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Research Article

# CDR (CDR<sub>1</sub>, CDR<sub>2</sub>, CDR<sub>3</sub>) Complementary-Determining Region Invertebrate Primitive Antibody from; Sea Star Modelization 3D with Human IGK

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### A B S T R A C T

CDR<sub>1</sub>, CDR<sub>2</sub>, CDR<sub>3</sub> determining regions were discovered in the IPA (Invertebrate Primitive Antibody) from sea star, for the first time, in an Invertebrate. Further more a modelization in 3D of this primitive antibody was given; it shares similar regions with IGKV1-5 human antibody.

**Keywords:** Invertebrates; sea star, CDR regions; IGKV1-5 human antibody

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### Introduction

10 years ago, we tried to clone, for the first time, the Asterias rubens sea star IGKappa gene by the use and the help of E. coli as amplifier<sup>1</sup>. It allowed, in a second time, to verify that

the Young Protein, or anti-HRP Protein recognizes the HRP antigen<sup>1,2</sup>.

In the present work we research Complementary Determining Regions called more briefly CDR<sub>1</sub>, CDR<sub>2</sub>, CDR<sub>3</sub> or Complementary-Determining Regions<sup>3,4</sup>.

First, anti-HRP sequence in nucleotids is given :

5'GGA TCC GGA GGA ATG CGTGGCAACATGGCGTCTATGGATGTTCTTCTT  
TGTCGTGGGATAACTTACAACGGAGTTGGCGATTACACGTTCGCG  
AGCAACCGTCGGACACTAGCGCGTGCAGGGGAGCACAGTGGTGCTTCAC  
TGCTCCGTTGAGCAGTACATAAACACCACGCCATCGTTGGTGGAGCCG  
TGACTCGGTACATGCCACAACAAAGACCTGAAACTGTCCAGTCTAAACA  
CCGACCAGCTCAAAGGTACTCGATTTCAGGCGACGCATCTGGGGGGAA  
TTCAACCTAAAATAGTGAACTTACCGCCACAGACGCCAGTTACCG  
CTGTCAGATG TAA GAA TTC3'

gga tcc gga gga atg cgt ggc aac atg gcg tct cta tgg atg ttc ttc ttt gtc gtg ggg  
G S G G M R G N M A S L W M F F F V V G

ata act tta caa ccg agt ttg gcg att tac acg ttt cgc gag caa ccg tcg gac act agc  
 I T L Q R S L A I Y T F R E Q P S D T S  
 gcg ttg cag ggg agc aca gtg gtg ctt cac tgc tcc gtt gag cag tac ata aac acc acg  
 A L Q G S T V V L H C S V E Q Y I N T T  
 gcc atc gtt tgg tgg agc cgt gac tgc atc agc cac aac gac ctg aaa ctg tcc  
 A I V W W S R D S V I S H N K D L K L S  
 agt cta aac acc gac cag ctc caa agg tac tcg att tca ggc gac gca tct cgg ggg gaa  
 S L N T D Q L Q R Y S I S G D A S R G E  
 ttc aac ctt aaa ata gtg aac ttt acc gec aca gac gec gec agt tac cgc tgt cag atg  
 F N L K I V N F T A T D A A S Y R C Q M  
 taa gaa ttc  
 - E F .

Or in Another way:

MRGNMASLWMFFFVVGITLQRSLAIYTFREQPSDTSALQGSTVVLHCSVEQYINTTAIVWWRSRDSVISHNKDLKLSSL-  
 NTDQLQRYSISGDASRGFNLKIVNFTATDAASYRCQMFA

## Results

2 Tables issued from IMGT resume the following analysis below: (**Tables 1,2**)

<https://www.imgt.org/3Dstructure-DB/cgi/DomainGapAlign.cgi> with default settings, 17/01/2024

IMGT/DomainGapAlign version: [4.10.3](#) (2021-12-06).

**Table 1:** Closest Reference Gene and Allele(s) from the IMGT V Domain Directory: (All Species).

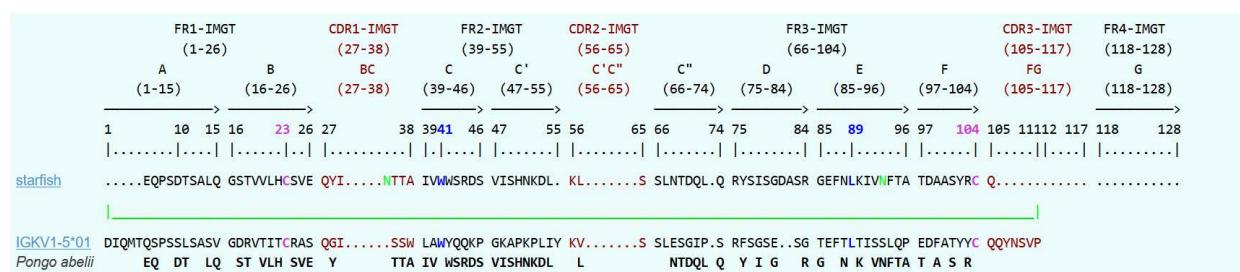
### • Closest reference gene and allele(s) from the IMGT V domain directory: (All species)

