ClustAlignPy

Multiple protein sequence alignment

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M2BI
Programmation 3 - Projet court

Introduction

Multiple Sequence Alignment (MSA)

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➔ Identification de motifs conservés

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➔ Identification de motifs conservés

➔ Analyse phylogénétique

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Multiple Sequence Alignment (MSA)

➔   Identification de motifs conservés

➔   Analyse phylogénétique

➔   Prédiction de structures protéiques

Introduction

Multiple Sequence Alignment (MSA)
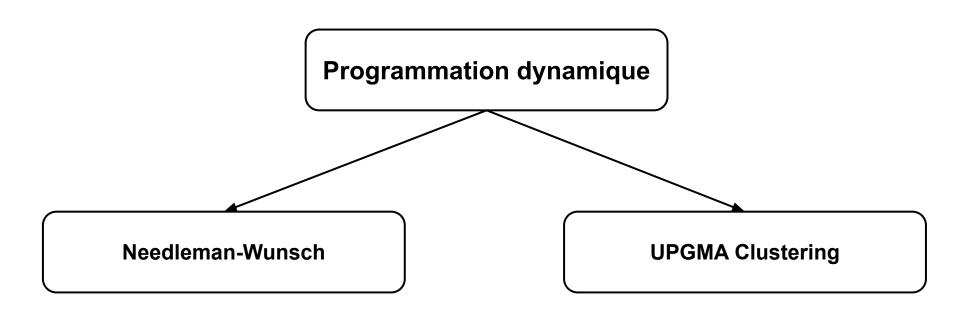
➔ Identification de motifs conservés

➔ Analyse phylogénétique

➔ Prédiction de structures protéiques

Processus Complexe et coûteux

Multiple Sequence Alignment (MSA)

Programmation dynamique

Needleman-Wunsch

UPGMA Clustering

Desmond G Higgins and Paul M Sharp. "Fast and sensitive multiple sequence alignments on a microcomputer". In:
Comput Appl Biosci 5.2 (Apr. 1989)

Matériels et Méthodes

- Matrice de substitution : BLOSUM 62

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- Pénalité de Gap fixe = -8.

Matériels et Méthodes

- Matrice de substitution : BLOSUM 62.

- Pénalité de Gap fixe = -8.

- Le match score est privilégié.

Matériels et Méthodes

Trois grandes étapes :

1 - Alignement par pair

```
>Seq1
TWDKATACPWPWGCG
>Seq2
TWPDKTTGCPC
>Seq3
AFTWSMTATGCWPT
```

```
>Seq1
TWDKATACPWPWGCG
>Seq2
TWPDKTTGCPC
>Seq3
AFTWSMTATGCWPT
```

Alignement deux à deux

two_seq_align()

pairwise_alignment_matrix()

>Seq1
TWDKATACPWPWGCG
>Seq2
TWPDKTTGCPC
>Seq3
AFTWSMTATGCWPT

two__seq_align()

pairwise_alignment_matrix()

Alignement deux à deux

	Seq1	Seq2	Seq3
Seq1	Nan	9	17
Seq2	Nan	Nan	25
Seq3	Nan	Nan	Nan

Matrice de score

14

distance = 1 - score_normalisé

score_to_distance()

Transformation en matrice de distance

	Seq1	Seq2	Seq3
Seq1	Nan	1	0.39
Seq2	Nan	Nan	0
Seq3	Nan	Nan	Nan

Matériels et Méthodes

Trois grandes étapes :

> 1 - Alignement par pair

> 2 - Clustering UPGMA

	Seq1	Seq2	Seq3
Seq1	Nan	1	0.39
Seq2	Nan	Nan	0
Seq3	Nan	Nan	Nan
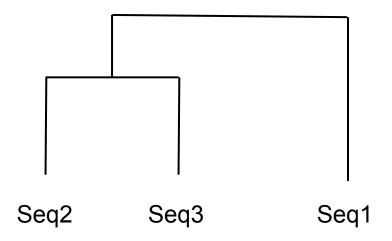
	Seq1	Seq2	Seq3
Seq1	Nan	1	0.39
Seq2	Nan	Nan	0
Seq3	Nan	Nan	Nan

$$d_{(C_i, C_j)} = \frac{|C_i| \cdot d_{(C_i, C_k)} + |C_j| \cdot d_{(C_j, C_k)}}{|C_i| + |C_j|}$$

upgma()

	(Seq2, Seq3)	Seq1
(Seq2, Seq3)	Nan	0.25
Seq3	Nan	Nan

Clustering UPGMA

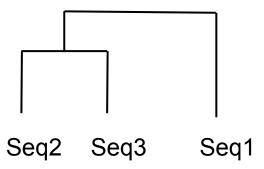# Matériels et Méthodes

Trois grandes étapes :

1 - Alignement par pair
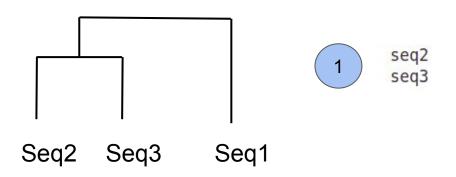
2 - Clustering UPGMA

