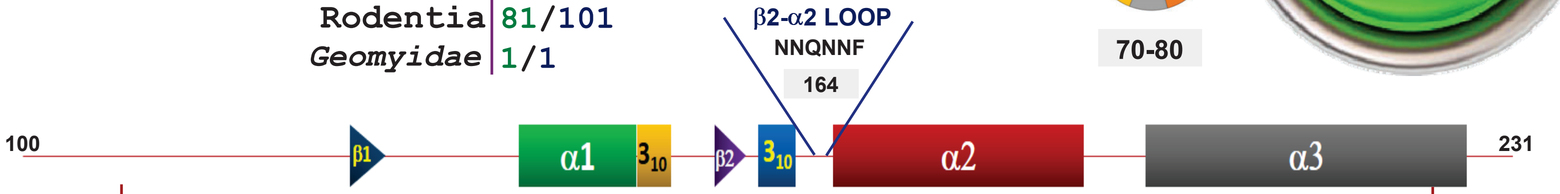
GenBank: BK064206

Thomomys bottae

Rodentia	81/101
Geomyidae	1/1

Distinct primary sequence across species





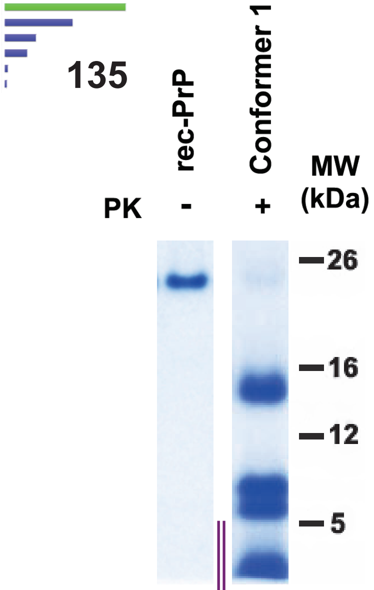
```
WNKPSKPKTSMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLLHFGNDYEDRYYRENMNRYPSQVYYKPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERMVEQMCITQYQKEAQAYYEPRS-
          NI                                 MI     W                 N    R                              I                        M  V     V      S     G S
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found



219 AA

Tm^{Exp}: ND

ΔΔG: ND

***In vitro* studies**

Not tested
TgVole (1x)

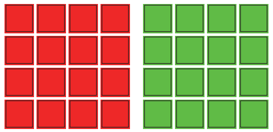
Not tested
Botta's pocket gopher

***In vivo* studies**

Not tested
TgVole (1x)

Not tested
Botta's pocket gopher

pLDDT
[87.29]



Protein code: 4580

Greater cane rat

GenBank: BK064162

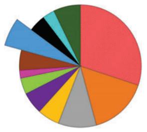
Thryonomys swinderianus

Rodentia 81/101
Thryonomyidae 1/1

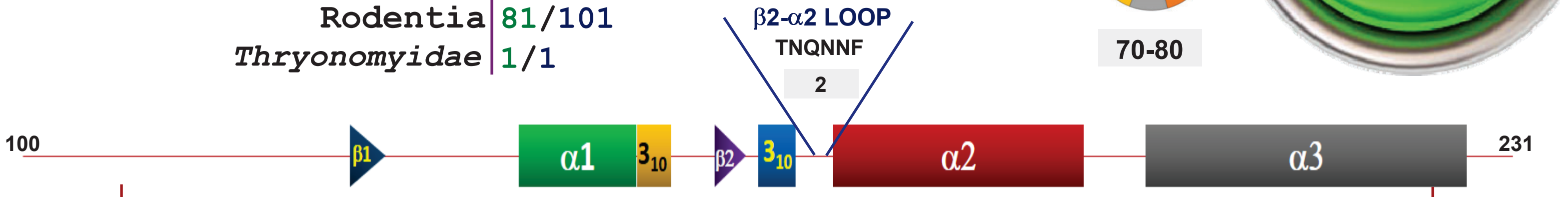
Distinct primary sequence across species

P79%

70.4



70-80

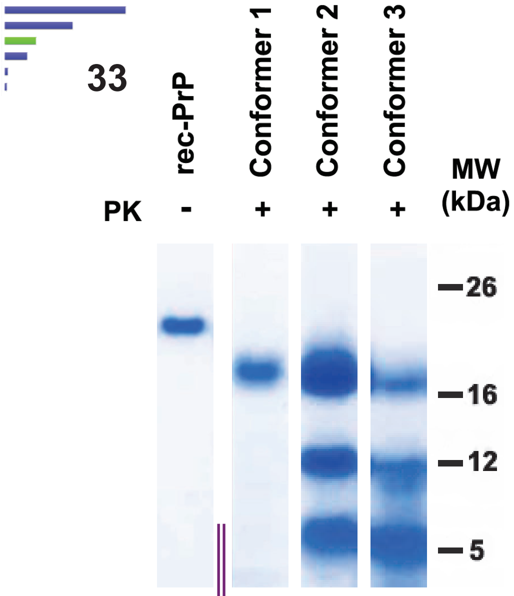


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPNQVYYKPVDQYTNQNNFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLEQMCTTQYQKESQAYYYQGSSG-
I M W R N H M V V EGR

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

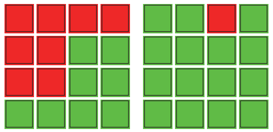
No deletions
No insertions
No polymorphic variants found

33



202 AA

3
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

Not tested
TgVole (1x)

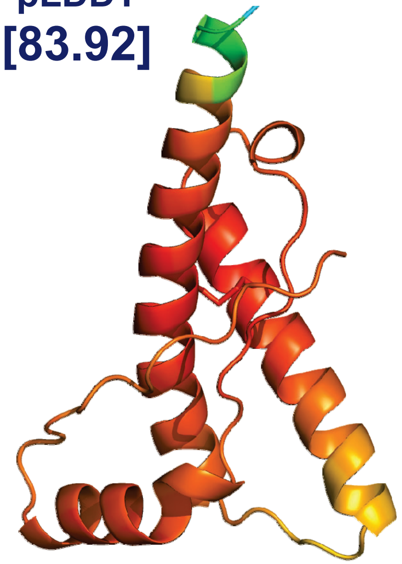
Not tested
Greater cane rat

In vivo studies

Not tested
TgVole (1x)

Not tested
Greater cane rat

pLDDT [83.92]



Protein code: 3776

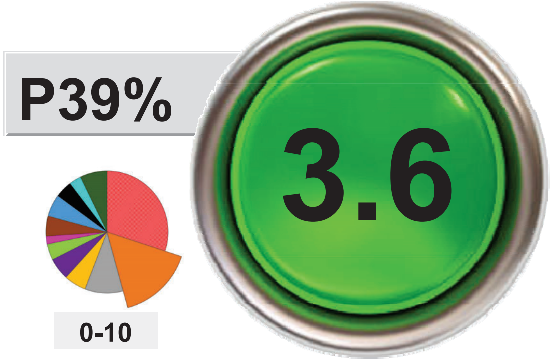
Plains viscacha rat

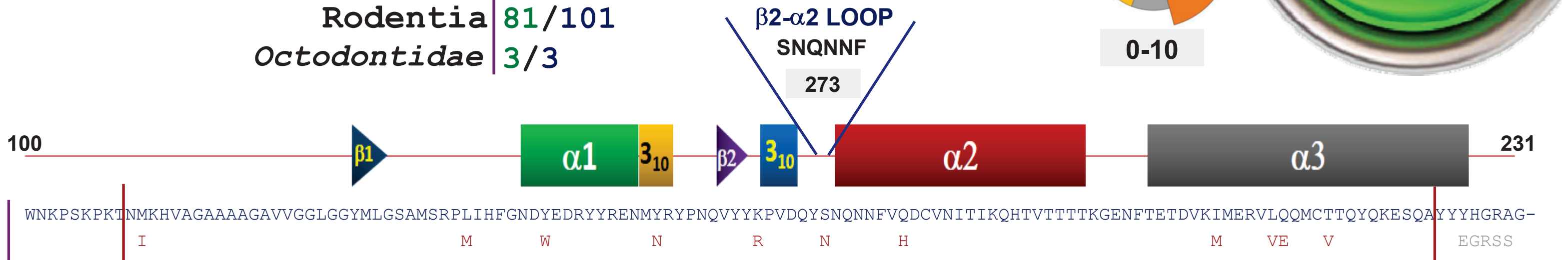
GenBank: BK064138

Tympanoctomys barrerae

Distinct primary sequence across species

Rodentia	81/101
Octodontidae	3/3

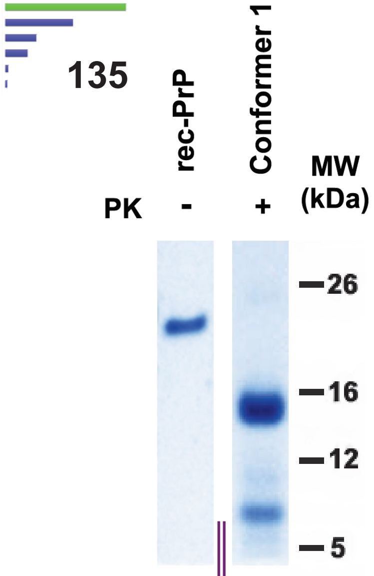




