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GenBank KC405565-KC405568

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Sent: Wednesday, April 17, 2013 4:36 AM

To: KAMARUL RAHIM BIN KAMARUDIN; physique481@yahoo.co.uk

Dear GenBank Submitter:

Thank you for your submission.

Based on the data submitted to us, the scheduled release date for your submission is:

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If this date is not correct, please let us know as soon as possible, otherwise this submission will be released on the date indicated above. The data would then be available over the network data servers which provide daily updates of GenBank data. The data are simultaneously made available to EMBL in Europe and the DNA Data Bank of Japan.

Minor changes may have been made to your original submission in order to conform to database annotation conventions. In particular, please review:

- Spelling
- Citation data (page span, etc.)
- Nomenclature ('official' gene names, product labels, etc.)
- Taxonomic and source data
- Feature spans and descriptions (particularly non-coding regions)

Additional edits may have been made to your submission, including:

- Exon spans adjusted to conform to the splice donor/acceptor consensus sequences, GT and AG, respectively
- Strings of N's at the ends of sequences and linker past the polyA tail removed
- Any mRNA or ribosomal RNA sequences submitted on the minus-strand have been reverse-complemented

If your submission contained unpublished organism names, the scientific names have been changed to temporary names. Please notify us when the organism names are published and we will update them accordingly.

Please send any revisions, including bibliographic information (e.g., conversion from unpublished to published), biological data (e.g., new features), or sequence data to:

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Since the flatfile record is a display format only and is not an editable format of the data, do not make changes directly to a flatfile. For complete information about different methods to update a sequence record, see: <http://www.ncbi.nlm.nih.gov/Genbank/update.html>

An accession number has been assigned to each nucleotide sequence and was previously provided to you. Note that during the processing, we have assigned protein identifiers to any proteins within the submission. This is fielded as /protein_id.

We strongly recommend that these numbers appear in any publication which reports or discusses these data, so that readers may easily retrieve your data from our databases.

Thank you once again for your submission.

Please reply using the original subject line. This will allow for faster processing of your correspondence.

Sincerely,

Lawrence Chlumsky, Ph. D.
GenBank Direct Submission Staff
gb-admin@ncbi.nlm.nih.gov

GenBank flat file:

LOCUS KC405565 588 bp DNA linear INV 16-APR-2013
 DEFINITION *Holothuria leucospilota* clone HLTNP1 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial.
 ACCESSION KC405565
 VERSION KC405565
 KEYWORDS .
 SOURCE mitochondrion *Holothuria leucospilota*
 ORGANISM *Holothuria leucospilota*
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Holothuroidea; Aspidochirotea; Aspidochirotida; Holothuriidae; *Holothuria*.
 REFERENCE 1 (bases 1 to 588)
 AUTHORS Kamarudin,K.R., Ngah,N., Tengku Abdul Hamid,T.H., Hashim,R. and Susanti,D.
 TITLE Genetic identification of *Holothuria* (*Mertensiothuria*) *leucospilota* (Brandt, 1835) and *Stichopus horrens* Selenka, 1867 from Pangkor Island, Malaysia using cytochrome oxidase subunit I
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 588)
 AUTHORS Kamarudin,K.R., Ngah,N., Tengku Abdul Hamid,T.H., Hashim,R. and Susanti,D.
 TITLE Direct Submission
 JOURNAL Submitted (20-DEC-2012) Kulliyah of Science, International Islamic University Malaysia, Jalan Istana, Bandar Indera Mahkota, Kuantan, Pahang Darul Makmur 25200, Malaysia
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 Sequencing Technology :: Sanger dideoxy sequencing
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 /identified_by="Kamarul Rahim Kamarudin"
 /note="collect between 8-9 November 2011; authority: *Holothuria* (*Mertensiothuria*) *leucospilota* (Brandt, 1835)"
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 301 ccagtactag caggagcaat aacaatggtg ctaaccgacc gaacataaa cacaaccttc
 361 ttcgaccccg cggggggagg agatcccata ctattccaac acctattttg attcttcggt
 421 caccagaag tctatatatt aatcctgcca ggcttcgga tgatattcca cgtaatagcc
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 LOCUS KC405566 627 bp DNA linear INV 16-APR-2013
 DEFINITION *Holothuria leucospilota* clone HLTNP3 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial.
 ACCESSION KC405566
 VERSION KC405566
 KEYWORDS .
 SOURCE mitochondrion *Holothuria leucospilota*
 ORGANISM *Holothuria leucospilota*
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Holothuroidea; Aspidochirotea; Aspidochirotida; Holothuriidae;

Holothuria.