3 - Alignement multiple

Alignement multiple

Seq2   Seq3   Seq1
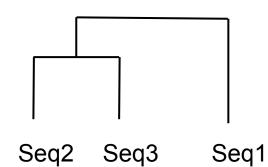
Alignement multiple


```
     seq2    --TWPDKTTGC-PC 11
  1  seq3    AFTWSMTATGCWPT 14
```

Seq2   Seq3   Seq1

Alignement multiple


```
     seq2   --TWPDKTTGC-PC  11
  1  seq3   AFTWSMTATGCWPT  14
```

multi_seq_align()

```
     seq2   --TWPDKTTGC--P--C-  11
  2  seq3   AFTWSMTATGC-WP--T-  14
     seq1   --TW-DKATACPWPWGCG  15
```

Results

1   **Aligner une séquence sur elle même**

Results

(1) **Aligner une séquence sur elle même**

ClustAlignPy

```
sp|P81026-0|GLUC1_ORENI        HSEGTFSNDYSKYLEDRKAQDFVRWLMNNKRSGAAE 36
sp|P81026-1|GLUC1_ORENI        HSEGTFSNDYSKYLEDRKAQDFVRWLMNNKRSGAAE 36
```

- Scores calculés correctement
- Traçage de l'alignement optimal est correcte

Results

2 **Tropomyosine : Alignement de 3 isoformes (~250 aa)**

Results

2 **Tropomyosine : Alignement de 3 isoformes (~250 aa)**

ClustAlignPy

```
sp|P06753-2|Isoform_2     -MAGI-TTIEAVK-RKIQVL-Q-QQAD-D---AEERA---E-RL---QREVEG---E--R-----R-A--  41
sp|P06753-3|Isoform_3     -MAGI-TTIEAVK-RKIQVL-Q-QQAD-D---AEERA---E-RL---QREVEG---E--R-----R-A--  41
sp|P06753|TPM3_HUMAN      MMEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTEDELDKYSEALKDAQE  70

sp|P06753-2|Isoform_2     R-E--Q-----AEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 103
sp|P06753-3|Isoform_3     R-E--Q-----AEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 103
sp|P06753|TPM3_HUMAN      KLELAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 140

sp|P06753-2|Isoform_2     KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESRCREMDEQIRLMDQNLKCLSA 173
sp|P06753-3|Isoform_3     KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESRCREMDEQIRLMDQNLKCLSA 173
sp|P06753|TPM3_HUMAN      KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESKCSELEEELKNVTNNLKSLEA 210

sp|P06753-2|Isoform_2     AEEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDKLKCTKEEHLCTQRMLDQTLL 243
sp|P06753-3|Isoform_3     AEEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEERLYSQLERNRLLSNELKLTLH 243
sp|P06753|TPM3_HUMAN      QAEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALN 280

sp|P06753-2|Isoform_2     DLNEM 248
sp|P06753-3|Isoform_3     DLCD- 247
sp|P06753|TPM3_HUMAN      DMTSI 285

Execution time: 3.08 seconds
```

Results

2 **Tropomyosine : Alignement de 3 isoformes (~250 aa)**

ClustAlignPy

```
sp|P06753-2|Isoform_2    -MAGI-TTIEAVK-RKIQVL-Q-QQAD-D---AEERA---E-RL---QREVEG---E--R-----R-A-- 41
sp|P06753-3|Isoform_3    -MAGI-TTIEAVK-RKIQVL-Q-QQAD-D---AEERA---E-RL---QREVEG---E--R-----R-A-- 41
sp|P06753|TPM3_HUMAN     MMEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTEDELDKYSEALKDAQE 70

sp|P06753-2|Isoform_2    R-E--Q-----AEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 103
sp|P06753-3|Isoform_3    R-E--Q-----AEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 103
sp|P06753|TPM3_HUMAN     KLELAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 140

sp|P06753-2|Isoform_2    KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESRCREMDEQIRLMDQNLKCLSA 173
sp|P06753-3|Isoform_3    KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESRCREMDEQIRLMDQNLKCLSA 173
sp|P06753|TPM3_HUMAN     KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESKCSELEEELKNVTNNLKSLEA 210

sp|P06753-2|Isoform_2    AEEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDKLKCTKEEHLCTQRMLDQTLL 243
sp|P06753-3|Isoform_3    AEEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEERLYSQLERNRLLSNELKLTLH 243
sp|P06753|TPM3_HUMAN     QAEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALN 280

sp|P06753-2|Isoform_2    DLNEM 248
sp|P06753-3|Isoform_3    DLCD- 247
sp|P06753|TPM3_HUMAN     DMTSI 285
```

Execution time: 3.08 seconds

Results

2

Tropomyosine : Alignement de 3 isoformes (~250 aa)

