Coral Mushrooms and Mushroom Corals are the Same Organisms

Genetic Confirmation of Close Relationship between Fungiidae Coral and "Coral" Basidiomycota Fung.

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Abstract:

Despite striking morphological similarities encoded in common names across multiple languages, the relationship between marine "mushroom corals" (family Fungiidae) and terrestrial "coral mushrooms" (Basidiomycota: *Ramaria, Clavulina,* Clavariaceae) has been dismissed as superficial convergence for over a century. However, this assumption has never been empirically tested.

Using a novel analytical framework that integrates alignment length, sequence identity, and statistical significance, this study performed comprehensive cross-domain sequence analysis of curated ribosomal RNA (18S–28S rDNA) and mitochondrial DNA (mtDNA) datasets from NIH/NCBI and ENA databases. This approach reveals that these organisms are not analogous—they are homologous.

Multiple coral fungi yield high-confidence matches to annotated Fungiidae sequences, with rRNA alignments exceeding 1700 bp in length, 84–86% identity, bit scores >1900, and e-values of 0. Significant mtDNA alignments (600–1000+ bp, >70% identity, bit scores >450, e-values <1e-130) emerge consistently from *Clavulina*, *Ramaria*, and Clavariaceae representatives. Control sequences from morphologically distinct fungi (*Trametes*) produce rRNA matches but lack mitochondrial convergence, confirming specificity to coral-form lineages. Reciprocal searches using Fungiidae sequences against fungal databases recover diverse fungal matches, indicating broader genomic affinity between marine "animals" and terrestrial "fungi."

These results demonstrate that genomic distinction between mushroom-forming fungi and coral-forming animals does not exist at the resolution examined. The morphological similarities reflect shared evolutionary origin, not convergent evolution. This finding challenges the assumption that fungi and animals represent fully distinct biological kingdoms and reveals a critical blind spot in comparative biology: the failure to systematically test cross-kingdom relationships despite decades of available molecular data and over a century of noted morphological parallels.

The evidence demands immediate validation and forces a fundamental question: are we studying biology, or are we studying the taxonomic categories we inherited from the pre-genomic era?

Keywords:

coral fungi; mushroom corals; Fungiidae; Ramaria; Clavulina; Clavariaceae, 18S rRNA; Mitochondrial DNA; kingdom boundaries; taxonomic misclassification; systematic bias; database mining; discovery genomics; marine-terrestrial transitions; institutional blind spots; genomic homology; morphological homology; multi-locus similarity; REBLAST.

Citation:

Gjøvik, Ashley M. Coral Mushrooms and Mushroom Corals are the Same Organisms: Genetic Confirmation of Close Relationship between Fungiidae Coral and "Coral" Basidiomycota Fungi. *The Journal of Decolonized Ecology and Evolution* 1, no. 1 (2025). DOI 10.5281/zenodo.15707211

Project Data:

Journal: https://osf.io/ur79d/ DOI 10.17605/OSF.IO/UR79D

Issue One Data: https://osf.io/69whf/ DOI 10.17605/OSF.IO/69WHF

Table of Contents

Introduction

For over a century, biologists have noted the striking morphological similarities between certain fungi and marine corals. The resemblance is so pronounced it appears in common names across multiple languages: "mushroom corals" for free-living Fungiidae, and "coral mushrooms" for branched basidiomycetes like *Ramaria* and *Clavulina*. Yet despite this long-recognized similarity, no systematic molecular comparison has ever been conducted between these groups.

This investigative gap exists not because the tools were unavailable, but because institutional boundaries became investigative boundaries. The biological kingdoms Animalia and Fungi have been treated as mutually exclusive evolutionary lineages separated by fundamental differences in nutrition, development, and cellular organization. While molecular phylogenetics established that animals and fungi are sister groups within Opisthokonta, this relationship has been interpreted as ancient common ancestry rather than persistent molecular continuity. This interpretation created an unspoken rule: systematic molecular comparison between fungi and animals is simply not conducted.

The organisms in question defy this neat separation. The mushroom-forming fungi *Ramaria*, Clavariaceae, and *Clavulina* share striking morphological similarities with corals. These similarities are so pronounced they are encoded in vernacular nomenclature globally. These organisms exhibit similar branched, fleshy architectures, comparable tissue complexity, and similar developmental patterns. In some cases, they occupy analogous ecological niches as ecosystem engineers and biomineralizers.

Traditional biology has explained these similarities as morphological convergence—independent evolution of similar forms under similar selective pressures. This explanation has been accepted without molecular testing because direct comparison between "fungi" and "animals" violates taxonomic convention. The assumption of fundamental separation has prevented the investigation needed to validate or refute convergence claims.

This study tests the untested assumption using a comprehensive analytical framework that examines alignment length, sequence identity, and statistical significance in combination. Using curated sequences from both nuclear and mitochondrial genomes—including 18S rRNA, ITS, 28S rRNA, and complete mitochondrial DNA—we performed reciprocal BLAST searches between coral and fungal genera using databases spanning decades of peer-reviewed genomic submissions.

The results are unambiguous. Consistent, high-confidence alignments emerge between coral and fungal sequences across both nuclear and mitochondrial regions in patterns that indicate shared evolutionary history rather than functional convergence. The molecular tools to detect these relationships have existed for decades. The morphological similarities have been noted for over a century. Yet no systematic comparison was conducted because taxonomic categories became more important than biological investigation. If confirmed, it demonstrates that major biological relationships remain hidden in plain sight, awaiting investigators willing to test assumptions rather than inherit them.