```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVQDCVNITIKQHTVTTTTKGENFTETDVKIMERVLQQMCTTQYQKESQAYYYHGRAG-
          I                         M     W        N       R    N     H                                M    VE   V                EGRSS
```

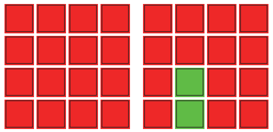
PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



202 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

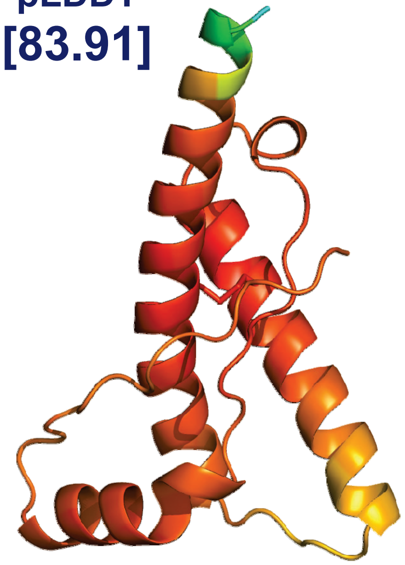
***In vitro* studies**

TgVole (1x)	Not tested
Plains viscacha rat	Not tested

***In vivo* studies**

TgVole (1x)	Not tested
Plains viscacha rat	Not tested

pLDDT
[83.91]



Protein code: 3322

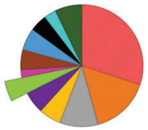
Chinese pygmy dormouse

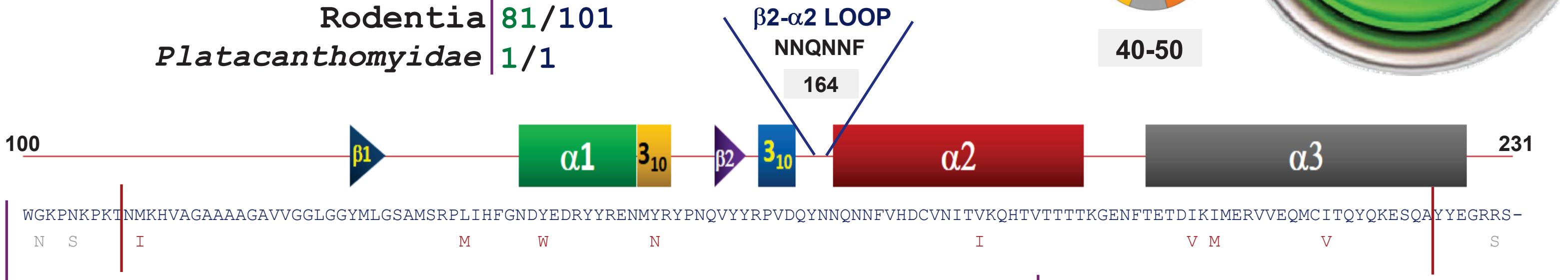
GenBank: BK064190

Typhlomys cinereus

Rodentia 81/101
Platacanthomyidae 1/1

P70% **46.4**

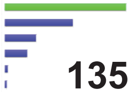


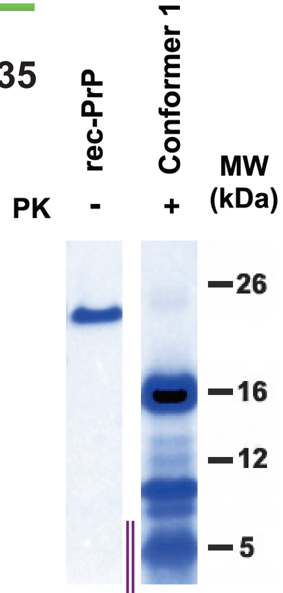


PrP sequence differs by 8 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

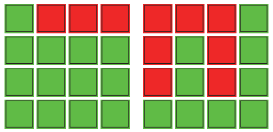
Distinct primary sequence across species





212 AA

1 Conformers



Tm^{Exp}: ND

ΔΔG: -13.72

***In vitro* studies**

Not tested
TgVole (1x)

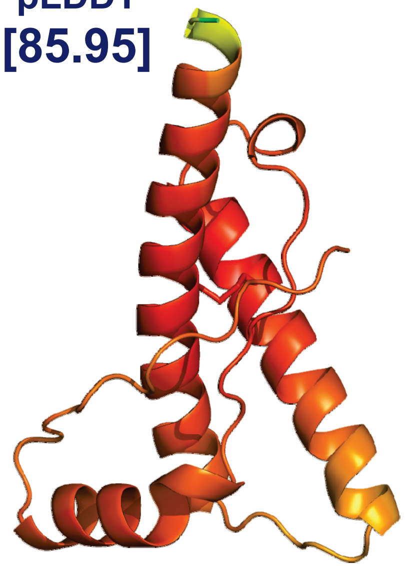
Not tested
Chinese pygmy dormouse

***In vivo* studies**

Not tested
TgVole (1x)

Not tested
Chinese pygmy dormouse

pLDDT [85.95]



Protein code: 4478

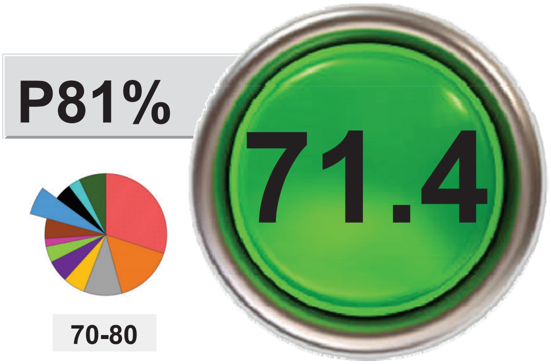
Giant white-tailed rat

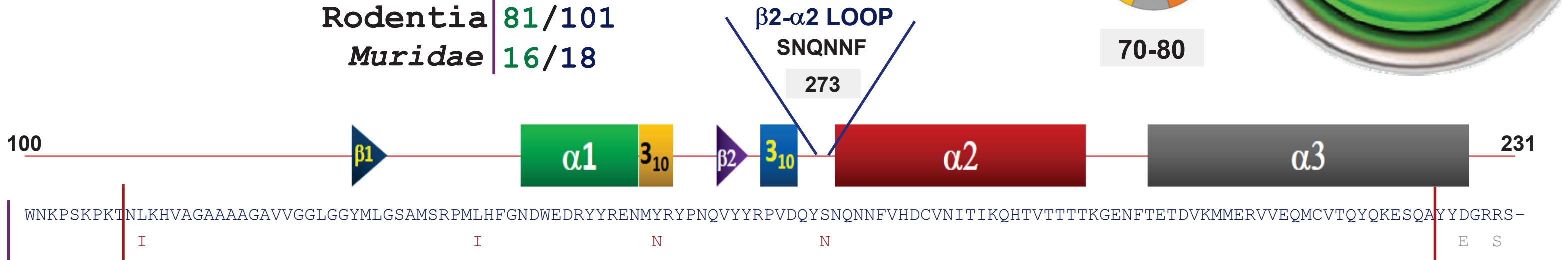
GenBank: BK064806

Uromys caudimaculatus

Rodentia	81/101
Muridae	16/18

Distinct primary sequence across species





WNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLGSAMSRPMLHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRRS-

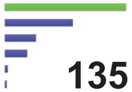
I I N N E S

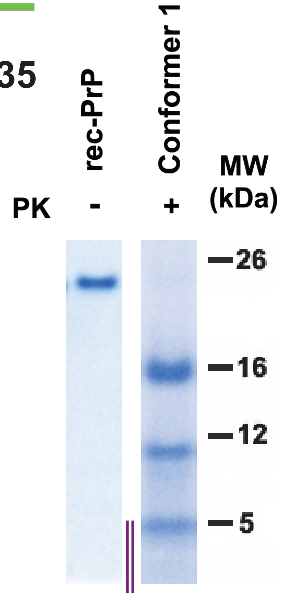
PrP sequence differs by 4 amino acids from the bank vole PrP (see in red)

No deletions

No insertions

No polymorphic variants found



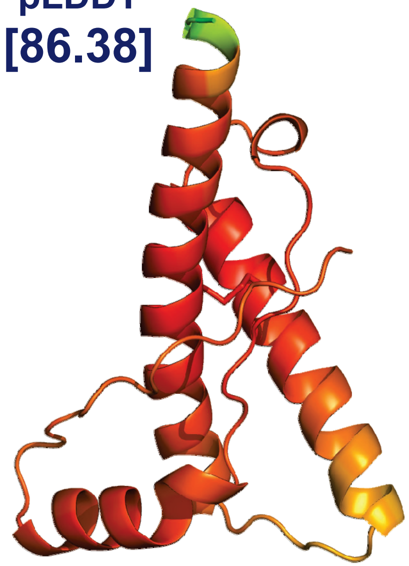


219 AA

Tm^{Exp}: ND

ΔΔG: -9.36

pLDDT [86.38]



***In vitro* studies**

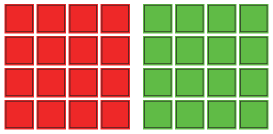
TgVole (1x) Not tested

Giant white-tailed rat Not tested

***In vivo* studies**

TgVole (1x) Not tested

Giant white-tailed rat Not tested



1 Conformers

Protein code: 3974

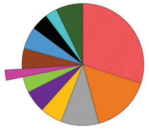
Unstriped ground squirrel

GenBank: BK064797

Xerus rutilus

Rodentia	81/101
Sciuridae	7/13

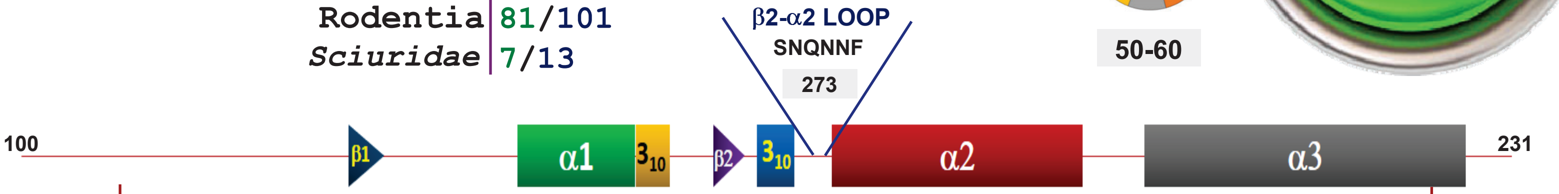
P73%



50-60

53.6

Distinct primary sequence across species

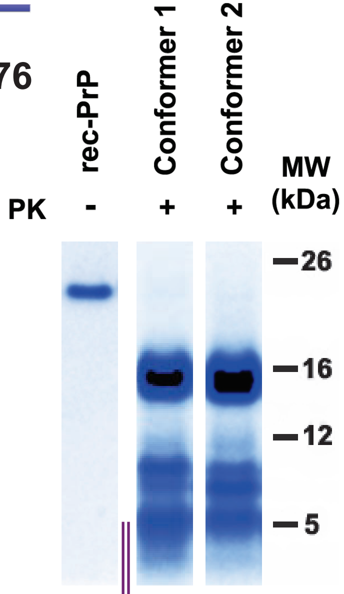