ClustAlignPy

```
sp|P06753-2|Isoform_2    -MAGI-TTIEAVK-RKIQVL-Q-QQAD-D---AEERA---E-RL---QREVEG---E--R-----R-A-- 41
sp|P06753-3|Isoform_3    -MAGI-TTIEAVK-RKIQVL-Q-QQAD-D---AEERA---E-RL---QREVEG---E--R-----R-A-- 41
sp|P06753|TPM3_HUMAN     MMEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTEDELDKYSEALKDAQE 70


sp|P06753-2|Isoform_2    R-E--Q-----AEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 103
sp|P06753-3|Isoform_3    R-E--Q-----AEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 103
sp|P06753|TPM3_HUMAN     KLELAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 140


sp|P06753-2|Isoform_2    KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESRCREMDEQIRLMDQNLKCLSA 173
sp|P06753-3|Isoform_3    KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESRCREMDEQIRLMDQNLKCLSA 173
sp|P06753|TPM3_HUMAN     KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESKCSELEEELKNVTNNLKSLEA 210


sp|P06753-2|Isoform_2    AEEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDKLKCTKEEHLCTQRMLDQTLL 243
sp|P06753-3|Isoform_3    AEEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEERLYSQLERNRLLSNELKLTLH 243
sp|P06753|TPM3_HUMAN     QAEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALN 280


sp|P06753-2|Isoform_2    DLNEM 248
sp|P06753-3|Isoform_3    DLCD- 247
sp|P06753|TPM3_HUMAN     DMTSI 285


Execution time: 3.08 seconds
```

Results

② **Tropomyosine : Alignement de 3 isoformes (~250 aa)**

ClustAlignPy

```
sp|P06753-2|Isoform_2    -MAGI-TTIEAVK-RKIQVL-Q-QQAD-D---AEERA---E-RL---QREVEG---E--R-----R-A-- 41
sp|P06753-3|Isoform_3    -MAGI-TTIEAVK-RKIQVL-Q-QQAD-D---AEERA---E-RL---QREVEG---E--R-----R-A-- 41
sp|P06753|TPM3_HUMAN     MMEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTEDELDKYSEALKDAQE 70

sp|P06753-2|Isoform_2    R-E--Q-----AEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 103
sp|P06753-3|Isoform_3    R-E--Q-----AEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 103
sp|P06753|TPM3_HUMAN     KLELAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 140

sp|P06753-2|Isoform_2    KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESRCREMDEQIRLMDQNLKCLSA 173
sp|P06753-3|Isoform_3    KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESRCREMDEQIRLMDQNLKCLSA 173
sp|P06753|TPM3_HUMAN     KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESKCSELEEELKNVTNNLKSLEA 210

sp|P06753-2|Isoform_2    AEEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDKLKCTKEEHLCTQRMLDQTLL 243
sp|P06753-3|Isoform_3    AEEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEERLYSQLERNRLLSNELKLTLH 243
sp|P06753|TPM3_HUMAN     QAEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALN 280

sp|P06753-2|Isoform_2    DLNEM 248
sp|P06753-3|Isoform_3    DLCD- 247
sp|P06753|TPM3_HUMAN     DMTSI 285
```

Execution time: 3.08 seconds

Results

2 **Tropomyosine : Alignement de 3 isoformes (~250 aa)**

ClustAlignPy

```
sp|P06753-2|Isoform_2    -MAGI-TTIEAVK-RKIQVL-Q-QQAD-D---AEERA---E-RL---QREVEG---E--R-----R-A-- 41
sp|P06753-3|Isoform_3    -MAGI-TTIEAVK-RKIQVL-Q-QQAD-D---AEERA---E-RL---QREVEG---E--R-----R-A-- 41
sp|P06753|TPM3_HUMAN     MMEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTEDELDKYSEALKDAQE 70

sp|P06753-2|Isoform_2    R-E--Q-----AEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 103
sp|P06753-3|Isoform_3    R-E--Q-----AEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 103
sp|P06753|TPM3_HUMAN     KLELAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENRALKDEE 140

sp|P06753-2|Isoform_2    KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESRCREMDEQIRLMDQNLKCLSA 173
sp|P06753-3|Isoform_3    KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESRCREMDEQIRLMDQNLKCLSA 173
sp|P06753|TPM3_HUMAN     KMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERTEERAELAESKCSELEEELKNVTNNLKSLEA 210

sp|P06753-2|Isoform_2    AEEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDKLKCTKEEHLCTQRMLDQTLL 243
sp|P06753-3|Isoform_3    AEEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEERLYSQLERNRLLSNELKLTLH 243
sp|P06753|TPM3_HUMAN     QAEKYSQKEDKYEEEIKILTDKLKEAETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALN 280

sp|P06753-2|Isoform_2    DLNEM 248
sp|P06753-3|Isoform_3    DLCD- 247
sp|P06753|TPM3_HUMAN     DMTSI 285
```