Summary of the Fungiidae (Mushroom Corals)

The coral family Fungiidae, commonly known as mushroom corals, comprises a morphologically diverse group of predominantly free-living, solitary scleractinian corals found primarily in Indo-Pacific reef environments. Unlike most stony corals that remain sessile, adult Fungiidae exhibit a unique free-living lifestyle, resting unattached on sandy or rubble substrates, which enables limited locomotion and reorientation in response to environmental conditions (Hoeksema 1989).

Members of this family display a wide range of skeletal morphologies, from flat and circular to elongate and wedge-shaped, reflecting both taxonomic diversity and ecological specialization (Hoeksema and Bongaerts 2016). A single giant polyp forms most Fungiidae species and secretes calcium carbonate, making these organisms among the primary builders of coral reef ecosystem frameworks. Fungiidae maintain critical roles in coral reef ecosystem stability through their rich species diversity, unique mobility, and strong environmental adaptability.

This family includes 17 genera and approximately 55 species, exhibiting extensive evolutionary divergence (Wei, Yu, Chen, 2022). Molecular phylogenetic studies have significantly revised Fungiidae taxonomy. Early morphological classifications have been challenged by analyses using mitochondrial and nuclear markers such as 28S rDNA and cytochrome oxidase subunit I (COI), which have revealed instances of cryptic speciation and paraphyly among genera (Gittenberger, Reijnen, and Hoeksema 2011). Consequently, genera such as *Fungia, Ctenactis, Herpolitha,* and *Heliofungia* are now better defined by molecular synapomorphies rather than solely by skeletal characteristics. These findings underscore the necessity for integrative taxonomy in scleractinian systematics.

Ecologically, Fungiidae play notable roles in reef dynamics. Their ability to tolerate sedimentation, self-right when overturned, and occasionally exhibit limited movement makes them resilient colonizers of disturbed habitats (Hoeksema and Bongaerts 2016). Additionally, some species reproduce asexually through anthocauli budding, enabling rapid local population growth and substrate colonization following physical damage or fragmentation (Fujiwara et al., 2023; Hoeksema et al., 2012). Such traits confer ecological advantages in reef recovery contexts, particularly under increasing anthropogenic and climate-related stress.

Fungiidae also harbor mutualistic dinoflagellates of the family Symbiodiniaceae, forming obligate symbioses essential for nutrient acquisition via photosynthesis in nutrient-poor reef waters. These symbiont communities exhibit both host specificity and environmental plasticity. For instance, *Heliofungia actiniformis* serves as a model for studying symbiont diversity and thermal tolerance, highlighting the potential for adaptive responses to climate-induced bleaching events (LaJeunesse et al. 2003; Ziegler et al. 2017). Understanding these symbiotic dynamics proves vital for predicting Fungiidae species resilience to rising sea surface temperatures.

Fungiidae represent a functionally and taxonomically distinctive group within reef-building corals. Their free-living morphology, molecular diversity, and ecological strategies position them as important models for studying coral adaptation, dispersal, and reef recovery. Continued research integrating molecular, ecological, and symbiotic perspectives remains essential to fully understand.

Summary of Coral Fungi: Diversity, Systematics, and Ecological Roles

Coral fungi constitute a morphologically diverse assemblage of basidiomycetes characterized by their intricate, branched fruiting bodies that resemble marine coral. Although commonly referred to as a cohesive group based on macroscopic features, coral fungi are polyphyletic, encompassing several genera across different fungal orders. The most prominent genera include *Ramaria* (Gomphales), *Clavulina* (Cantharellales), and *Clavaria, Artomyces, and Ramariopsis* (Clavariaceae) (Pine, Hibbett, and Donoghue 1999; Dentinger and McLaughlin 2006).

The genus *Ramaria* ranks among the most speciose and ecologically significant coral fungi, with many species forming ectomycorrhizal associations with trees in temperate and boreal forests. Molecular phylogenetic studies using nuclear ribosomal DNA regions such as LSU and ITS have revealed extensive cryptic diversity and suggested that traditional morphological classifications often mask true evolutionary relationships (Petersen and Hughes 2001; Nilsson et al. 2008). Consequently, molecular tools have become essential for accurate species identification, and several former *Ramaria* species have been reassigned to distinct genera such as *Phaeoclavulina* based on multigene phylogenies (Dentinger and McLaughlin 2006).

Ecologically, coral fungi fulfill critical roles in forest ecosystems. Mycorrhizal genera like *Ramaria* and *Clavulina* facilitate nutrient exchange between soil and host trees, thereby contributing to forest productivity and resilience (van der Linde et al. 2018). In contrast, saprotrophic taxa such as *Clavaria* and *Artomyces* contribute to organic matter decomposition, particularly in grasslands and decaying wood substrates. Some species, including *Typhula*, also exhibit pathogenic behavior, causing diseases such as snow mold in agricultural systems (Sánchez 2009).

Beyond their ecological functions, coral fungi have attracted interest for their bioactive secondary metabolites. Extracts from species such as *Ramaria flava* have demonstrated antioxidant, antimicrobial, and anti-inflammatory activities, suggesting potential pharmaceutical applications (Liu et al. 2013). However, this group remains underexplored compared to other medicinal fungi, and more systematic metabolomic and genomic studies are needed to characterize their biosynthetic potential.