REFERENCE 1 (bases 1 to 627)
AUTHORS Kamarudin,K.R., Ngah,N., Tengku Abdul Hamid,T.H., Hashim,R. and Susanti,D.
TITLE Genetic identification of Holothuria (Mertensiothuria) leucospilota (Brandt, 1835) and Stichopus horrens Selenka, 1867 from Pangkor Island, Malaysia using cytochrome oxidase subunit I
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 627)
AUTHORS Kamarudin,K.R., Ngah,N., Tengku Abdul Hamid,T.H., Hashim,R. and Susanti,D.
TITLE Direct Submission
JOURNAL Submitted (20-DEC-2012) Kulliyah of Science, International Islamic University Malaysia, Jalan Istana, Bandar Indera Mahkota, Kuantan, Pahang Darul Makmur 25200, Malaysia

COMMENT ##Assembly-Data-START##
Assembly Method :: Clustal X v. 2.1
Sequencing Technology :: Sanger dideoxy sequencing
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authority: Holothuria (Mertensiothuria) leucospilota (Brandt, 1835)"
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CDS <1..>627
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601 tgagcccacc atatgttcac agtaggt

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DEFINITION Stichopus horrens clone SHP1 cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial.
ACCESSION KC405567
VERSION KC405567
KEYWORDS .
SOURCE mitochondrion Stichopus horrens (warty sea cucumber)
ORGANISM Stichopus horrens
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Holothuroidea; Aspidochirotacea; Aspidochirotida; Stichopodidae;
Stichopus.
REFERENCE 1 (bases 1 to 624)
AUTHORS Kamarudin,K.R., Ngah,N., Tengku Abdul Hamid,T.H., Hashim,R. and Susanti,D.
TITLE Genetic identification of Holothuria (Mertensiothuria) leucospilota (Brandt, 1835) and Stichopus horrens Selenka, 1867 from Pangkor Island, Malaysia using cytochrome oxidase subunit I
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 624)
AUTHORS Kamarudin,K.R., Ngah,N., Tengku Abdul Hamid,T.H., Hashim,R. and Susanti,D.
TITLE Direct Submission
JOURNAL Submitted (20-DEC-2012) Kulliyah of Science, International Islamic University Malaysia, Jalan Istana, Bandar Indera Mahkota, Kuantan

University Malaysia, Jalan Istana, Bandar Indera Mahkota, Kuantan,
Pahang Darul Makmur 25200, Malaysia

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Sequencing Technology :: Sanger dideoxy sequencing
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    121 ccactttcga gaaacattgc gcacgccgga gggtcagtgg atttgcccat tttttcccta
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    241 atgcgaacac cgggagttac ttttgatcga cttcctttat ttgtttggtc ggtttttata
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    481 tttggaatga tttcccacgt aatagctcac tacagaggaa agcaagaacc ctttggtcac
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DEFINITION    Stichopus horrens clone SHP2 cytochrome oxidase subunit I (COI)
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ACCESSION    KC405568
VERSION      KC405568
KEYWORDS     .
SOURCE       mitochondrion Stichopus horrens (warty sea cucumber)
   ORGANISM  Stichopus horrens
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             Holothuroidea; Aspidochirotacea; Aspidochirotida; Stichopodidae;
             Stichopus.
REFERENCE    1 (bases 1 to 627)
   AUTHORS   Kamarudin,K.R., Ngah,N., Tengku Abdul Hamid,T.H., Hashim,R. and
             Susanti,D.
   TITLE     Genetic identification of Holothuria (Mertensiothuria) leucospilota
             (Brandt, 1835) and Stichopus horrens Selenka, 1867 from Pangkor
             Island, Malaysia using cytochrome oxidase subunit I
   JOURNAL   Unpublished
REFERENCE    2 (bases 1 to 627)
   AUTHORS   Kamarudin,K.R., Ngah,N., Tengku Abdul Hamid,T.H., Hashim,R. and
             Susanti,D.
   TITLE     Direct Submission
   JOURNAL   Submitted (20-DEC-2012) Kulliyah of Science, International Islamic
             University Malaysia, Jalan Istana, Bandar Indera Mahkota, Kuantan,
             Pahang Darul Makmur 25200, Malaysia
COMMENT     ##Assembly-Data-START##
Assembly Method      :: Clustal X v. 2.1
Sequencing Technology :: Sanger dideoxy sequencing
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121 cccccacttt cgagaaacat tgcgcacgcc ggagggtcag tggatttggc cattttttcc
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481 ggatttgaa tgattccca cgtaatagct cactacagag gaaagcaaga accctttggc
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601 caccatatgt ttacagttag aatggac
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