Execution time: 3.08 seconds

Results

2 **Tropomyosine : Alignement de 3 isoformes (~250 aa)**

Clustal 0(1.2.4)

```
sp|P06753|TPM3_HUMAN     -----MMEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTE 55
sp|P06753-2|Isoform_2    MAGITTIEAVKRKIQVLQQQADD------------------------------------- 23
sp|P06753-3|Isoform_3    MAGITTIEAVKRKIQVLQQQADD------------------------------------- 23
                             :**:*:*:*:*: : ::

sp|P06753|TPM3_HUMAN     DELDKYSEALKDAQEKLELAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 115
sp|P06753-2|Isoform_2    -----AEERAERLQREVEGERRAREQAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 78
sp|P06753-3|Isoform_3    -----AEERAERLQREVEGERRAREQAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 78
                             .*  :  *.::*  .:   :*****************************

sp|P06753|TPM3_HUMAN     EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 175
sp|P06753-2|Isoform_2    EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 138
sp|P06753-3|Isoform_3    EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 138
                         ***********************************************************

sp|P06753|TPM3_HUMAN     DLERTEERAELAESKCSELEEELKNVTNNLKSLEAQAEKYSQKEDKYEEEIKILTDKLKE 235
sp|P06753-2|Isoform_2    DLERTEERAELAESRCREMDEQIRLMDQNLKCLSAAEEKYSQKEDKYEEEIKILTDKLKE 198
sp|P06753-3|Isoform_3    DLERTEERAELAESRCREMDEQIRLMDQNLKCLSAAEEKYSQKEDKYEEEIKILTDKLKE 198
                         **************:* *::*::: : :***.*.*  ********************

sp|P06753|TPM3_HUMAN     AETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALNDMTSI    285
sp|P06753-2|Isoform_2    AETRAEFAERSVAKLEKTIDDLEDKLKCTKEEHLCTQRMLDQTLLDLNEM    248
sp|P06753-3|Isoform_3    AETRAEFAERSVAKLEKTIDDLEERLYSQLERNRLLSNELKLTLHDLCD-    247
                         **********************:.* .   .    .. *. :* *: .
```

Results

2 **Tropomyosine : Alignement de 3 isoformes (~250 aa)**

Clustal 0(1.2.4)

```
sp|P06753|TPM3_HUMAN      -----MMEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTE 55
sp|P06753-2|Isoform_2     MAGITTIEAVKRKIQVLQQQADD------------------------------------- 23
sp|P06753-3|Isoform_3     MAGITTIEAVKRKIQVLQQQADD------------------------------------- 23
                               :**:*:*:*:*:  :  : ::

sp|P06753|TPM3_HUMAN      DELDKYSEALKDAQEKLELAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 115
sp|P06753-2|Isoform_2     -----AEERAERLQREVEGERRAREQAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 78
sp|P06753-3|Isoform_3     -----AEERAERLQREVEGERRAREQAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 78
                              .*   :  *.::*   .:   :*****************************

sp|P06753|TPM3_HUMAN      EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 175
sp|P06753-2|Isoform_2     EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 138
sp|P06753-3|Isoform_3     EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 138
                          ***********************************************************

sp|P06753|TPM3_HUMAN      DLERTEERAELAESKCSELEEELKNVTNNLKSLEAQAEKYSQKEDKYEEEIKILTDKLKE 235
sp|P06753-2|Isoform_2     DLERTEERAELAESRCREMDEQIRLMDQNLKCLSAAEEKYSQKEDKYEEEIKILTDKLKE 198
sp|P06753-3|Isoform_3     DLERTEERAELAESRCREMDEQIRLMDQNLKCLSAAEEKYSQKEDKYEEEIKILTDKLKE 198
                          **************:* *::*::: : :***.*.*  *******************

sp|P06753|TPM3_HUMAN      AETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALNDMTSI    285
sp|P06753-2|Isoform_2     AETRAEFAERSVAKLEKTIDDLEDKLKCTKEEHLCTQRMLDQTLLDLNEM    248
sp|P06753-3|Isoform_3     AETRAEFAERSVAKLEKTIDDLEERLYSQLERNRLLSNELKLTLHDLCD-    247
                          **********************:.* .   .    .. *. :* *: .
```

Results

(2) **Tropomyosine : Alignement de 3 isoformes (~250 aa)**

Clustal 0(1.2.4)

```
sp|P06753|TPM3_HUMAN     -----MMEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTE 55
sp|P06753-2|Isoform_2    MAGITTIEAVKRKIQVLQQQADD------------------------------------- 23
sp|P06753-3|Isoform_3    MAGITTIEAVKRKIQVLQQQADD------------------------------------- 23
                          :**:*:*:*:*:  : ::
```

```
sp|P06753|TPM3_HUMAN     DELDKYSEALKDAQEKLELAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 115
sp|P06753-2|Isoform_2    -----AEERAERLQREVEGERRAREQAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 78
sp|P06753-3|Isoform_3    -----AEERAERLQREVEGERRAREQAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 78
                          .*  :  *.::*  .:   :***************************
```

```
sp|P06753|TPM3_HUMAN     EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 175
sp|P06753-2|Isoform_2    EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 138
sp|P06753-3|Isoform_3    EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 138
                         ***********************************************************
```

```
sp|P06753|TPM3_HUMAN     DLERTEERAELAESKCSELEEELKNVTNNLKSLEAQAEKYSQKEDKYEEEIKILTDKLKE 235
sp|P06753-2|Isoform_2    DLERTEERAELAESRCREMDEQIRLMDQNLKCLSAAEEKYSQKEDKYEEEIKILTDKLKE 198
sp|P06753-3|Isoform_3    DLERTEERAELAESRCREMDEQIRLMDQNLKCLSAAEEKYSQKEDKYEEEIKILTDKLKE 198
                         **************:* *::*::: : :***.*.*  ********************
```

```
sp|P06753|TPM3_HUMAN     AETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALNDMTSI      285
sp|P06753-2|Isoform_2    AETRAEFAERSVAKLEKTIDDLEDKLKCTKEEHLCTQRMLDQTLLDLNEM      248
sp|P06753-3|Isoform_3    AETRAEFAERSVAKLEKTIDDLEERLYSQLERNRLLSNELKLTLHDLCD-      247
                         **********************:.*  .   .. *. :* *:  .
```