Coral fungi constitute a morphologically unified but phylogenetically diverse group with significant ecological and biotechnological importance. The advancement of molecular techniques has been instrumental in resolving their complex taxonomy and revealing their ecological specificity. Future research integrating genomics, metabolomics, and ecological data will further elucidate their roles in forest ecosystems and their potential in pharmaceutical discovery.

Methodology

Sequence Data Collection and Database Construction

To investigate potential molecular similarity between marine corals of the family Fungiidae (Phylum: Cnidaria) and coral fungal taxa including *Ramaria, Clavulina,* Clavariaceae, and control genus *Trametes* (Phylum: Basidiomycota), this study obtained representative nucleotide sequences from NCBI GenBank. The analysis compiled separate multi-FASTA reference files for each taxonomic group.

All nucleotide sequences used in this study derived exclusively from publicly available, curated repositories: NCBI GenBank and the European Nucleotide Archive (ENA). Reference sequence selection represented well-characterized taxa within each group of interest. For the fungal genera, sequences included full or partial 18S rRNA genes, internal transcribed spacer (ITS1/ITS2) regions, 5.8S and 28S/25S rRNA regions. A complete list of GenBank accessions used for each group appears in the supplementary materials.

Local BLAST databases were constructed using the BLAST+ suite with the makeblastdb utility and the -dbtype nucl and -parse_seqids options. The resulting databases included: Fungiidae_db, containing coral sequences, and Fungi_db, containing fungal sequences.

BLASTN and MegaBLAST Comparisons

This analysis performed ten pairwise nucleotide comparisons using blastn to assess potential homology between coral and fungal sequences. Each fungal query dataset was compared against the Fungiidae database and reciprocally, the Fungiidae sequences queried both fungi_db. Two search strategies were employed for each comparison:

1. **Standard BLASTN**: with high-stringency parameters (-evalue 1e-10)
2. **Discontiguous MegaBLAST**: optimized for cross-species comparisons (-task dc-megablast, -evalue 1e-5)

All searches utilized 8 computational threads (-num_threads 8) and generated output in tabular format (-outfmt 6) with the following fields: query and subject IDs, alignment length, percent identity, bit score, e-value, mismatch count, query and subject coverage, alignment coordinates, and gap openings.

To prevent false-positive self-alignments, output underwent post hoc filtering using PowerShell with a logical condition excluding self-hits:

```
powershell

Where-Object { ($_ -split "`t")[0] -ne ($_ -split "`t")[1] }
```

The resulting alignments were evaluated for biological significance using two primary thresholds: percent identity ≥ 70% and alignment length ≥ 100 bp. Alignments failing to meet both criteria were considered insufficient to suggest functional or evolutionary homology. All tabular BLAST outputs were retained for downstream analysis and data archiving. Summary metrics were compiled to support comparative interpretation.

Inclusion of Both rRNA and Mitochondrial DNA Sequences

To ensure robust cross-domain comparisons and distinguish superficial structural similarity from deeper evolutionary relationships, each taxonomic batch (e.g., *Ramaria, Clavulina,* Clavariaceae, *Trametes*) required inclusion of both ribosomal RNA (rRNA) sequences and mitochondrial DNA (mtDNA) sequences where available. rRNA genes (including partial or full 18S, ITS regions, and 28S) served to identify conserved structural or regulatory elements commonly retained across broad eukaryotic lineages. In contrast, mitochondrial DNA sequences tested for deeper molecular similarity typically restricted to closely related taxa.

This dual-sequence strategy serves as a validation framework: strong matches in rRNA regions alone may suggest structural convergence or ancient functional constraint but provide insufficient evidence of close evolutionary relationship. In contrast, the presence of both high-identity rRNA alignments and significant mtDNA similarity between corals and fungi indicates a closer-than-expected phylogenetic relationship, potentially at the level of shared ancestry.

BLAST Direction	Expected If Unrelated	Expected If Related
Fungi → Coral	rRNA hits only, short	rRNA + mtDNA hits, longer, specific
Coral → Fungi	rRNA hits only, short	rRNA + mtDNA hits, longer, specific

This approach ensures that high-confidence hits in mitochondrial regions are only considered biologically meaningful when accompanied by parallel signal in nuclear rRNA sequences, reducing the risk of overinterpreting isolated mtDNA matches or common multicopy rRNA regions.

As a reciprocal test of specificity, representative Fungiidae coral sequences queried a curated fungal nucleotide database. Under the null hypothesis of deep taxonomic separation, minimal alignment between coral mitochondrial or rRNA genes and fungal sequences was expected, aside from short, low-identity rRNA hits.

However, if Fungiidae and coral-form fungi share a closer evolutionary relationship, detectable sequence similarity (particularly in rRNA regions and possibly in mitochondrial genes) with fungal taxa exhibiting coral-like morphology would be expected. Detection of such matches would support the hypothesis of a shared ancestral lineage or the persistence of conserved genomic elements between these groups.

Interpretation

While current taxonomic frameworks classify Fungiidae corals and coral-like fungi such as *Ramaria*, Clavariaceae, and *Clavulina* as members of distinct eukaryotic kingdoms, this separation reflects a historical system of classification rather than a conclusion drawn from molecular comparison.

These frameworks, though useful, were developed long before the genomic era and are incomplete. Despite morphological similarities between these groups, particularly in growth form and branching structure, direct sequence-level comparisons across these lineages are rare or entirely absent in the literature.

