

# Hla-E Gene from *Ophiocomina Nigra* (Echinodermata-Invertebrates). Bioinformatics Data

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## Abstract

HLA-E gene from MHC system has been recently discovered, in our laboratory, in Invertebrates. Blasts were performed against different species to find or not homologies. Results were given in the precedent communication.

## Introduction:

In 2020, we discovered for the first time, MHC genes in Invertebrates and particularly in Echinodermata [1, 2]. More recently, in 2022 a biosynthesis of HLA-E (ClassI, MHC) gene from *O.nigra* was performed [3]. The aim of this work is to analyse HLA-E DNA sequence.

## Material and Methods:

**Starting material: dna sequence of HLA-E transcriptome:**

```
TGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCG
GATCACGAGGTCAGGAGATCGAGACCATCCTGGCT
AACACAGTGAAACCCCGTCTCTACTAAAAATACAA
AAAATTAGCCGGGCGTGGTGGCGGGCGCCTGTAGT
CCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGC
GTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAG
ATCGCGCCACTGCACTCCAGCCTGGGCGACAGAGC
GAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAA
AA
```

## Results and conclusion

**1. Blastn original sequence:** Database: Standard databases were used

We also optimize for: Highly similar sequences (megablast)

We recall that Molecule type is dna

Its query length is 281

We find more than 100 sequences producing significant alignments

First results appear in the **table** below:



Table 1

Description	Scientific name	Max score	Total score	Query cover	E. Value	Per. Ident	Acc Len	Accession
Pan troglodytes chromosomes unknow clone CH251-153M19, complete sequence	Pan troglodytes	514	9982	100%	2e-141	99.64%	184578	AC280142.1
Pan troglodytes BAC clone CH251-501A13 from chromosomes unknow, complete sequence	Pan troglodytes	514	10636	100%	2e-141	99.64%	181275	AC185293.4
Homo sapiens clone RP11-92L24 from 2 from chromosomes unknow, complete sequence	Homo sapiens	514	2329	100%	9e-141	99.64%	137248	AC019051.8
Eukaryotic synthetic construct chromosome 13	Homo sapiens	508	1.314e+06	100%	9e-140	99.29%	960898 78	CP034516.1

2. **Blastn original sequence:** The Molecule type is again dna with a query length of 281

The Database which is used consists in: Non-redundant protein sequences (nr)

We obtain more than 100 sequences producing significant alignments

The table is recapitulated as following in **Table 2:**

Table 2

Description	Scientific name	Max score	Total score	Query cover	E. Value	Per. Ident	Acc Len	Accession
Hypothetical protein EGM_09670 [Macaca fascicularis]	Macaca fascicularis	149	149	91%	1e-44	91.86%	89	EHH59533.1
hCG2030582 [Homo sapiens]	Homo sapiens	135	135	90%	5e-39	83.53%	102	EAW48014.1
Low quality protein: histone demethylase UTY [Chlorocebus sabaeus]	Chlorocebus sabaeus	129	219	91%	7e-36	87.50%	166	XP_037863302.1
<u>hypothetical protein</u> CRU82_14500 [Staphylococcus aureus]	Staphylococcus aureus	124	124	71%	7e-35	92.54%	72	PGG78133.1

### Conclusion:

Results summarized in the 2 tables show homologies between the *Ophiocoma nigra* HLA-E gene and various proteins issued from *Staphylococcus aureus* to human Chromosome 13 which is sometimes implicated in human trisomy We note also a strong homology with *Macaca fascicularis*.: 91,86% of identity.

Mainly we retain that *O.nigra* HLA-E gene exists in” its own right” and in its amplification in plasmid [3].

### References:

1. Leclerc M. (2020) Evidence of MHC Class I and Class II Genes in Echinodermata. 2(1): 59-61.
2. Leclerc M. (2021) Biosynthesis « De Novo » of the Ophiurid *Ophiocoma Nigra* I $\gamma$  Gene.1(1): 1-4.
3. Leclerc M. (2022) Ophiurid *Ophiocoma Nigra* HLA-E Gene Synthesis in PUC-GW-KAN Plasmid or HLA-E Echinodermata Gene Biosynthesis « De Novo » in *E. Coli Senu Lato* Plasmid. J Virol Viral Dis 2(1).