Results

(2) **Tropomyosine : Alignement de 3 isoformes (~250 aa)**

Clustal 0(1.2.4)

⚠️ Gap affine

```
sp|P06753|TPM3_HUMAN     -----MMEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTE 55
sp|P06753-2|Isoform_2    MAGITTIEAVKRKIQVLQQQADD------------------------------------- 23
sp|P06753-3|Isoform_3    MAGITTIEAVKRKIQVLQQQADD------------------------------------- 23
                              :**:*:*:*:*:  :  : ::

sp|P06753|TPM3_HUMAN     DELDKYSEALKDAQEKLELAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 115
sp|P06753-2|Isoform_2    -----AEERAERLQREVEGERRAREQAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 78
sp|P06753-3|Isoform_3    -----AEERAERLQREVEGERRAREQAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 78
                             .*  :  *.::*  .:   :*************************************

sp|P06753|TPM3_HUMAN     EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 175
sp|P06753-2|Isoform_2    EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 138
sp|P06753-3|Isoform_3    EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 138
                         ***********************************************************

sp|P06753|TPM3_HUMAN     DLERTEERAELAESKCSELEEELKNVTNNLKSLEAQAEKYSQKEDKYEEEIKILTDKLKE 235
sp|P06753-2|Isoform_2    DLERTEERAELAESRCREMDEQIRLMDQNLKCLSAAEEKYSQKEDKYEEEIKILTDKLKE 198
sp|P06753-3|Isoform_3    DLERTEERAELAESRCREMDEQIRLMDQNLKCLSAAEEKYSQKEDKYEEEIKILTDKLKE 198
                         **************:* *::*::: : :***.*.*  *******************

sp|P06753|TPM3_HUMAN     AETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALNDMTSI  285
sp|P06753-2|Isoform_2    AETRAEFAERSVAKLEKTIDDLEDKLKCTKEEHLCTQRMLDQTLLDLNEM  248
sp|P06753-3|Isoform_3    AETRAEFAERSVAKLEKTIDDLEERLYSQLERNRLLSNELKLTLHDLCD-  247
                         *********************:.*  .   .   .. *. :* *: .
```

Results

⚠️ Gap fixe

(2) **Tropomyosine : Alignement de 3 isoformes**

Clustal 0(1.2.4)

⚠️ Gap affine

```
sp|P06753|TPM3_HUMAN     -----MMEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKKLKGTE 55
sp|P06753-2|Isoform_2    MAGITTIEAVKRKIQVLQQQADD------------------------------------- 23
sp|P06753-3|Isoform_3    MAGITTIEAVKRKIQVLQQQADD------------------------------------- 23
                            :**:*:*:*:*:  :  : ::

sp|P06753|TPM3_HUMAN     DELDKYSEALKDAQEKLELAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 115
sp|P06753-2|Isoform_2    -----AEERAERLQREVEGERRAREQAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 78
sp|P06753-3|Isoform_3    -----AEERAERLQREVEGERRAREQAEAEVASLNRRIQLVEEELDRAQERLATALQKLE 78
                             .*   :  *.::*  .:   :*****************************

sp|P06753|TPM3_HUMAN     EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 175
sp|P06753-2|Isoform_2    EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 138
sp|P06753-3|Isoform_3    EAEKAADESERGMKVIENRALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEG 138
                         ***********************************************************

sp|P06753|TPM3_HUMAN     DLERTEERAELAESKCSELEEELKNVTNNLKSLEAQAEKYSQKEDKYEEEIKILTDKLKE 235
sp|P06753-2|Isoform_2    DLERTEERAELAESRCREMDEQIRLMDQNLKCLSAAEEKYSQKEDKYEEEIKILTDKLKE 198
sp|P06753-3|Isoform_3    DLERTEERAELAESRCREMDEQIRLMDQNLKCLSAAEEKYSQKEDKYEEEIKILTDKLKE 198
                         **************:* *::*::: : :***.*.*  ******************

sp|P06753|TPM3_HUMAN     AETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALNDMTSI   285
sp|P06753-2|Isoform_2    AETRAEFAERSVAKLEKTIDDLEDKLKCTKEEHLCTQRMLDQTLLDLNEM   248
sp|P06753-3|Isoform_3    AETRAEFAERSVAKLEKTIDDLEERLYSQLERNRLLSNELKLTLHDLCD-   247
                         *********************:.*  .   .   .. *. :* *:  .
```