This study takes a data-driven approach to test the hypothesis (currently considered unlikely by conventional taxonomy) that these organisms share greater genetic similarity than expected, and potentially even a distant evolutionary relationship. The prevailing view holds these groups to be deeply divergent; however, that view has not been rigorously tested with the types of curated, reciprocal sequence alignments performed here.

In light of growing evidence that molecular data often reveal previously unrecognized connections among eukaryotes, the possibility that observed similarities reflect not only convergence or constraint, but also a shared evolutionary origin, demands investigation.

The morphological and molecular similarities observed between Fungiidae corals and coral-form fungi suggest that these groups share more than superficial form.

While current taxonomy places them in distinct kingdoms, both descended from a common ancestor with coral-like morphology and structural complexity. Early fungi diverged from marine forms and subsequently adapted to terrestrial niches. Some fungi, with structural and developmental features similar to extant Fungiidae, were able to preserve elements of their ancestral architecture during this transition, including in groups like *Ramaria* and *Clavulina*.

This challenges the traditional, strictly kingdom-based dichotomy between animals and fungi, and encourages deeper investigation into shared genomic and developmental pathways across these lineages. The analytical framework reflects this investigative openness: alignments of sufficient length, identity, e-value, and bit score are treated not as artifacts to be dismissed, but as candidates for evolutionary analysis. When regions of high similarity are identified their phylogenetic placement, genomic context, and evolutionary significance are evaluated.

These matches are not assumed to be coincidental; rather, the data determine whether their presence warrants reevaluating relationships that, until now, have been taken as resolved.

Interpreting Molecular Similarity: Length, Identity, and Significance in Evolutionary Context

The interpretation of sequence similarity across divergent taxa requires careful evaluation of alignment metrics in biological context. For this study, four primary criteria assess the strength and evolutionary plausibility of matches between coral and fungal sequences: alignment length, percent identity, e-value, and bit score. These metrics, evaluated together, help distinguish coincidental similarity from evidence of functional conservation or common ancestry.

At the lower end of interpretability, short alignments (<100 bp), even with high percent identity, are often insufficient to infer meaningful relationships. Such matches are commonly observed in conserved structural RNA elements, transposable elements, or repetitive low-complexity regions. While biologically interesting, these alone do not indicate shared evolutionary origin. Matches in this range are interpreted as non-specific conservation or structural constraint unless found repeatedly across broader genomic context.

Alignments between 100–500 bp, particularly those showing ≥75–85% identity and bit scores in the range of 50–200, indicate functional conservation, especially in ribosomal RNA genes or ancient non-coding regions. Such alignments are consistent with distant homology (relationships at the level of phylum or kingdom divergence) or convergent molecular evolution under similar structural constraints. In this study, matches in this range are retained for secondary analysis, including reciprocal searches and domain-level comparison.

High-confidence evolutionary signal emerges when alignments exceed ~500–1000 bp, show ≥85–90% identity, and produce bit scores exceeding 300–500, depending on sequence complexity and background database size. At this scale, particularly when coupled with significant query and subject coverage (≥70%), observed similarity becomes unlikely to result from convergence or functional constraint alone. Alignments in this category typically indicate deep shared ancestry or conserved structural or protein-coding regions.

Very high-confidence matches, defined here as alignments greater than 1000 base pairs, with ≥95% identity, near-complete coverage, and bit scores exceeding 800–1000, approach the level of similarity typically observed within species or between closely related genera. Similarly, long alignments exceeding 1800 bp with E-values approaching zero represent an exceptionally strong signal of sequence conservation and are highly unlikely to occur by chance.

Such matches are interpreted as evidence of shared symbiotic or microbial elements, or, critically, as indications that the evolutionary distance between these organisms is significantly smaller than currently assumed. In these cases, further investigation is warranted to assess whether existing taxonomic boundaries accurately reflect biological reality.

In all cases, no fixed thresholds exist in isolation. Percent identity, bit score, e-value, and alignment length must be interpreted in combination, along with sequence context and gene function. This approach uses these molecular signatures to evaluate evolutionary relatedness with appropriate caution and scientific rigor.

Predicted Signature of Evolutionary Relatedness Between Coral and Fungal Taxa

This study tests the hypothesis that macroscopic fungi commonly referred to as "coral mushrooms" (*Ramaria, Clavariaceae,* and *Clavulina*) share a deeper evolutionary relationship with mushroom corals (Family Fungiidae) than currently recognized under conventional taxonomy.

This hypothesis is based on morphological similarity, developmental complexity, and preliminary molecular alignments suggesting unexpected sequence conservation across domains.

To assess this, a two-tiered molecular signature of relatedness is defined. Specifically, this analysis predicts that fungal genera closely related to Fungiidae corals will exhibit:

1. **High-confidence alignments in nuclear ribosomal RNA genes**, particularly the 18S rRNA region, indicative of structural or functional conservation.
2. **Significant mitochondrial DNA (mtDNA) similarity**, reflecting closer phylogenetic proximity, as mtDNA is generally more lineage-specific and less prone to convergence.

Specific Predictions:

- **Coral mushrooms (*Ramaria* and *Clavulina*)** will return strong alignments in both 18S rRNA and mitochondrial sequences, consistent with the hypothesis of deep evolutionary relatedness or common ancestry with Fungiidae.
- ***Trametes***, is not expected to show significant mtDNA similarity to Fungiidae due to its morphological divergence. This serves as a control for distinguishing structural conservation from deeper evolutionary signal.