Species	Gene and allele	Domain	Domain label	Smith-Waterman score	% identity	Overlap	Show alignment
Pongo abelii	<a href="#">IGKV1-5*01</a>	1	V-KAPPA	121	33.3	90	<input checked="" type="radio"/>
Pongo pygmaeus	<a href="#">IGKV1-8*01</a>	1	V-KAPPA	121	33.3	90	<input type="radio"/>
Homo sapiens	<a href="#">IGKV1-5*03</a>	1	V-KAPPA	119	33.3	90	<input type="radio"/>
Homo sapiens	<a href="#">IGKV1-5*04</a>	1	V-KAPPA	119	33.3	90	<input type="radio"/>
Homo sapiens	<a href="#">IGKV1-5*05</a>	1	V-KAPPA	119	33.3	90	<input type="radio"/>

Species	Gene and allele	Domain	Domain label	Smith-Waterman score	% identity	Overlap
Pongo pygmaeus	<a href="#">IGKJ4*01</a>	1		7	100.0	1

**Table 2:** Alignments with the Closest Reference Gene and Allele(s) from the IMGT V Domain Directory: (All Species)

### • Alignment with the closest gene and allele from the IMGT V domain directory: (All species)



>starfish|IGKV1-5\*01|33.3||Pongo abelii

EQPSDTSALQ GSTVVLHCSVE QYI.....NTTA IVWWRSRDS VISHNKDL.KL.....SSLNTDQL.QRYSISGDASRGFNLKIVNF  
 TATDAASYRCQ.

The conserved amino acids (positions 23, 41, 89, 104) are found in the starfish sequence.

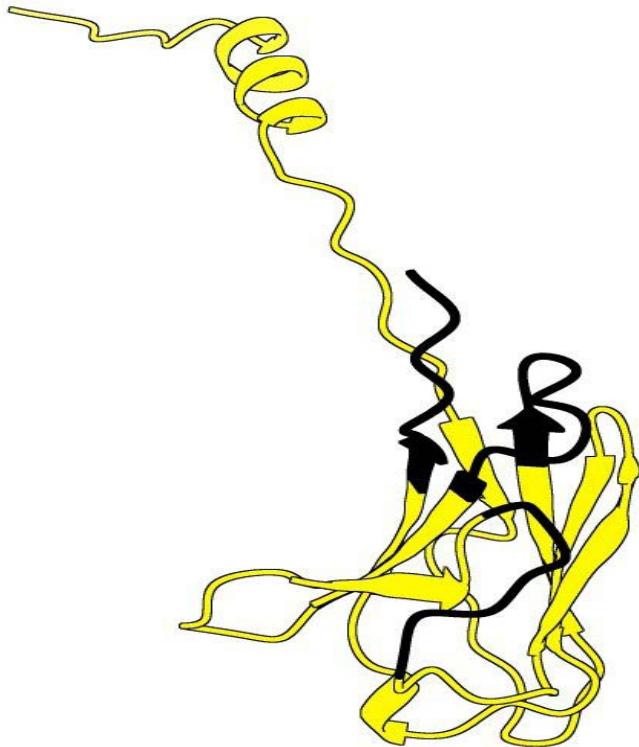
This molecule appears to have an IG AA sequence as seen from the above analysis.

If it aligns with the Pongo IGKV1-5, the percentage of alignment is 33%, so it is a sequence that seems to have similarities to an IGKV gene when it comes to conserved amino acids.

It appears clearly that CDR1 and CDR2 exist in the sea star primitive antibody and less clearly for CDR3 (1 amino acid which is conserved).

**Undoubtedly:** These new parameters corroborate the existence of an Invertebrate Primitive Antibody and NOT IG-LIKE as it is often said. We recall also the discovery by us of T and B sea star lymphocytes<sup>5</sup>. Humoral specific response<sup>6</sup>, Genomic data<sup>7</sup> with specially Invertebrate MHC genes.

ALL these elements assess the existence of an IPA : Invertebrate Primitive Antibody which shares strong sequence alignments(at least for CDR1 and CDR2) with the Primate : Pongo pygmaeus<sup>erences</sup>. More recently, in a work concerning Modelizations in 3D of the sea star anti-HRP protein, we found a CDR3 region (see below this modelization when compared to AlphaFold prediction of IGKV1-503 from Homo sapiens (**Figure 1**).



**CDR1**

**Figure 1:** Alpha Fold prediction of IGKV1-5\*03 Homo sapiens in black sea star CDR1, CDR2, CDR3(at the left) determining regions.

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