```
WSKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQEAQAYYQRGSS-
 N  S    I                               M      W          N         R      N              I                 V M          V    K S    EGR
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

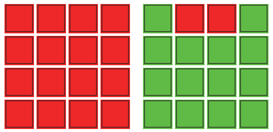
No deletions
No insertions
No polymorphic variants found

76



213 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -13.01

In vitro studies

TgVole (1x) — Propagate

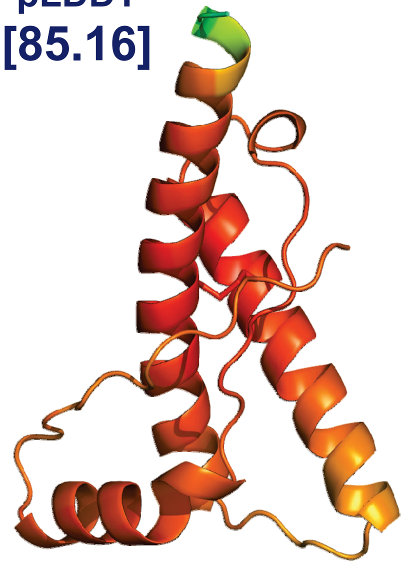
Unstriped ground squirrel — Not tested

In vivo studies

TgVole (1x) — Ongoing

Unstriped ground squirrel — Not tested

pLDDT
[85.16]



Protein code: 3962

Meadow jumping mouse

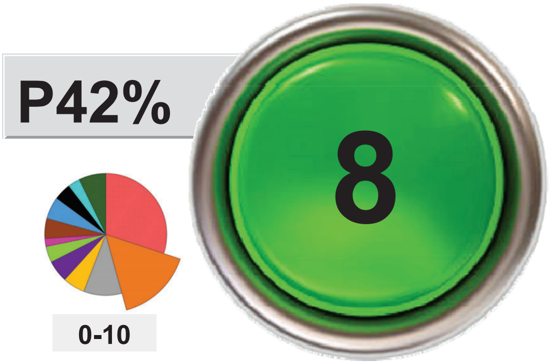
GenBank: BK064139

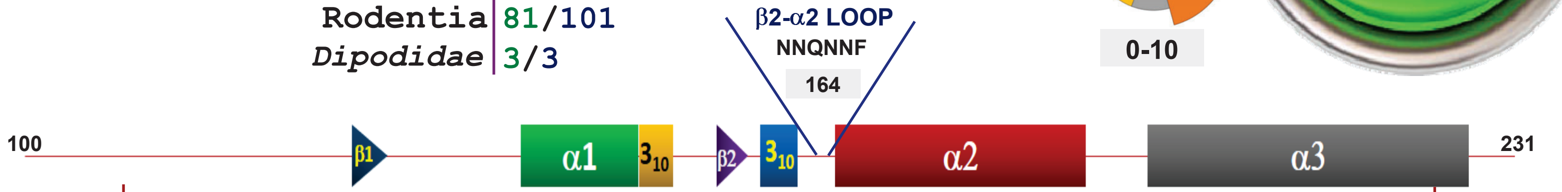
Zapus hudsonius

Rodentia 81/101
Dipodidae 3/3

Distinct primary sequence across species

P42%



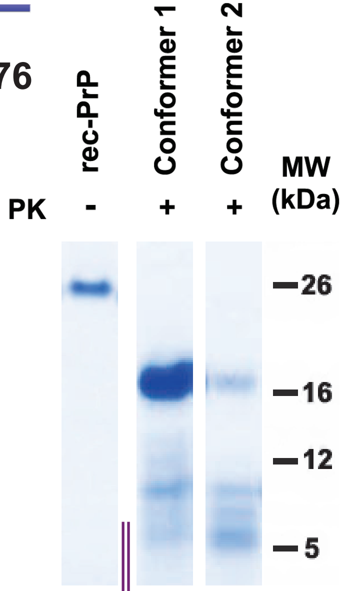


```
WNKPNKPKTNMKHMAGAAAAGAVVGGLGGYMLGSAMSRPSMSFGNEYEDRYYRENMNRYPSQVYYKPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYQKEAQAYQEGRRS-
     S     I  V                            MIH   DW              N    R                    I                    M         V      S  Y   S
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

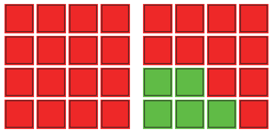
No deletions
No insertions
No polymorphic variants found

76



219 AA

2 Conformers



Tm^{Exp}: ND

ΔΔG: -9.25

In vitro studies

TgVole (1x) Not tested

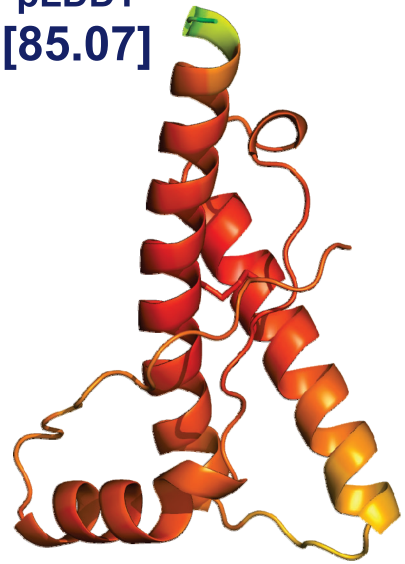
Meadow jumping mouse Not tested

In vivo studies

TgVole (1x) Not tested

Meadow jumping mouse Not tested

pLDDT [85.07]



Protein code: 3323

Chinese tree shrew

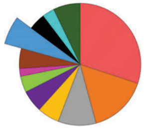
GenBank: XM_006163978

Tupaia belangeri chinensis

Scandentia 2/2
Tupaiidae 2/2

P82%

71.8



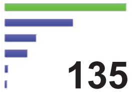
70-80

β2-α2 LOOP
SNQNNF
273

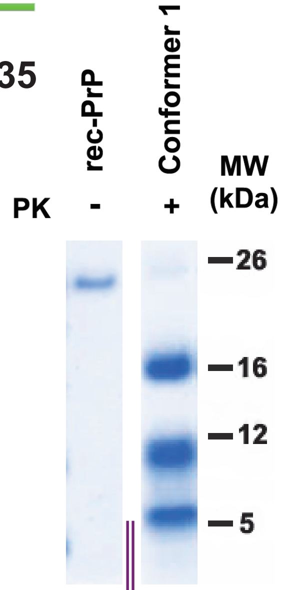
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSVMSRPMIHFGSDYEDRYYRENMNRYPNQVYYKPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQEARASYYNSS-
           I                          A           N W                      R      N                                        V M          V      K SQ Y EGR S
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

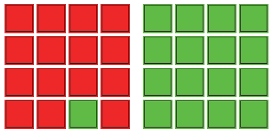


135



220 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

Chinese tree shrew Not tested

In vivo studies

TgVole (1x) Not tested

Chinese tree shrew Not tested

pLDDT
[93.79]

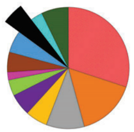
Distinct primary sequence across species

Protein code: 1093

Large treeshrew

GenBank: AY133035

P89%



80-90

89.3

Tupaia tana

Scandentia 2/2
Tupaiidae 2/2

β2-α2 LOOP
SNQNNF
273

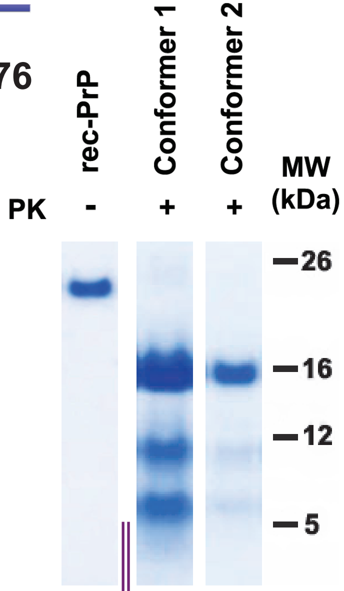
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSVMSRPMIHFGSDYEDRYYRENMNRYPNQVYYYKPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQQEARASYYSSS-
           I                       A         N W                     R     N                                     V M          V     K SQ Y EGR S
```