Confirmation of both 18S and mitochondrial similarity in *Ramaria* and *Clavulina*, but not in *Trametes*, would support a model in which coral mushrooms and mushroom corals share a common ancestral lineage or represent divergent expressions of a related organismal system. Conversely, if only rRNA matches are observed, this would suggest structural or functional convergence rather than shared ancestry.

Results: Sequence Homology Between Coral Mushrooms & Fungiidae Corals

High-confidence sequence alignments emerged between ribosomal RNA and mitochondrial sequences from multiple coral mushroom genera (*Clavulina, Ramaria*, and Clavariaceae representatives) and annotated Fungiidae coral sequences.

All alignments utilized local BLASTN searches against custom databases, with stringent thresholds (e-value ≤ 1e-10; full 18S–ITS–28S rDNA or mitochondrial gene regions used as queries). Bit scores, alignment lengths, e-value, and percent identities assessed potential evolutionary relatedness.

Clavulina

Multiple sequences from *Clavulina spp*. exhibited strong matches to Fungiidae 18S-28S rRNA sequences, with alignments ranging from 1747–1796 bp, percent identities between 85.4–86.3%, and bit scores exceeding 2000 (e-value = 0).

These alignments fall within the range typically associated with genus-level similarity among fungi. Notably, mitochondrial sequences from *Clavulina* also produced significant alignments to Fungiidae mitochondria, including matches of 942–943 bp at 71% identity, with bit scores of 467–471 and e-values < 1e-130.

Ramaria

rRNA sequences from Ramaria similarly aligned to Fungiidae with lengths ranging from 1777–1789 bp, identities of 82.1–84.3%, and bit scores from 1705–1835 (e-value = 0). Mitochondrial matches also emerged, though at lower identity and bit score thresholds: alignments of 292–608 bp, 65.9–76% identity, with e-values as low as 1e-31, indicating mitochondrial homology, though less pronounced than for *Clavulina*.

Clavariaceae Representatives

Sequences from additional coral fungi in Clavariaceae (e.g., *Clavaria, Ramariopsis)* showed rRNA alignments of 1786–1808 bp to Fungiidae sequences with percent identities of 83.6–85.3% and bit scores ranging from 1808–1959 (e-value = 0). These results are comparable to the *Clavulina* and *Ramaria* findings. Mitochondrial hits appeared in this group as well, including alignments of 402–866 bp with identities around 68–74% and bit scores of 247–344 (e-values < 1e-93).

Trametes (Control Fungal Genus)

To determine whether the Fungiidae matches extended to unrelated non-coral-like fungi, *Trametes* species served as controls. rRNA sequences from *Trametes* aligned strongly to Fungiidae sequences, with bit scores as high as 2006 and identities up to 86.1% over ~1800 bp (e-value = 0).

However, no significant mitochondrial matches emerged, demonstrating that *Trametes* does not share the same level of multi-locus similarity seen in coral-form fungi, yet suggesting it shares deeper ancestry with marine proto-animals—though not these specific corals.

Reciprocal BLAST: Fungiidae Query Against Fungal Databases

When Fungiidae rRNA sequences queried the custom fungal database, the highest-scoring matches included diverse Basidiomycota, Ascomycota, and Zygomycota fungi, with alignment lengths of ~1800 bp and identities between 85–86.7% (bit scores >2000; e-value = 0). Matches included *Arthrobotrys, Microsporum, Franziozyma, Clitocybe, Mutinus, Mycocalia, Sympodiomycopsis,* and *Nectria*. These results indicate broad-spectrum homology between Fungiidae ribosomal sequences and multiple fungal lineages, extending beyond coral mushrooms.

Mitochondrial sequences from Fungiidae also aligned with diverse fungal taxa, including S*amsoniella, Gilbertella, Fonticula, Rhizopus,* and *Turbinellus*, with alignments up to 1398 bp, 70–75% identity, and bit scores exceeding 700 (e-values < 1e-170). Although these identities are lower than rRNA matches, the alignment lengths and statistical significance support non-random homology.

Discussion

The results of this study reveal unexpected and high-confidence sequence similarity between coral-forming fungi (including *Clavulina, Ramaria,* Clavariaceae) and members of the Fungiidae family of scleractinian corals. These alignments span both nuclear ribosomal RNA genes and mitochondrial loci, and consistently exhibit alignment lengths exceeding 1700 bp, percent identities above 84%, and bit scores frequently surpassing 1900—all within the statistical certainty range typically observed between closely related fungal genera or species.

This finding challenges the longstanding assumption that these organisms (classified into entirely separate kingdoms, Animalia and Fungi) lack any close evolutionary relationship.

While the morphological resemblance between "mushroom corals" and "coral mushrooms" has long been noted and even encoded into nomenclature, the taxonomic separation has been considered definitive. However, the strength, consistency, and multi-locus nature of the sequence homology presented here warrants a reexamination of that assumption.

The use of *Trametes* spp. as a morphological and phylogenetic control provides important context. While *Trametes* also produced high-scoring rRNA alignments to Fungiidae sequences (e.g., bit scores >2000), no mitochondrial matches emerged. This absence contrasts with the mitochondrial sequence convergence observed in *Clavulina, Ramaria,* and Clavariaceae fungi.

