

## Short Commentary

### Sea Star *Asterias Rubens* Fab Gene and Bioinformatic Data

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#### ABSTRACT

The *Asterias rubens* Fab gene was isolated in 2016. Its transcriptome was analyzed in bioinformatics according the method of Marchler-Bauer. Identities mainly with other sea star genomes were repertoried in the precedent report.

#### INTRODUCTION

The objective of this work is to analyze Fab DNA sequence from the sea star *Asterias rubens* (Asterids, Echinodermata) which belong to Invertebrates [1].

**Our Starting material is the following DNA sequence which is translated in 5'-3'**

```
CAGAGTACCAGGTGCTGTGTTGACATCAGCACTTT
CTGAATCCACCTCCATTGGTTGATCCACTTCCTCTT
CACTATAGTTGACGATTTGATATCAACACTGTCACC
TGTAAGCGCATCAACACCGCTTGTATATCAACAG
ACGATCTCCTTTGTGGATCCACTTTTTGATCGGTGG
ATAGAGGCGGAGTGGATGACTCCATCTTTGCTAAT
GTTTTGTCATCGGCTAATGTTGATGAACCTTTCTCA
GCTTTTACCTCGGCTTCACATCCACTGTTTGGTTTT
CTGATTTACGGAAACAGTTGATGTGCTTTTACTG
GATCCACTGACTTATCAGCCAATGTTCCCTGCGGAG
TTGTTGATGTACTTTGTTGAGAGATGGCTGTGAAGG
GATTTGTGGCGGGATCGAAGGAAGCTCCTAAGCCT
TCCTCCCCTGGGGTTGGCGTTTCTAGAAGCGAGGA
ATCTTTGGCATCTTCGAAACACAAGGGATGGTATGT
CCTGGAGTTGAACCTGACAGCATCTCAGTTTCCA
AACCTCTTCATCTTCATCAAAGAATTGCTCAAACGG
CTCATGACACAGAGAACACATCTCATCGCCAGTGA
CGTTTCCATCAATAGCCACACAGAGGATGCCATCTT
TATCAGTTTACTGCTGACGATCTCCTCAAAGA
AACTGCTCCTCTCTTCATCCACTTCGTTGATTTCTTC
AAAGTCCAACCACTGATCGACTTCATAGAACCACT
TCCTGGACTGAACAGCCTTCACTCCATCCTTCTCAC
GACGATTCTGACGGAAGTGCCAGTCCAGATGTTTC
CGATATCTGTCCATTTTCATCAATGACAAAGCGCATA
CCA
```

#### RESULTS

##### 1. Blastn original sequence Data base:

Standard data bases (nr.) have been used [2,3] and optimized for highly similar sequences (megablast)

The DNA molecule included a query length of 863

Among sequences producing significant alignments, 5 sequences were selected as shown in **Table 1**.

The graphic summary follows below **Figure 1**.

##### 2. BlastX original sequence:

As precedingly the Molecule type is DNA. The characteristics were the following:

- Query length: 863
- Genetic code: Standard
- Database: Non-redundant protein sequences (nr)
- Sequences producing significant alignments: more than 100 sequences were found as shown below in **Table 2**.

The graphic summary was resumed as shown below **Figure 2**.

#### Conclusion

No putative conserved domains as homologies with Ig domains have been found. Such homologies were detected with the Fc receptor gene from *Asterias rubens* [4].

In the present study alignment sequences present mainly analogies between Fc receptor genes and sophisticated proteins which belong especially to *Asterias rubens* (Protein Pcf11-like: 99, 19 %identities) or other starfishes at a less degree. **Table 2** corroborates these same results.

We retain Fab gene and Fc receptor gene exist in Echinodermata as it was already demonstrated in 2016.

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**Table 1.** Selection of Asterid sequences.

Description	Scientific name	Max score	Total score	Query cover	E. Value	Per. Ident	Acc Len	Accession
Predicted: <i>Asterias rubens</i> pre-mRNA cleavage complex 2 protein Pcf11-like (LOC117293273) mRNA	<i>Asterias rubens</i>	1555	1555	100%	0.0	99.19%	7600	XM_03377550/8.1
<i>Asterias rubens</i> genome assembly, chromosome 8	<i>Asterias rubens</i>	833	1576	100%	0.0	98.93%	21693562	LR699099.1
Predicted: <i>Acanthaster planci</i> uncharacterized LOC110976864 (LOC110976864), transcript variant X	<i>Acanthaster planci</i>	309	309	49%	4e-79	79.72%	9401	XM_022230513.1
Predicted: <i>Acanthaster planci</i> uncharacterized LOC110976864 (LOC110976864), transcript variant X	<i>Acanthaster planci</i>	309	309	49%	4e-79	99.29%	9455	XM_022230512.1
<i>Marthasterias glacialis</i> , genome assembly, chromosome: 10	<i>Marthasterias glacialis</i>	152	152	10%	6e-32	95.74%	25093327	OU452228.1