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

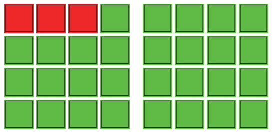
Distinct primary sequence across species

76



220 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: ND

In vitro studies

TgVole (1x) Not tested

Large treeshrew Not tested

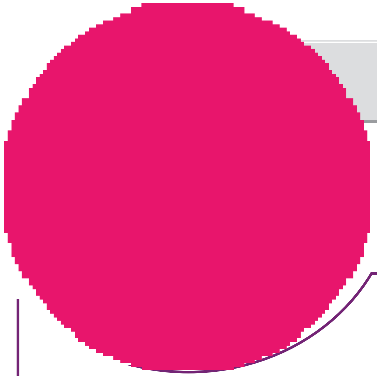
In vivo studies

TgVole (1x) Not tested

Large treeshrew Not tested

pLDDT
[94.29]

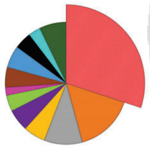
Protein code: 1371



Dugong

GenBank: BK063981

P29%



0

0

Dugong dugon

Sirenia 1/2

Dugongidae 0/1

Steller's sea cow
Hydrodamalis gigas

1 species sharing the same primary sequence

β2-α2 LOOP
SSQNNF
42

WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPNQVYYYRPVNEYSSQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYEKEFQAYQRGSS-

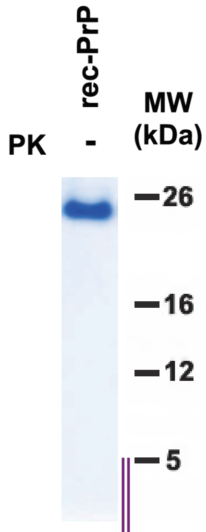
I M W DQ NN I M V Q S YE R S

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

ΔΔG: ND



220 AA

NO MISFOLDING

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

0
Conformers

pLDDT
[88.27]

Protein code: 3138

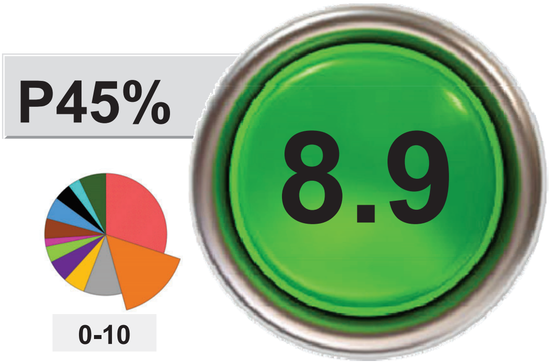
West Indian manatee

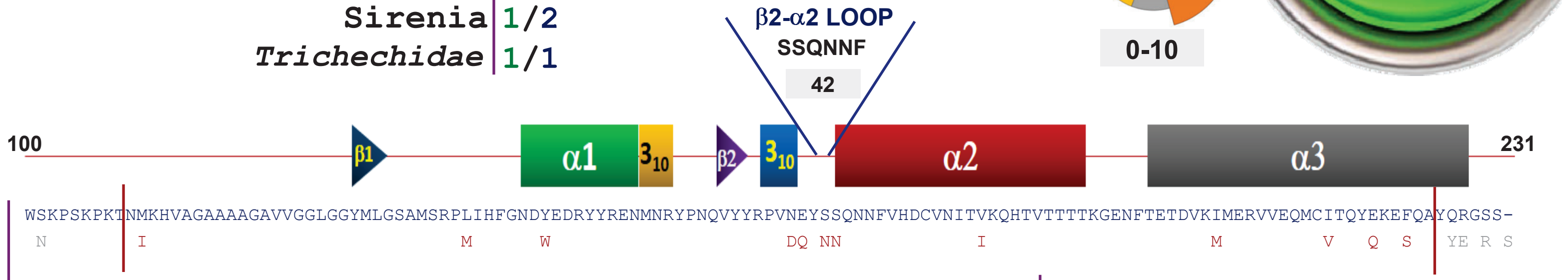
GenBank: AY133056

Trichechus manatus

Sirenia 1/2
Trichechidae 1/1

P45%



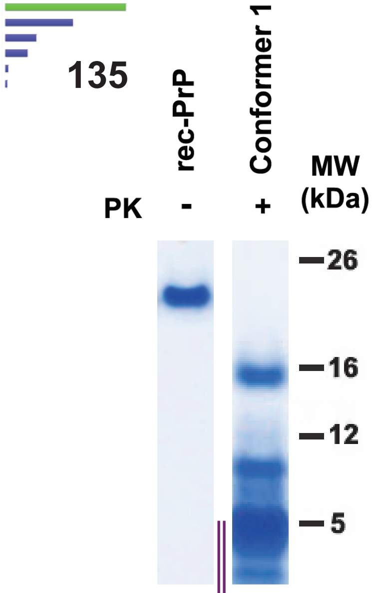


`WSKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPNQVYYRPVNEYSSQNNFVHDCVNITVKQHTVTTTTKGENFTETDVKIMERVVEQMCITQYEKEFQAYQRGSS-`

`N I M W DQ NN I M V Q S YE R S`

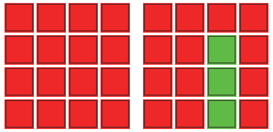
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found



220 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: ND

***In vitro* studies**

TgVole (1x) Not tested

West Indian manatee Not tested

***In vivo* studies**

TgVole (1x) Not tested

West Indian manatee Not tested

pLDDT
[88.15]

Distinct primary sequence across species

Protein code: 0959

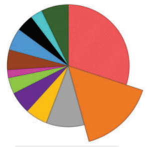
Star-nosed mole

GenBank: XM_012728373

Condylura cristata

Soricomorpha 7/12
Talpidae 4/6

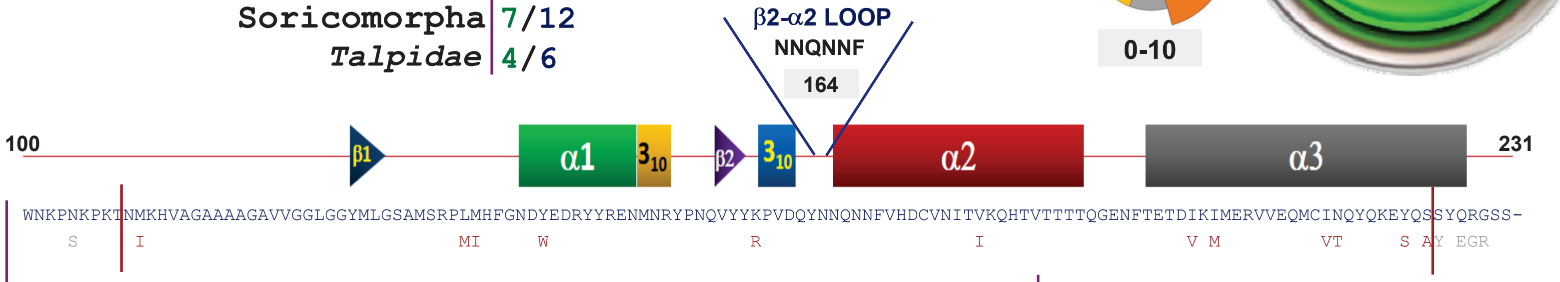
P36%



0-10

3.2

Distinct primary sequence across species

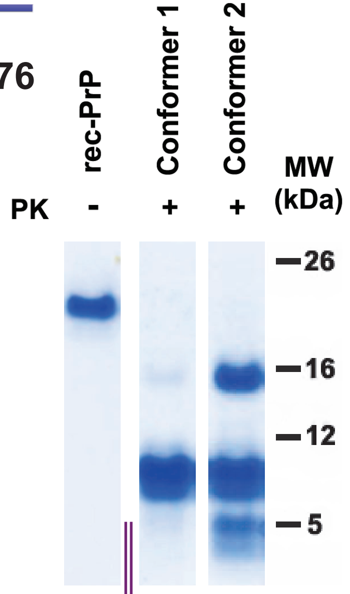


WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNDYEDRYYRENMNRYPNQVYYKPVDQYNNQNNFVHDCVNITVKQHTVTTTTQGENFTETDIKIMERVVEQMCINQYQKEYQSSYQRGSS-
S I MI W R I V M VT S AY EGR

PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

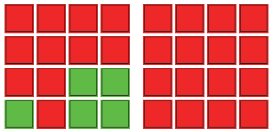
No deletions
No insertions
No polymorphic variants found