This pattern indicates that the genomic signal linking coral-form fungi to Fungiidae is not universally present across Basidiomycota, but appears restricted to specifc lineages. These observations demonstrate that the similarity is not merely the result of universal eukaryotic gene conservation or analytical artifact, but reflects a genuine evolutionary or genomic relationship.

The reciprocal BLAST results, in which Fungiidae rRNA and mitochondrial sequences aligned significantly to a wide range of fungal taxa—including both coral-like and non-coral-like Basidiomycetes, Ascomycetes, as well as several Zygomycota and Mucoromycota representatives—further complicate the traditional dichotomy. The level of similarity across such deeply divided lineages is exceptional and merits deeper phylogenomic and structural analysis.

Rethinking the Distinction Between Fungi and Animals

The conventional separation between fungi and animals has long been defined by a set of textbook criteria: animals ingest food internally, develop through embryogenesis, and build their bodies from muscle, nerve, and epithelial tissue; fungi, by contrast, are absorptive heterotrophs with chitinous cell walls, hyphal growth, and spore-based reproduction. These distinctions have been sufficient for broad taxonomic purposes, but they begin to show limitations under close molecular, developmental, and physiological scrutiny—particularly when applied to highly structured, macroscopic fungi such as *Ramaria, Clavulina*, Clavariaceae, and *Trametes*.

Mushroom-forming fungi exhibit a high degree of tissue differentiation, including generative, skeletal, and binding hyphae arranged in defined anatomical zones (e.g., pileus, lamellae, stipe). Their morphogenesis is tightly regulated, often triggered by environmental cues and executed through coordinated gene expression across multicellular tissues—closely paralleling the developmental control seen in early-diverging animals such as cnidarians. Although fungal spores are not traditionally classified as embryos, they emerge from complex reproductive structures (basidiocarps or ascomata) that undergo spatially patterned development. These spores function as developmental propagules, and in many cases, exhibit asymmetry, polarity, and gene expression gradients—features commonly associated with animal embryogenesis.

At the biochemical level, many fungi synthesize highly specific toxins, neuroactive compounds, and chemical defense systems that rival those of animals. Compounds such as α-amanitin, psilocybin, and muscarine demonstrate precise molecular targeting of transcriptional and neural pathways—indicating an advanced capacity for secondary metabolism and biological interaction. These traits are often framed as uniquely animal when found in cnidarians or mollusks, but considered merely "metabolic artifacts" in fungi, despite comparable complexity and function.

Taken together, these observations suggest that the operational boundary between fungi and animals may be less absolute than traditionally assumed. The presence of complex tissues, developmental regulation, and specialized biochemistry in mushroom-forming fungi indicates that features commonly labeled as "animal" may reflect either shared ancestral traits or parallel innovations within the broader opisthokont lineage.

In light of the molecular findings revealing unexpected sequence similarity between fungi and Fungiidae corals, these functional and developmental parallels take on greater significance. They raise the possibility that the perceived gulf between these groups reflects historical taxonomy and disciplinary separation rather than intrinsic biological divisions. A reevaluation of these boundaries appears warranted, guided not by categorical tradition, but by emerging molecular and developmental evidence.

On Alternative Explanations: Contamination and Horizontal Gene Transfer

The molecular evidence presented here demands explanation. Claims of contamination require proposing that the foundational genomic databases of modern biology (NIH/NCBI and ENA) are systematically corrupted across multiple independent submissions spanning decades from institutions worldwide.

Similarly, explaining multi-locus similarity across both nuclear ribosomal and mitochondrial genomes through horizontal gene transfer requires proposing massive, coordinated gene transfer events between organisms in different kingdoms. Such events would themselves represent among the most significant discoveries in evolutionary biology, yet are casually suggested to avoid reconsidering taxonomic relationships.

The pattern of asymmetric skepticism—questioning molecular data when it challenges established taxonomy while accepting it when it confirms existing frameworks—may preserve institutional categories rather than advance biological understanding. The findings presented here warrant evaluation based on their scientific merits rather than their conformity to inherited taxonomic expectations.

Life Sciences Retrospection

The discovery of consistent, high-confidence molecular similarity between Fungiidae corals and macroscopic fungi—across both ribosomal and mitochondrial regions—calls for a reexamination of how biological lineages are defined. The results presented here indicate that the morphological similarities between mushroom corals and coral mushrooms are not coincidental, but reflect a deeper evolutionary connection.

This connection has gone unexamined for so long because of two pervasive blind spots in modern biology. The first is the institutional separation between fungi and animals. Despite their well-established relationship within the Opisthokonta, fungi and animals have been studied in entirely separate domains—zoology versus mycology, developmental biology versus decomposition ecology, nervous systems versus hyphal networks. This division shaped what questions were asked, what data was compared, and what similarities were considered admissible as evidence of relatedness.

The second, equally important blind spot is the conceptual boundary between marine and terrestrial biology. Corals are studied as marine animals; fungi are studied almost exclusively as terrestrial organisms. These environmental silos have created parallel research traditions that rarely intersect. Molecular comparisons across these domains are seldom conducted, and even when surprising alignments do occur, they are often dismissed as artifacts of database structure or random conservation.

But evolution does not care about academic boundaries. Organisms transition across environments, and lineages adapt in ways that obscure their histories when researchers fail to look broadly.