Results

3 **Collagène : Alignement de 10 isoformes (~ 600-900 aa)**

Results

③ Collagène : Alignement de 10 isoformes (~ 600-900 aa)

ClustAlignPy

```
sp|P25067|CO8A2_HUMAN    YLEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGMGKPGLHGQPGPAGPPGFSRMGKAGPPGLPG 132
NP_005193.1              YLEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGMGKPGLHGQPGPAGPPGFSRMGKAGPPGLPG 132
XP_022283551.1           YLEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMGKAGPPGLPG 127
XP_004472303.2           HLEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMGKAGPPGLPG 133
XP_036767792.2           YLEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGMGKPGLHGQPGPAGPPGFSRMGKAGPPGLPG 135
XP_067581583.1           LKEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMGKAGPPGLPG 117
XP_032509941.1           LKEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMGKAGPPGLPG 117
XP_005353298.3           YLEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMGKAGPPGLPG 176
XP_034505092.1           ---MPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMGKAGPPGLPG 67
XP_030679284.1           YLEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMGKAGPPGLPG 350


sp|P25067|CO8A2_HUMAN    KVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGITIPGKPGAQGVPGPPGFQGEPGPQGEPGPPGDR 202
NP_005193.1              KVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGITIPGKPGAQGVPGPPGFQGEPGPQGEPGPPGDR 202
XP_022283551.1           KAGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGIAVPGKPGPQGVPGPPGFGGEPGPQGEPGPPGDR 197
XP_004472303.2           KTGPPGQPGPQGEPGIRGHQGLRGPPGTPGLPGPSGIAVPGKPGPQGVPGPPGFRGEPGTHGEPGPPGDR 203
XP_036767792.2           KVGSPGQPGLRGEPGIQGDQGLRGPPGPPGLPGPSGIAVPGKPGPQGIPGPPGFRGEPGPQGEPGPPGDR 205
XP_067581583.1           KVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGIAVPGKPGPQGVPGPPGFGGEPGPQGEPGPPGDR 187
XP_032509941.1           KVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGIAVPGKPGPQGVPGPPGFGGEPGPQGEPGPPGDR 187
XP_005353298.3           KVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGITVPGKPGAQGMPGPPGFRGEPGPQGEPGPRGDR 246
XP_034505092.1           KAGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGIAVPGKPGPQGVPGPPGFGGEPGPQGEPGPPGDR 137
XP_030679284.1           KVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGITIPGKPGAQGVPGPPGFQGEPGPQGEPGPPGDR 420


sp|P25067|CO8A2_HUMAN    GLKGDNGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDGLPGAPGDKGESGPPGVPGPRGEPGAVGPK 272
NP_005193.1              GLKGDNGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDGLPGAPGDKGESGPPGVPGPRGEPGAVGPK 272
XP_022283551.1           GLKGDNGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDGLPGAPGDKGESGPPGVPGPRGEPGALGPK 267
XP_004472303.2           GLKGDNGVGQPGLPGPPGQGGAPGPPGLPGPAGMGKPGLDGLPGAPGDKGESGAPGVPGPSGEPGAVGPK 273
XP_036767792.2           GLKGDNGVGQPGLPGTPGQGGAPGPPGLPGPAGPDKGESGLPGVPGPRGEPGDLGPK 275
XP_067581583.1           GLKGENGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDGFPGAPGDKGESGPPGLPGPRGEPGALGPK 257
XP_032509941.1           GLKGENGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDGFPGAPGDKGESGPPGLPGPRGEPGALGPK 257
XP_005353298.3           GLKGDTGVGQPGLPGAPGQTGAPGPPGLPGPAGLGKPGLDGIPGAPGDKGDSGPPGVPGSRGEPGVMGPK 316
XP_034505092.1           GLKGDNGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDGLPGAPGDKGESGPPGVPGPRGEPGAVGPK 207
XP_030679284.1           GLKGDNGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDGLPGAPGDKGESGPPGVPGPRGEPGAVGPK 490
```

