



# Mitochondrial DNA Part A

## DNA Mapping, Sequencing, and Analysis

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MITOGENOME ANNOUNCEMENT

**Complete mitochondrial genome of yellowfin goby  
(*Acanthogobius hasta*)**

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**Abstract**

Yellowfin goby (*Acanthogobius hasta*) belongs to the Perciformes Gobiidae. In this study, we sequenced the complete mitochondrial genome of *A. hasta*. The complete mitochondrial genome was determined to be 16,663 bp in length including 13 protein-coding genes, 22 transfer RNAs (tRNAs), 2 ribosomal RNAs (rRNAs) and 1 control region. The complete mitochondrial genome of *A. gueldenstaedti* provides basic genome data for relative studies on Acipenseriformes.

**Keywords**

*Acanthogobius hasta*, Gobiidae, mitochondrial genome, Perciformes

**History**

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*Acanthogobius hasta* is one of the species in the goby family. It is also well known with the common name yellowfin goby by people. The Gobiodei, which is one of the largest families of marine fishes and comprises more than 2000 species, is widely distributed all over the world. They form a big biological group, thus they play an important role in the marine environment. Besides, gobies exhibit significantly diverse morphological characteristics and habits, making them have a certain value in evolutionary biology (Sun, 2009). Previous study showed complete mitogenome in *Acanthogobius* genera of *A. hasta*, which was applicable to molecular phylogenetics in the suborder Gobiodei (Kima et al., 2004).

Our sample was collected from Bohai gulf, China. Total genomic DNA was extracted with the DNeasy Tissue Kit (Qiagen, Valencia, CA). Seven pairs of PCR primers were designed for amplification of the mitogenome sequence with previously reported method (Xu et al., 2014). We annotated the complete genome sequence using MitoAnnotator (Iwasaki et al., 2013).

The complete mitogenome of *A. hasta* (GenBank accession number KJ958906) was 16,663 bp in length containing 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and a control region (Table 1) which is a typical mitogenome structure of other vertebrates. The overall base composition of the full-sequence mitogenome was T 26.9%, C 27.9%, A 27.7%, and G 17.4%, with a slight A/T bias of 54.6%. The control region D-loop was located between tRNA<sup>Pro</sup> and tRNA<sup>Phe</sup> with 984 bp in length. ND6 and 8 tRNA genes were encoded on the L-strand and the rest were encoded on the H-strand.

Table 1. Characteristics of the mitochondrial genome of *A. hasta*.

Gene	Location		Size nucleotide (bp)	Codon		Intergenic nucleotide (bp)*	Strand†
	Start	End		Start	End		
tRNA <sup>Phe</sup>	1	68	68				H
12SrRNA	69	1010	942			0	H
tRNA <sup>Val</sup>	1012	1083	72			1	H
16SrRNA	1085	2774	2775			1	H
tRNA <sup>Leu</sup>	2775	2848	74			0	H
ND1	2849	3823	975	ATG	TAG	0	H
tRNA <sup>Ile</sup>	3827	3896	70			3	H
tRNA <sup>Gln</sup>	3896	3966	71			−1	L
tRNA <sup>Met</sup>	3966	4034	69			−1	H
ND2	4035	5081	1047	ATG	TAG	0	H
tRNA <sup>Trp</sup>	5081	5152	72			−1	H
tRNA <sup>Ala</sup>	5155	5224	70			2	L
tRNA <sup>Asn</sup>	5228	5301	74			3	L
tRNA <sup>Cys</sup>	5335	5401	67			33	L
tRNA <sup>Tyr</sup>	5402	5472	71			0	L
COX1	5474	7033	1560	ATG	TAA	1	H
tRNA <sup>Ser</sup>	7029	7099	71			−5	L
tRNA <sup>Asp</sup>	7103	7173	71			3	H
COX2	7175	7874	700	ATG	TAG	1	H
tRNA <sup>Lys</sup>	7867	7942	76			−8	H
ATPase8	7944	8111	168	ATG	TAA	1	H
ATPase6	8102	8785	684	ATG	TAA	−10	H
COX3	8785	9569	785	ATG	TAA	−1	H
tRNA <sup>Gly</sup>	9570	9640	71			0	H
ND3	9641	9991	351	ATG	TAA	0	H
tRNA <sup>Arg</sup>	9991	10,058	68			−1	H
ND4L	10,059	10,355	297	ATG	TAA	0	H
ND4	10,349	11,729	1381	ATG	TAA	−7	H
tRNA <sup>His</sup>	11,730	11,798	69			0	H
tRNA <sup>Ser</sup>	11,799	11,866	68			0	H
tRNA <sup>Leu</sup>	11,872	11,943	72			5	H

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(continued)

Table 1. Continued

Gene	Location		Size nucleotide (bp)	Codon		Intergenic nucleotide (bp)*	Strand†
	Start	End		Start	End		
ND5	11,944	13,785	1842	ATG	TAA	0	H
ND6	13,778	14,299	522	ATG	TAA	−8	L
tRNA <sup>Glu</sup>	14,300	14,368	69			0	L
Cytb	14,373	15,513	1141	ATG	TAA	4	H
tRNA <sup>Thr</sup>	15,514	15,585	72			0	H
tRNA <sup>Pro</sup>	15,613	15,681	69			27	L
D-loop	15,682	16,665	984			0	

\*Numbers correspond to the nucleotides separating different genes, negative numbers indicate overlapping nucleotides between adjacent genes; †H and L denote heavy and light strands.

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### Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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