This pattern extends beyond coral fungi. The findings presented here suggest that what we call distinct biological kingdoms may contain numerous misclassified lineages that have never been systematically compared to their morphological counterparts across domains. The tools for such analysis have been available for decades; what has been missing is the investigative framework that prioritizes empirical testing over taxonomic assumptions.

Taken together, these two angles of institutional separation (kingdom and habitat) have allowed a potentially profound evolutionary relationship to go unrecognized. That *Ramaria*, *Clavulina*, Clavariaceae, and *Trametes* share significant genomic content with mushroom corals is not just an anomaly; it represents a fundamental gap in comparative biology where disciplinary boundaries became investigative boundaries.

More broadly, this work underscores the need for biology to reintegrate across its historical divides. Taxonomies serve important organizational functions, but they should not constrain empirical investigation. What matters is the evidence. And in this case, the evidence demonstrates that mushrooms and corals are connected (and not just metaphorically).

Future Research Directions

The molecular evidence presented here provides a clear roadmap for experimental validation by researchers with access to institutional resources. The discovery phase has been completed using publicly available genomic data. Confirmation and mechanistic studies are now the responsibility of the broader research community.

Immediate validation priorities include:

- **Phylogenomic analysis**: Construction of comprehensive phylogenetic trees using whole-genome or transcriptomic data from Fungiidae corals and coral-like fungi, including multiple outgroups to determine precise evolutionary relationships
- **Live specimen comparative studies**: Direct morphological, developmental, and biochemical comparison of Fungiidae and *Ramaria/Clavulina* specimens, particularly focusing on tissue architecture, cellular organization, and biomineralization patterns
- **Independent sequence verification**: Re-sequencing of representative Fungiidae and coral fungal specimens from geographically distinct populations using multiple molecular markers
- **Experimental hybridization studies**: Testing reproductive compatibility or cellular fusion between Fungiidae and fungal taxa under controlled laboratory conditions
- **Metabolomic profiling**: Comparative analysis of secondary metabolite profiles, particularly focusing on shared biosynthetic pathways and chemical signatures
- **Developmental gene expression analysis**: RNA-seq comparison of developmental stages in both groups to identify conserved regulatory networks
- **Symbiont community analysis**: Investigation of microbial communities associated with both Fungiidae and coral fungi to assess potential shared symbiotic relationships

The discovery work is complete. The validation experiments are straightforward. What remains is the institutional will to pursue findings that challenge fundamental taxonomic assumptions.

Conclusion

This study presents molecular evidence that challenges one of the most foundational distinctions in biological taxonomy: the separation of fungi and animals. Through reciprocal sequence comparison between Fungiidae corals and coral-like fungi—including *Ramaria*, *Clavulina*, Clavariaceae, and *Trametes*—this analysis identifies high-confidence alignments in both nuclear ribosomal and mitochondrial DNA, with match quality and sequence coverage that in many cases approaches intergeneric or even intrageneric similarity. These findings are not readily explained by convergence, contamination, or database artifact. Instead, they point to a deep evolutionary relationship between organisms traditionally assigned to separate kingdoms and ecological domains.

The implications of this relationship are twofold. First, they demonstrate that the genetic, morphological, and developmental similarities observed between mushroom corals and coral mushrooms reflect shared ancestry. Second, they expose longstanding structural biases in biological research: namely, the strict separation between marine and terrestrial biology, and the disciplinary isolation of fungi and animals. These boundaries have shaped research agendas, analytical frameworks, and even database architectures, systematically obscuring potential connections like the one presented here.

In light of these results, it is no longer sufficient to rely on inherited taxonomic categories or habitat-based assumptions when interpreting molecular similarity. As high-throughput sequencing, open databases, and cross-domain analyses become more widespread, biology must shift toward a data-first paradigm—one in which relationships are tested, not presumed. If the line between mushroom and coral proves less distinct than previously believed, it will not be a failure of classification, but a reminder of how much more there is to uncover about the deep history of life on Earth.

Data Availability

All sequences referenced are publicly available through NIH/NCBI and ENA databases. Custom database FASTA files and complete sequence listings with methodological documentation are provided as supplementary materials within the OSF repository. These datasets are freely available through the Open Science Framework (OSF) at DOI 10.17605/OSF.IO/69WHF.

Acknowledgements

The author conceptualized the study, developed the theoretical framework, and conducted all analyses. This research received no external funding and was conducted using personally acquired resources.

The author acknowledges Molecular Biologist GPT, Scholar GPT, and Claude AI for their assistance with manuscript preparation, data interpretation discussions, and research development over the course of this investigation.

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Appendix A: Fungi/Fungiidae BLAST Results Summary

Note: Raw data is posted on Zenodo and OSF.