Clustal 0(1.2.4)

```
XP_036767792.2           LEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGMGKPGLHGQPGPAGPPGFSRMG 126
XP_005353298.3           LEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMG 167
XP_004472303.2           LEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMG 124
XP_067581583.1           KEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMG 108
XP_032509941.1           KEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMG 108
sp|P25067|CO8A2_HUMAN    LEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGMGKPGLHGQPGPAGPPGFSRMG 123
NP_005193.1              LEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGMGKPGLHGQPGPAGPPGFSRMG 123
XP_030679284.1           LEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMG 341
XP_034505092.1           --MPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMG 58
XP_022283551.1           LEMPLPLLPMDLKGEPGPPGKPGPRGPPGPPGFPGKPGTGKPGLHGQPGPAGPPGFSRMG 118
                         ***************************************** *******************


XP_036767792.2           KAGPPGLPGKVGSPGQPGLRGEPGIQGDQGLRGPPGPPGLPGPSGIAVPGKPGPQGIPGP 186
XP_005353298.3           KAGPPGLPGKVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGITVPGKPGAQGMPGP 227
XP_004472303.2           KAGPPGLPGKTGPPGQPGPQGEPGIRGHQGLRGPPGTPGLPGPSGIAVPGKPGPQGVPGP 184
XP_067581583.1           KAGPPGLPGKVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGIAVPGKPGPQGVPGP 168
XP_032509941.1           KAGPPGLPGKVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGIAVPGKPGPQGVPGP 168
sp|P25067|CO8A2_HUMAN    KAGPPGLPGKVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGITIPGKPGAQGVPGP 183
NP_005193.1              KAGPPGLPGKVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGITIPGKPGAQGVPGP 183
XP_030679284.1           KAGPPGLPGKVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGITIPGKPGAQGVPGP 401
XP_034505092.1           KAGPPGLPGKVGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGIAVPGKPGPQGVPGP 118
XP_022283551.1           KAGPPGLPGKAGPPGQPGLRGEPGIRGDQGLRGPPGPPGLPGPSGIAVPGKPGPQGVPGP 178
                         **********.* ***** :*****:*.******** ********** ::***** **:***


XP_036767792.2           PGFRGEPGPQGEPGPPGDRGLKGDNGVGQPGLPGTPGQGGAPGPPGLPGPAGLGKPGLDG 246
XP_005353298.3           PGFRGEPGPQGEPGPRGDRGLKGDTGVGQPGLPGAPGQTGAPGPPGLPGPAGLGKPGLDG 287
XP_004472303.2           PGFRGEPGTHGEPGPPGDRGLKGDNGVGQPGLPGPPGQGGAPGPPGLPGPAGMGKPGLDG 244
XP_067581583.1           PGFGGEPGPQGEPGPPGDRGLKGENGVGQPGFPGAPGQGGAPGPPGLPGPAGLGKPGLDG 228
XP_032509941.1           PGFGGEPGPQGEPGPPGDRGLKGENGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDG 228
sp|P25067|CO8A2_HUMAN    PGFQGEPGPQGEPGPPGDRGLKGDNGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDG 243
NP_005193.1              PGFQGEPGPQGEPGPPGDRGLKGDNGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDG 243
XP_030679284.1           PGFQGEPGPQGEPGPPGDRGLKGDNGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDG 461
XP_034505092.1           PGFGGEPGPQGEPGPPGDRGLKGDNGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDG 178
XP_022283551.1           PGFGGEPGPQGEPGPPGDRGLKGDNGVGQPGLPGAPGQGGAPGPPGLPGPAGLGKPGLDG 238
                         *** **** :***** *******:.*******:** *** *********::*******:******
```

Results

3

Collagène : Alignement de 10 isoformes (~ 600-900 aa)

ClustAlignPy

```
sp|P25067|CO8A2_HUMAN   --------------------------------------------------P----L----------------- 8
NP_005193.1             --------------------------------------------------P----L----------------- 8
XP_022283551.1          --------------------------------------------------P----L----------------- 5
XP_004472303.2          --------------------------------------------------P----L------------F-- 9
XP_036767792.2          --------------------------------------------------P----L--S----------L-- 10
XP_067581583.1          --------------------------------------------------------L----------------- 3
XP_032509941.1          --------------------------------------------------------L----------------- 3
XP_005353298.3          --P------------------------A----E----------P--L-VL-VA----G--------LV- 35
XP_034505092.1          --------------------------------------------------------------------------- 0
XP_030679284.1          RRPSRGSGGRGGVGRAARERVCGGGSAWVSGREAAVRGRAGRAGPGGAPALAVAVERGGRRPRPDAPLLP 140

sp|P25067|CO8A2_HUMAN   ----------------------------------S--S---L--------------L----- 12
NP_005193.1             ----------------------------------S--S---L--------------L----- 12
XP_022283551.1          ----------------------------------A--------------------L----- 7
XP_004472303.2          ----------------------------------P--P---P-----------------P-------- 13
XP_036767792.2          ----------------------------------L--P---P--------------P----- 14
XP_067581583.1          ----------------------------------T-------------------------- 4
XP_032509941.1          ----------------------------------T-------------------------- 4
XP_005353298.3          ----------------------T-----------P--S---P-S---------------LC-------- 42
XP_034505092.1          --------------------------------------------------------------------------- 0
XP_030679284.1          PAHSGSRKGPPAERRGTPPARTPDPDAARPAADAPARSPRRPGSPRGPGAAPGGRARRPCLCWELPRPLR 210

sp|P25067|CO8A2_HUMAN   -------L------L--L---LV-LVLGCGPRASSGGGAGGAAGYAPVKYIQPMQKGPVGPPFREGKGQ 62
NP_005193.1             -------L------L--L---LV-LVLGCGPRASSGGGAGGAAGYAPVKYIQPMQKGPVGPPFREGKGQ 62
XP_022283551.1          -------L------P--L---LP-LLLGCGPRAATGGGAGGAAGYAPVKYVQPMHKGPAGPPFREGKGQ 57
XP_004472303.2          -------P------L--L---LL-LLLGSGLRAASGGGAGGAAGYAPVKHVQPMQKGPVGPPFREGKGQH 63
XP_036767792.2          -------S------L--LP--VL-LVLGFSPRAATSGGASAAAGYAPVKYIQPMQKGPVGPPFREGKGQ 65
XP_067581583.1          -------R------L--I---LS-SALR-S-KNCSH-GIDQEA-EAQTTEVTAGLVS-AG-TFR-GPSD 47
XP_032509941.1          -------R------L--I---LS-SALR-S-KNCSH-GIDQEA-EAQTTEVTAGLVS-AG-TFR-GPSD 47
XP_005353298.3          --SASTEAMQG--APM-TLPSLLL-LLLGCGPRVSSGGGVGGAAGYAPVKYVQPRQKGPVGPPFREGKGQ 106
XP_034505092.1          --------------------------------------------------------------------------- 0
XP_030679284.1          PESTSTDAMRGTLTPLSSLLLLLLVLGCGPRASSGGGAGGAAGYAPVKYIQPMQKGPVGPPFREGKGQ 280
```