76



216 AA

2
Conformers



Tm^{Exp}: ND

ΔΔG: -0.07

In vitro studies

TgVole (1x) Not tested

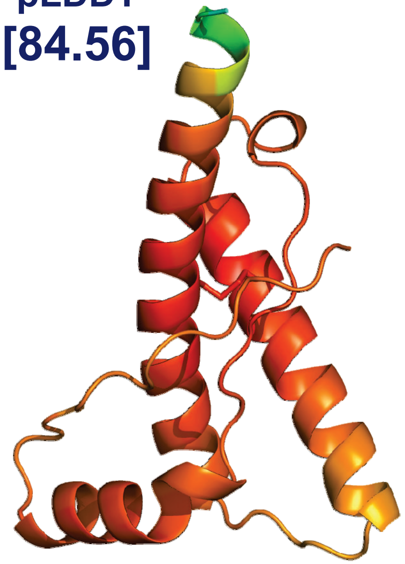
Star-nosed mole Not tested

In vivo studies

TgVole (1x) Not tested

Star-nosed mole Not tested

pLDDT
[84.56]



Protein code: 1138

Greater white-toothed shrew

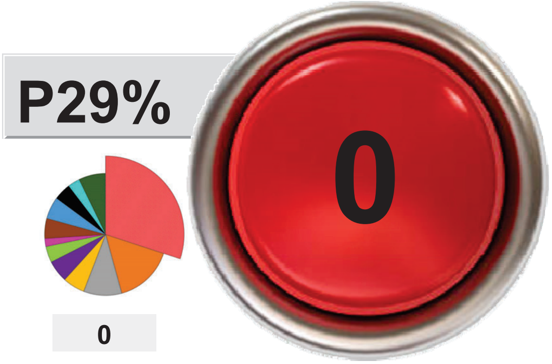
GenBank: OR47280

Crocidura russula

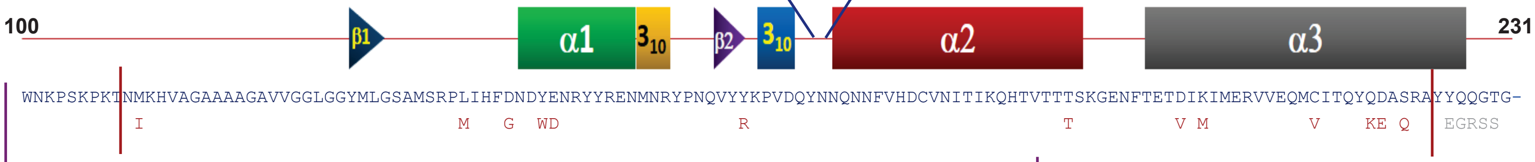
Soricomorpha 7/12
Soricidae 2/5

Distinct primary sequence across species

P29%



β2-α2 LOOP
NNQNNF
164



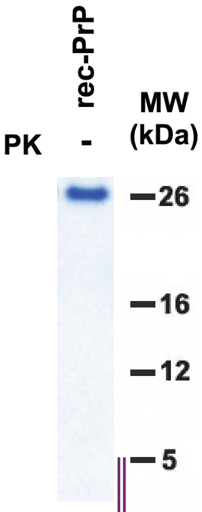
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFDNDYENRYYRENMNRYPNQVYYKPVDQYNNQNNFVHDCVNITIKQHTVTTTSKGENFTETDIKIMERVVEQMCITQYQDASRAYYQQGTG-
          I                       M   G  WD                  R                             T       V M         V    KE Q   EGRSS
```

PrP sequence differs by 13 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

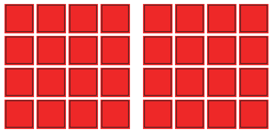
ΔΔG: -18.73



233 AA

NO MISFOLDING

0
Conformers



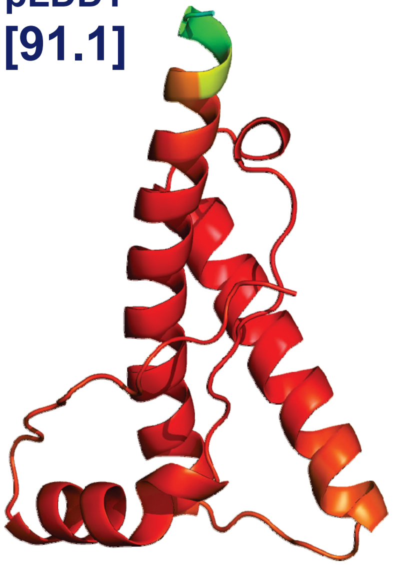
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[91.1]



Protein code: 4606

Pyrenean desman

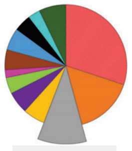
GenBank: BK063927

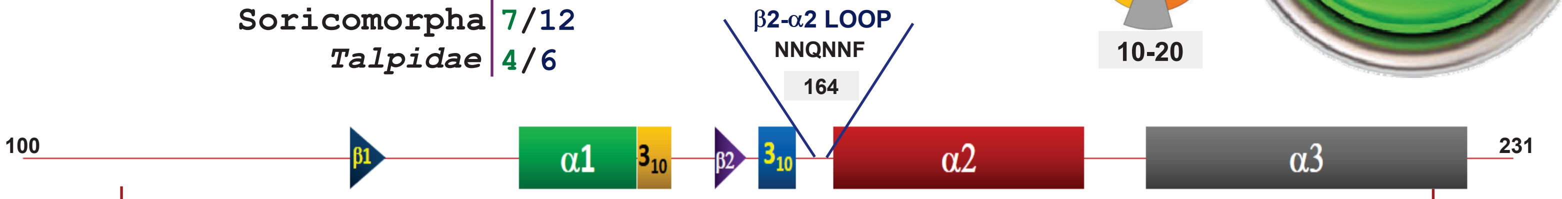
Galemys pyrenaicus

Soricomorpha 7/12
Talpidae 4/6

Distinct primary sequence across species

P51% **16.6**



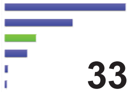


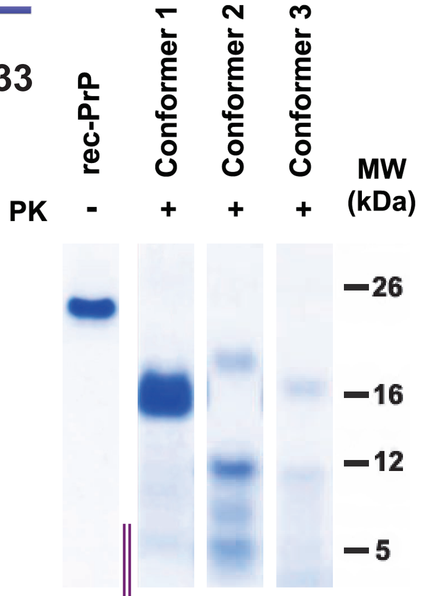
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLVHFGNDYEDRYYRENMNRYPNQVYYKPVDQYNNQNNFVHDCVNITVKQHTVTTTTQGENFTETDIKIMERVVEQMCITQYQKEYQASYQRGSS-

I MI W R I V M V S Y EGR

PrP sequence differs by 10 amino acids from the bank vole PrP (see in red)

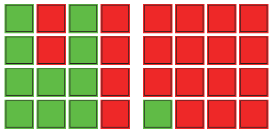
No deletions
No insertions
No polymorphic variants found





215 AA

3 Conformers



Tm^{Exp}: ND

ΔΔG: -9.42

In vitro studies

TgVole (1x) Not tested

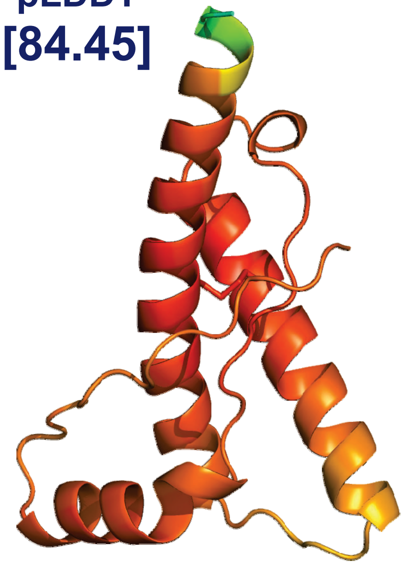
Pyrenean desman Not tested

In vivo studies

TgVole (1x) Not tested

Pyrenean desman Not tested

pLDDT
[84.45]



Protein code: 2562

Eastern mole

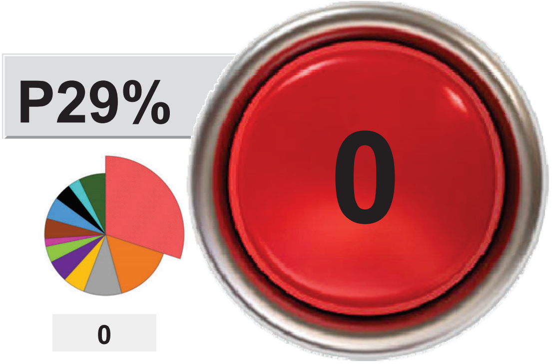
GenBank: BK063985

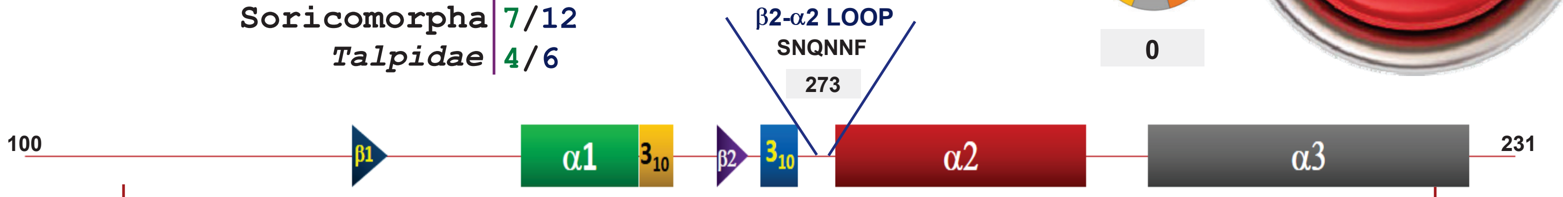
Scalopus aquaticus

Soricomorpha 7/12
Talpidae 4/6

Distinct primary sequence across species

P29%





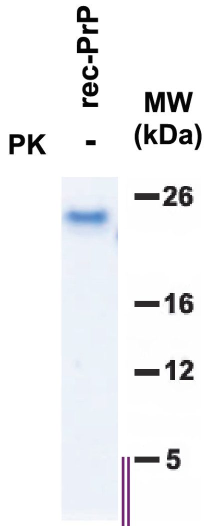
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLMHFDSDYENRYYRENMNRYPNQVYYKPVDQYSNQNNFVHDCVNITVKQHTVTTTTQGENFTETDIKIMERVVEQMCITQYQKEYQSAYQRGAS-