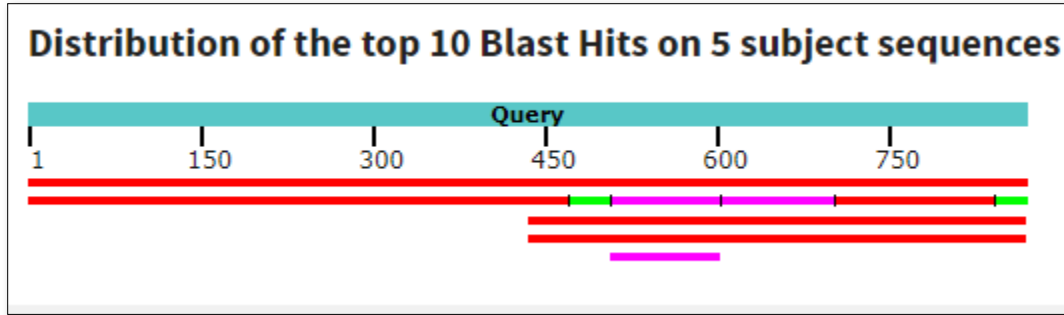


Figure 1. Selection of Asterid sequences.

Table 2. Alignment sequences.

Description	Scientific name	Max score	Total score	Query cover	E. Value	Per. Ident	Acc Len	Accession
Pre-mRNA cleavage complex 2 protein Pcf11-like [Asterias rubens]	<i>Asterias rubens</i>	536	536	99%	1e-171	98.61%	2426	XP_033631399.1
Uncharacterized protein LOC110976864 isoform X2 [Acanthaster planci]	<i>Acanthaster planci</i>	262	262	95%	2e-75	52.35%	2775	XP_022086205.1
Uncharacterized protein LOC110976864 isoform X1 [Acanthaster planci]	<i>Acanthaster planci</i>	262	262	95%	2e-75	52.35%	2793	XP_022086204.1
Low Quality Protein: pre-mRNA cleavage complex 2 protein Pcf11-like [Patiria miniata]	<i>Patiria miniata</i>	261	261	94%	5e-75	52.44%	2640	XP_038055691.1

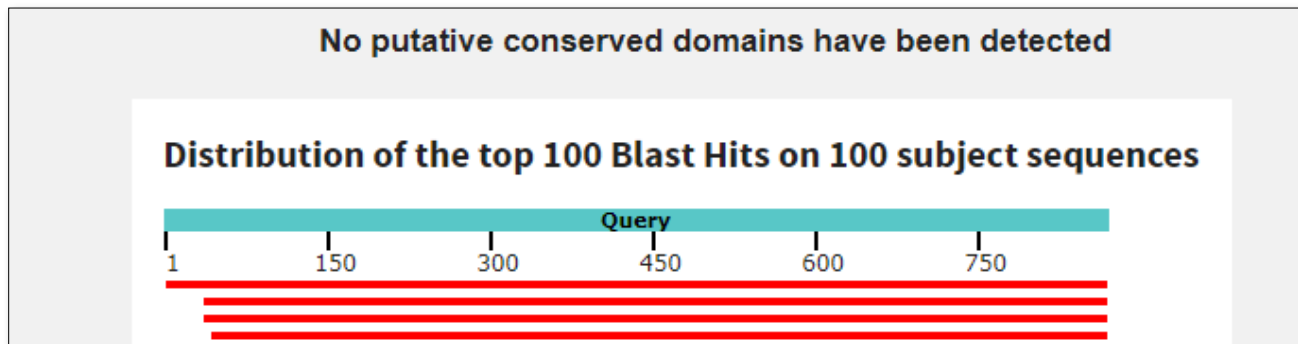


Figure 2. Alignment sequences.

## REFERENCES

1. Leclerc M, Kresdorn N (2016) Evidence of Fab Fragment Gene in an Invertebrate: The Sea Star *Asterias*. *Int J Biotech and Bioeng* 2(1): 37-38.
2. Marchler-Bauer A, Bo Y, Han L, He J, Lanczycki CJ, et al. (2017) CDD/SPARCLE: Functional classification of proteins via subfamily domain architectures. *Nucleic Acids Res* 45(D1): D200-D203.
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4. Leclerc M (2022) IJBA submitted.