Clustal 0(1.2.4)

```
XP_036767792.2          --------------------------------------------------------------------------- 0
XP_005353298.3          --------------------------------MHS--------------------------------------- 3
XP_004472303.2          --------------------------------------------------------------------------- 0
XP_067581583.1          --------------------------------------------------------------------------- 0
XP_032509941.1          --------------------------------------------------------------------------- 0
sp|P25067|CO8A2_HUMAN   --------------------------------------------------------------------------- 0
NP_005193.1             --------------------------------------------------------------------------- 0
XP_030679284.1          LAVAVERGGRRPRPDAPLLPPAHSGSRKGPPAERRGTPPARTPDPDAARPAADAPARSPR 180
XP_034505092.1          --------------------------------------------------------------------------- 0
XP_022283551.1          --------------------------------------------------------------------------- 0

XP_036767792.2          -------------------------------------------------------------MRGALA 6
XP_005353298.3          --------GE-VYFQIPALEICFLITTEFPAEPLVLVAGLVTPSPSLCSASTEAMQGAPM 54
XP_004472303.2          -------------------------------------------------------------MRGAPT 6
XP_067581583.1          ----------------------------------------------------------------M 1
XP_032509941.1          ----------------------------------------------------------------M 1
sp|P25067|CO8A2_HUMAN   -----------------------------------------------------------MLGTLT 6
NP_005193.1             -----------------------------------------------------------MLGTLT 6
XP_030679284.1          RPGSPRGPGAAPGGGRARRPCLCWELPRPLRP---------------ESTSTDAMRGTLT 224
XP_034505092.1          --------------------------------------------------------------------------- 0
XP_022283551.1          -------------------------------------------------------------MRGP-- 4

XP_036767792.2          PLSLLPPPSLLPVLLVLGFSPRAATSGGASAAAGYAPVKYVQPMQKGPVGPPFREGKGQY 66
XP_005353298.3          -------TLPSLLLLLLGCGPRVSSGGGVGGAAGYAPVKYVQPRQKGPVGPPFREGKGQY 107
XP_004472303.2          PL--FPPPPPLLLLLLLGSGLRAASGGGAGGGAGYAPVKHVQPMQKGPVGPPFREGKGQH 64
XP_067581583.1          KL--TR-LILSSALRSKNCSHGIDQEA----------EAQTTEVTAGLVSAGTFRGPSDL 48
XP_032509941.1          KL--TR-LILSSALRSKNCSHGIDQEA----------EAQTTEVTAGLVSAGTFRGPSDL 48
sp|P25067|CO8A2_HUMAN   PL--SS-LLLLLLVLVLGCGPRASSGGGAGGAAGYAPVKYIQPMQKGPVGPPFREGKGQY 63
NP_005193.1             PL--SS-LLLLLLVLVLGCGPRASSGGGAGGAAGYAPVKYIQPMQKGPVGPPFREGKGQY 63
XP_030679284.1          PL--SS-LLLLLLVLVLGCGPRASSGGGAGGAAGYAPVKYIQPMQKGPVGPPFREGKGQY 281
XP_034505092.1          --------------------------------------------------------------------------- 0
XP_022283551.1          -----L-ALLPLLPLLLGCGPRAATGGGAGGAAGYAPVKYVQPMHKGPAGPPFREGKGQY 58
```

Results

3   **Collagène : Alignement de 10 isoformes (~ 600-900 aa)**

8 minutes !

```
Execution time: 447.53 seconds
```

Limitations

Limitations

- Pénalité de gap fixe -> ne représente pas la réalité biologique

Limitations

- Pénalité de gap fixe -> ne représente pas la réalité biologique

- Processus lent sur les grandes séquences / données

Merci pour votre attention !