          I                         MI  GN WD                   R    N                    I                     V M          V        S AY EGRS
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

Tm^{Exp}: ND

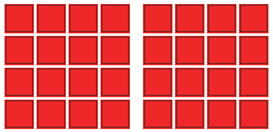
ΔΔG: -8.06



224 AA

NO MISFOLDING

0
Conformers



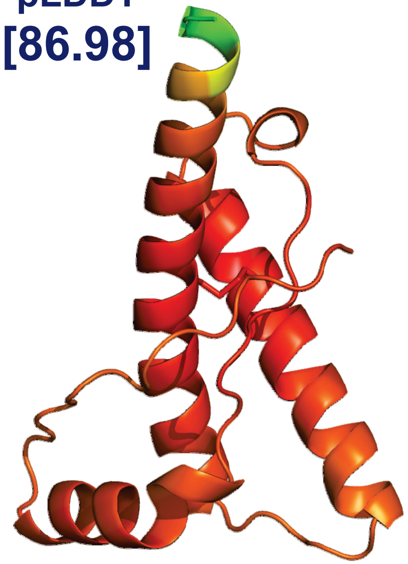
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[86.98]



Protein code: 3142

Hispaniolan solenodon

GenBank: BK063984

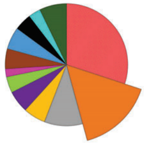
Solenodon paradoxus woodi

Soricomorpha	7/12
Solenodontidae	1/1

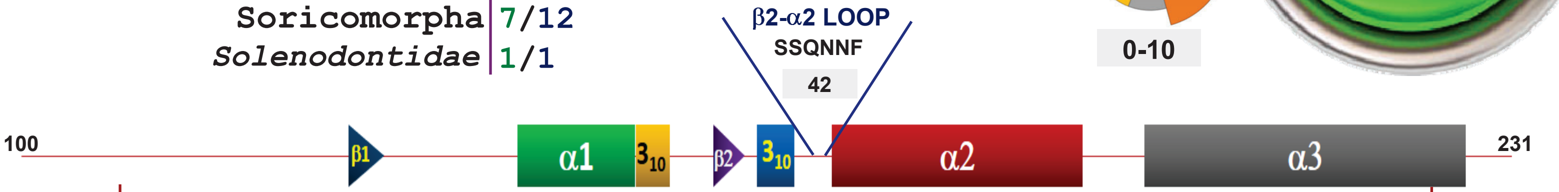
Distinct primary sequence across species

P45%

8.9



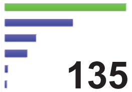
0-10



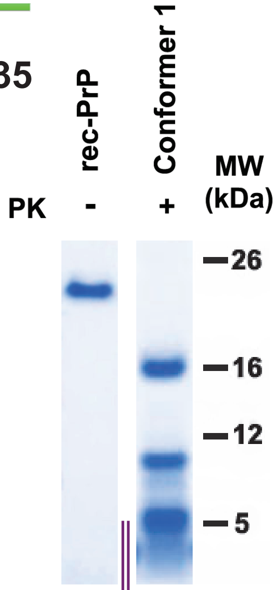
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYLVGSAMSRPMLHFGNDYEDRYYRENMYRYPSQVYYKPMDQYSSQNNFVHDCVNITIKQHTVTTTTKGENFTETDIKMMERVVEQMCTTQYQREYQSFSQRGAS-
          I                   ML        I     W         N   N    R V   NN                               V           V    K S AYYEGRS
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

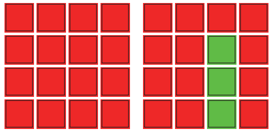


135



220 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -8.12

***In vitro* studies**

TgVole (1x) Not tested

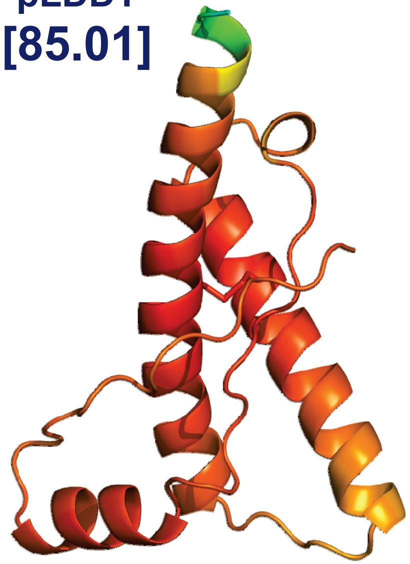
Hispaniolan solenodon Not tested

***In vivo* studies**

TgVole (1x) Not tested

Hispaniolan solenodon Not tested

pLDDT
[85.01]



Protein code: 3141

Common shrew

GenBank: BK064940

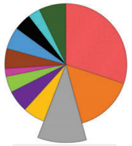
Sorex araneus

Soricomorpha 7/12
Soricidae 2/5

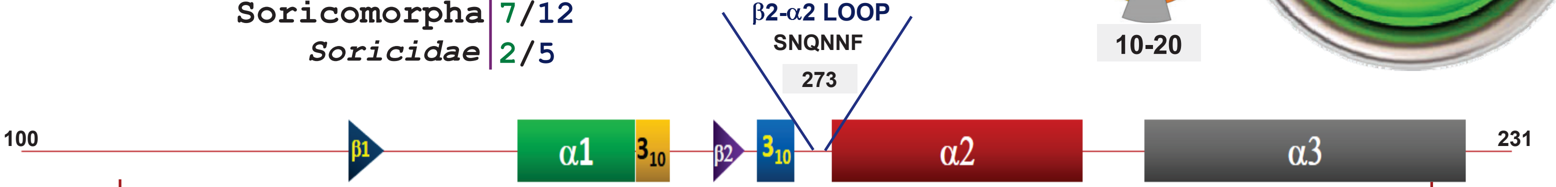
1 species sharing the same primary sequence

Maritime shrew
Sorex maritimensis

P53%



10-20

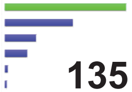


WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNMTVKQHTVTTTSKGENFTETDVKIMERVVEQMCITQYREAAQASYLQGDS-

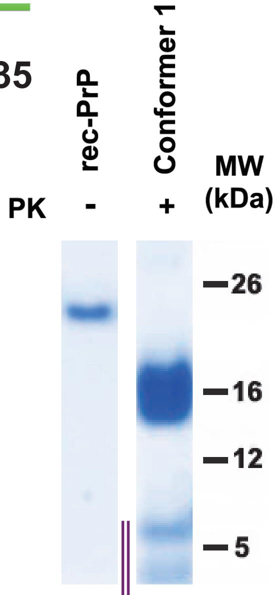
I MI W N R N I I T M V QKES Y EGRS

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

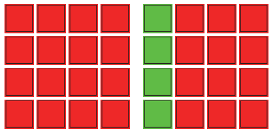


135



213 AA

1
Conformers



Tm^{Exp}: ND

ΔΔG: -14.08

In vitro studies

TgVole (1x) Not tested

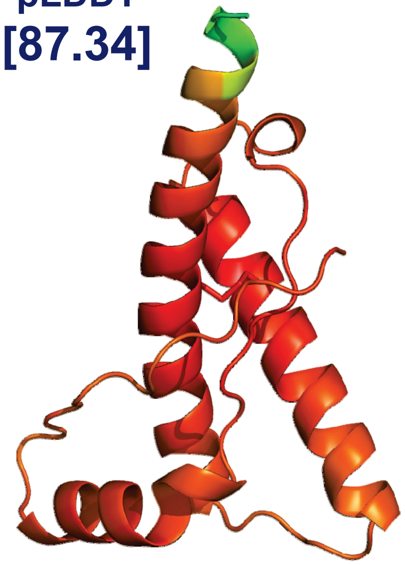
Common shrew Not tested

In vivo studies

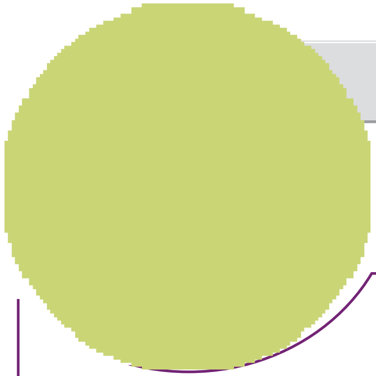
TgVole (1x) Not tested

Common shrew Not tested

pLDDT
[87.34]



Protein code: 0976



Cinereous shrew

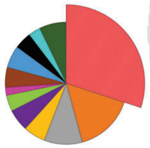
GenBank: BK063915

Sorex cinereus

Soricomorpha 7/12

Soricidae 2/5

P29%



0

0

1 species sharing the same primary sequence

Smoky shrew
Sorex fumeus

β2-α2 LOOP
SNQNNF
273

```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNDYEDRYYRENMYRYPNQVYYKPVDQYSNQNNFVHDCVNMTVKQHTVTTTSKGENFTETDVKIMERVVEQMCITQYREAAQASYMQGYN-
          I                            MI     W         N        R     N           I I        T           M         V   QKES  Y EGRSS
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

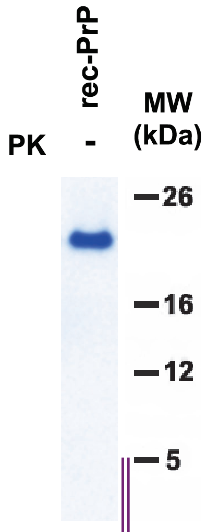
No deletions

No insertions

No polymorphic variants found

Tm^{Exp}: ND

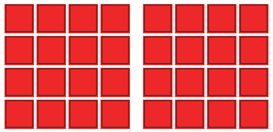
ΔΔG: -4.11



212 AA

NO MISFOLDING

0
Conformers



In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[93.25]

Protein code: 1352

American water shrew

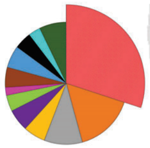
GenBank: BK064220

Sorex palustris

Soricomorpha 7/12
Soricidae 2/5

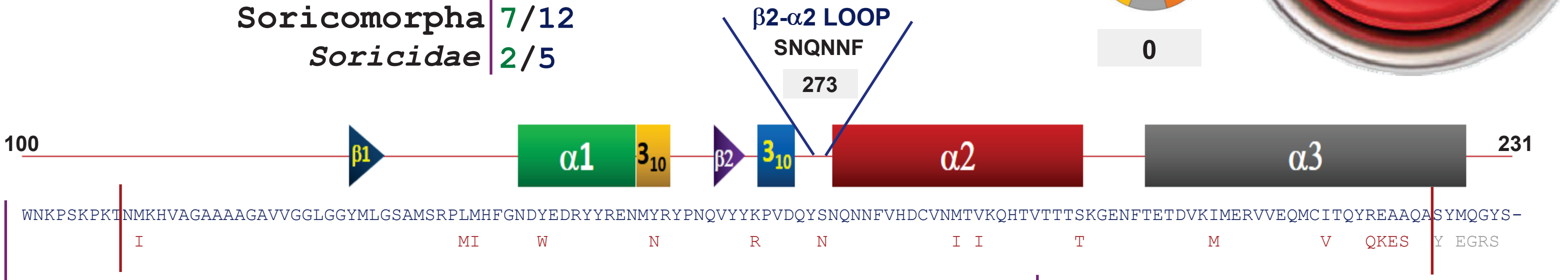
Distinct primary sequence across species

P29%



0

0



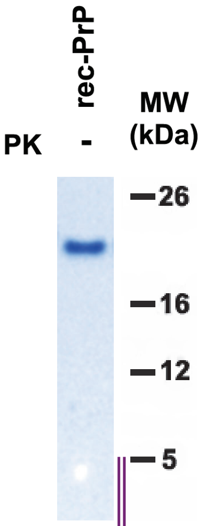
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNDYEDRYYRENMYRYPNQVYYYKPVDQYSNQNNFVHDCVNMTVKQHTVTTTSKGENFTETDVKIMERVVEQMCITQYREAAQASYMQGYS-
           I                                      MI      W          N          R      N            I I         T              M           V   QKES  Y EGRS
```

PrP sequence differs by 16 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

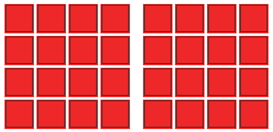
Tm^{Exp}: ND

ΔΔG: -9.15



212 AA

NO MISFOLDING



0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT [92.83]

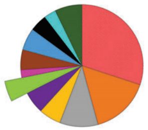
Protein code: 4817

Etruscan shrew

GenBank: BK064203

P69%

44.6



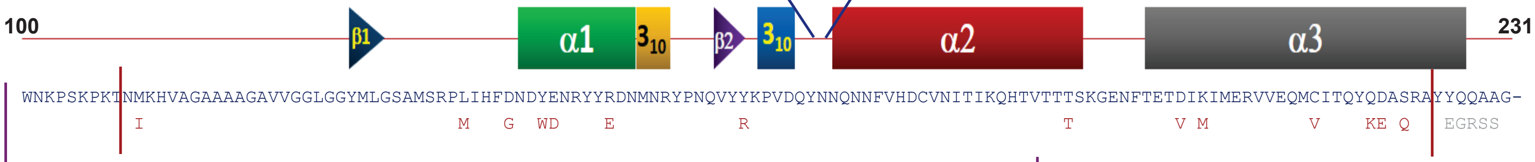
40-50

Suncus etruscus

Soricomorpha 7/12
Soricidae 2/5

Distinct primary sequence across species

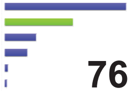
β2-α2 LOOP
NNQNNF
164



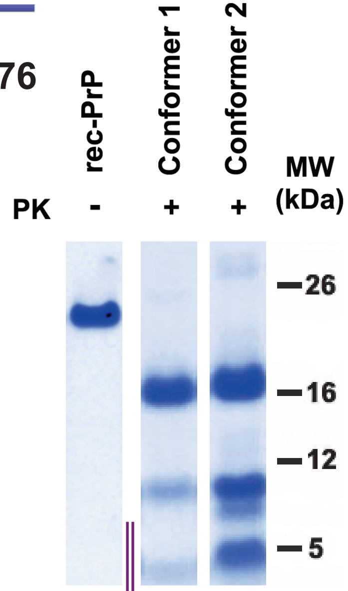
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFDNDYENRYYRDNMNRYPNQVYYKPVDQYNNQNNFVHDCVNITIKQHTVTTTSKGENFTETDIKIMERVVEQMCITQYQDASRAYYQQAAG-
          I                          M   G  WD   E      R                                T        V M       V   KE Q  EGRSS
```

PrP sequence differs by 14 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

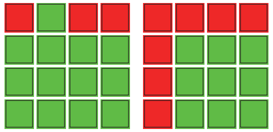


76



215 AA

2 Conformers



Tm^{Exp}: ND

ΔΔG: -3.98

***In vitro* studies**

TgVole (1x) Not tested

Etruscan shrew Not tested

***In vivo* studies**

TgVole (1x) Not tested

Etruscan shrew Not tested

pLDDT
[87.71]

Protein code: 4534

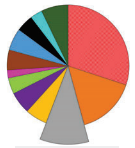
European mole

GenBank: AY133042

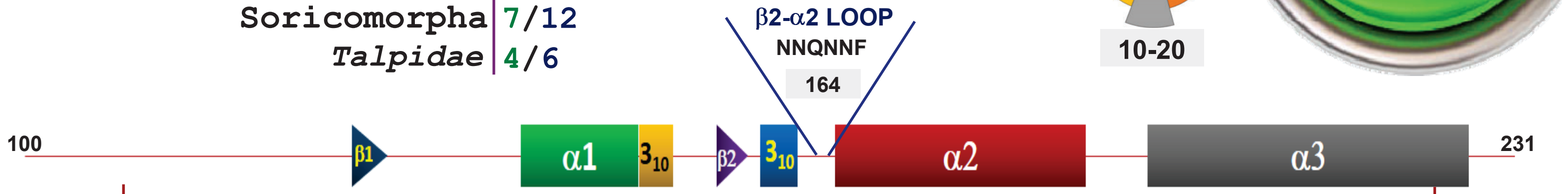
Talpa europaea

Soricomorpha 7/12
Talpidae 4/6

P54%



10-20



WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNEYEDRYYRDNMNRYPNQVYYKPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQKEYQASYQRGAS-

I MI DW E R I V M V S Y EGRS

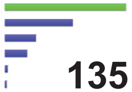
PrP sequence differs by 12 amino acids from the bank vole PrP (see in red)

No deletions

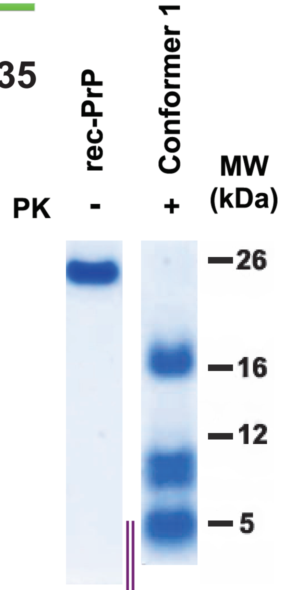
No insertions

No polymorphic variants found

Distinct primary sequence across species



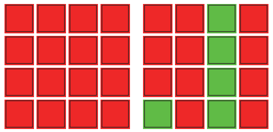
135



224 AA

1

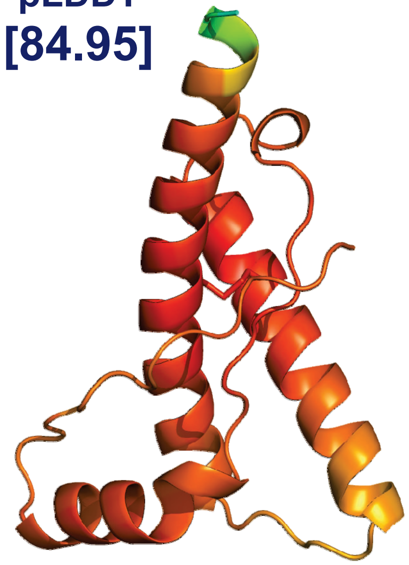
Conformers



Tm^{Exp}: ND

ΔΔG: -2.87

pLDDT [84.95]



In vitro studies

TgVole (1x) Not tested

European mole Not tested

In vivo studies

TgVole (1x) Not tested

European mole Not tested

Protein code: 0974

Spanish mole

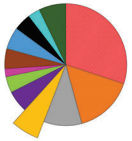
GenBank: BK063986

Talpa occidentalis

Soricomorpha	7/12
Talpidae	4/6

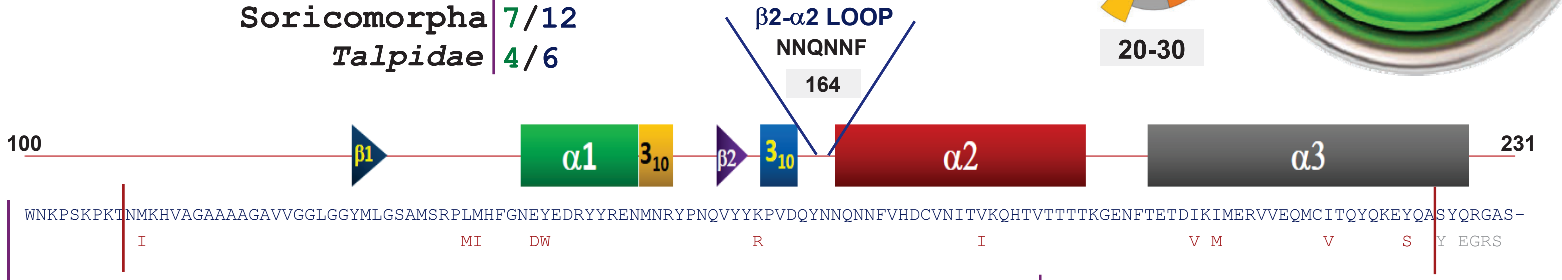
P57%

22.9



20-30

Distinct primary sequence across species



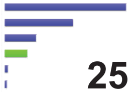
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLMHFGNEYEDRYYRENMNRYPNQVYYKPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQKEYQASYQRGAS-
           I                          MI    DW                      R                    I                          V M        V      S  Y EGRS
```

PrP sequence differs by 11 amino acids from the bank vole PrP (see in red)

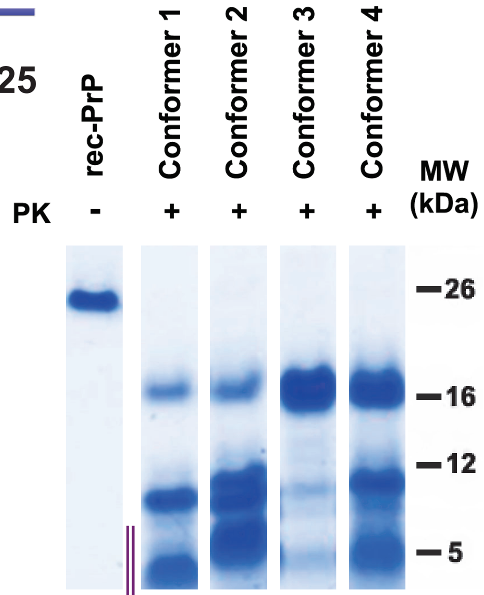
No deletions

No insertions

No polymorphic variants found



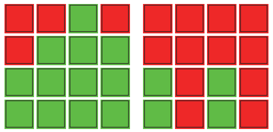
25



224 AA

4

Conformers



Tm^{Exp}: ND

ΔΔG: -3.35

In vitro studies

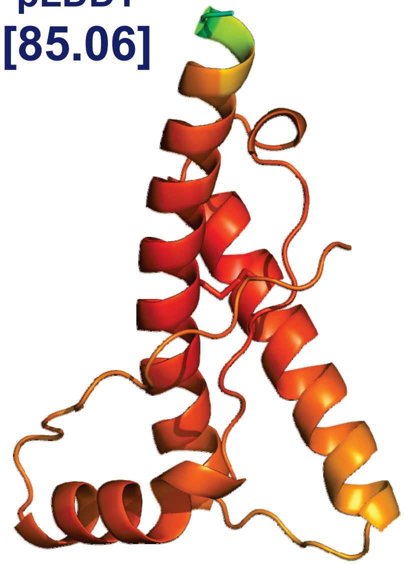
TgVole (1x)	Not tested
Spanish mole	Not tested

In vivo studies

TgVole (1x)	Not tested
Spanish mole	Not tested

pLDDT

[85.06]



Protein code: 3143

Gracile shrew mole

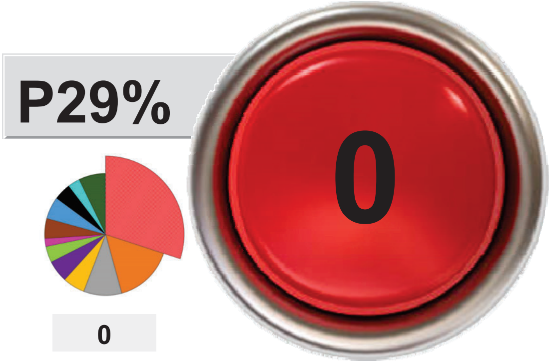
GenBank: BK063987

Uropsilus gracilis

Soricomorpha 7/12
Talpidae 4/6

Distinct primary sequence across species

P29%



β2-α2 LOOP
NNQNNF
164

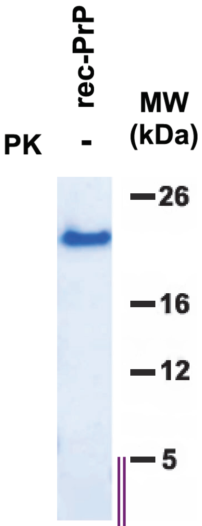
```
WNKPNKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCINQYQKEYQASYQRDAS-
    S    I                               M      W                                   I                     V M        VT     S  Y EGRS
```

PrP sequence differs by 9 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

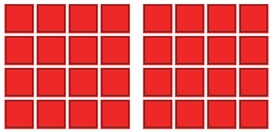
Tm^{Exp}: ND

ΔΔG: -5.6



215 AA

NO MISFOLDING



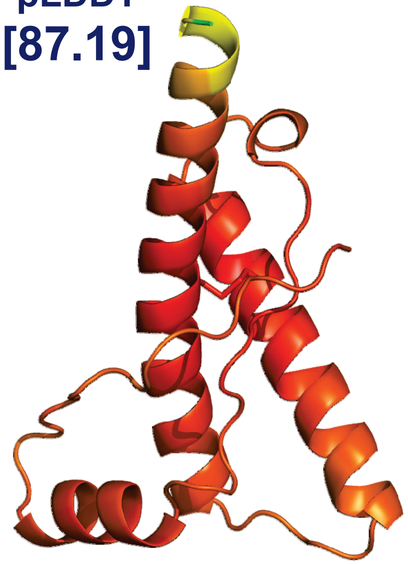
In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[87.19]



Protein code: 3144

Aardvark

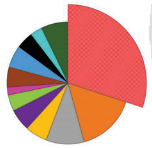
GenBank: AY133058

Orycteropus afer

Tubulidentata 0/1
Orycteropodidae 0/1

Distinct primary sequence across species

P29%



0

0

β2-α2 LOOP
SSENNF
8

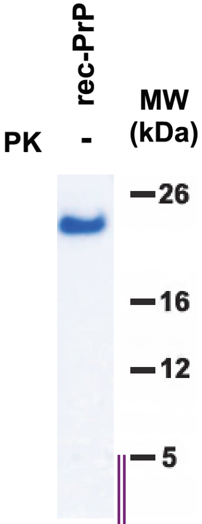
```
WNKPSKPKTNMKHVAGAAAAGAVVGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVNEYSSENNFVHDCVNITVKQHTTTTTTKGENFTETDIKIMERVVEQMCMTQYQKEFQAYQRGSS-
          I                          M      W         N           DQ NNQ             I    V                 V M         V      S   YE R S
```

PrP sequence differs by 15 amino acids from the bank vole PrP (see in red)

No deletions
No insertions
No polymorphic variants found

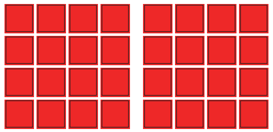
Tm^{Exp}: ND

ΔΔG: ND



212 AA

NO MISFOLDING



0
Conformers

In vitro studies

NOT APPLICABLE

In vivo studies

NOT APPLICABLE

pLDDT
[92.56]

Protein code: 4930