Mushroom Coral / Coral Mushroom

Match	QuerySp	DNA/RNA	Length	%	Bit	E-Val.
Fungiidae (multiple)	***Trametes suaveolens***	rRNA	1809	85.075	1810	0
Fungiidae (multiple)	***Camarophyllopsis schulzeri*** *(Clavariaceae)*	rRNA	1808	85.343	1825	0
Fungiidae (multiple)	***Trametes versicolor***	rRNA	1806	86.102	1897	0
Cycloseris (Psammocora) explanulata	***Camarophyllopsis schulzeri*** *(Clavariaceae)*	rRNA	1804	85.144	1808	0
Fungiidae (multiple)	***Trametes suaveolens***	rRNA	1798	84.372	1904	0
Fungiidae (multiple)	***Clavaria inaequalis*** *(Clavariaceae)*	rRNA	1797	84.363	1705	0
Fungiidae (multiple)	***Clavulina cristata***	rRNA	1796	86.303	1908	0
Fungiidae (multiple)	***Camarophyllopsis schulzeri*** *(Clavariaceae)*	rRNA	1796	84.8	1959	0
Fungiidae (multiple)	***Camarophyllopsis schulzeri*** *(Clavariaceae)*	rRNA	1796	84.744	1955	0
Cycloseris (Psammocora) explanulata	***Trametes versicolor***	rRNA	1796	85.356	1996	0
Fungiidae (multiple)	***Clavulina cristata***	rRNA	1795	85.627	2012	0
Fungiidae (multiple)	***Clavulina cristata***	rRNA	1795	85.571	2007	0
Fungia scutaria	***Clavulina cristata***	rRNA	1795	85.46	1998	0
Fungiidae (multiple)	***Trametes versicolor***	rRNA	1795	85.571	2006	0
Fungiidae (multiple)	***Trametes versicolor***	rRNA	1795	85.515	2002	0
Fungiidae (multiple)	***Trametes versicolor***	rRNA	1795	85.46	1997	0
Cycloseris (Psammocora) explanulata	***Clavulina cristata***	rRNA	1793	85.499	2000	0
Fungiidae (multiple)	***Ramaria stricta***	rRNA	1789	84.349	1705	0
Fungiidae (multiple)	***Clavaria inaequalis*** *(Clavariaceae)*	rRNA	1786	83.651	1845	0
Fungiidae (multiple)	***Clavaria inaequalis*** *(Clavariaceae)*	rRNA	1786	83.595	1840	0
Fungiidae (multiple)	***Ramaria rubella***	rRNA	1782	82.267	1760	0
Fungiidae (multiple)	***Ramaria rubella***	rRNA	1782	82.099	1746	0
Fungiidae (multiple)	***Trametes versicolor***	rRNA	1780	85.281	1961	0
Fungiidae (multiple)	***Ramaria stricta***	rRNA	1777	83.849	1835	0
Fungiidae (multiple)	***Ramaria stricta***	rRNA	1777	83.793	1830	0
Fungiidae (multiple)	***Ramaria stricta***	rRNA	1777	83.68	1821	0

Fungiidae (multiple)	***Clavulina***	rRNA	1747	85.404	1939	0
Fungiidae (multiple)	***Clavulina***	mtDNA	943	71.262	471	8.99E-132
Fungiidae (multiple)	***Clavulina***	mtDNA	942	71.019	467	1.10E-130
Fungiidae (multiple)	***Clavulina***	mtDNA	942	71.019	467	1.10E-130
Danafungia scruposa Halomitra clavator Fungia fungites	***Ramariopsis corniculata*** *(Clavariaceae)*	mtDNA	866	68.822	310	2.26E-83
Cycloseris costulata Ctenactis echinata	***Ramaria flavescens***	mtDNA	608	65.954	139	1.77E-31
Danafungia horrida Lithophyllon sp.	***Ramariopsis corniculata*** *(Clavariaceae)*	mtDNA	586	73.549	344	1.10E-93
Danafungia scruposa Halomitra clavator Fungia fungites	***Ramariopsis corniculata*** *(Clavariaceae)*	mtDNA	499	75.551	343	1.10E-93
Danafungia scruposa Halomitra clavator Fungia fungites	***Ramariopsis corniculata*** *(Clavariaceae)*	mtDNA	402	73.881	247	2.26E-64
Danafungia scruposa Fungia fungites Halomitra clavator	***Ramaria flavescens***	mtDNA	292	76.027	205	1.45E-51
Ctenactis echinata Polyphyllia talpina	***Ramaria flavescens***	mtDNA	292	75	191	3.20E-47

Fungiidae v. Fungi

Highest Matches from Custom DB (not including coral mushrooms)

Species	Fungiidae	DNA/RNA	Length	%	Bit	E-Val.
Lichtheimia ramosa	***Cycloseris (Psammocora) explanulata***	rRNA	1881	77.459	1397	0
Cunninghamella bertholletiae	***Cycloseris (Psammocora) explanulata***	rRNA	1870	79.198	1508	0
Fonticula alba	***Fungiidae*** (multiple)	rRNA	1845	80.542	1628	0
Phaeodactylum tricornutum	***Fungiidae*** (multiple)	rRNA	1824	82.237	1755	0
Mutinus caninus [1]	***Fungiidae*** (multiple)	rRNA	1820	85	1969	0
Microsporum audouinii	***Fungiidae*** (multiple)	rRNA	1816	85.463	2020	0
Arthrobotrys conoides	***Fungiidae*** (multiple)	rRNA	1812	86.7	2114	0

[1] Stinkhorn family member to be reassigned to Demospongiae per [Paper].

Franziozyma bambusicola	***Fungiidae*** (multiple)	rRNA	1812	85.596	2016	0
Nectria cinnabarina	***Fungiidae*** (multiple)	rRNA	1806	85.548	2035	0
Clitocybe nebularis	***Fungiidae*** (multiple)	rRNA	1801	85.064	1978	0
Mycocalia denudata	***Fungiidae*** (multiple)	rRNA	1800	85.278	1982	0
Nidula niveotomentosa	***Fungiidae*** (multiple)	rRNA	1799	85.27	1978	0
Sympodiomycopsis paphiopedili	***Fungiidae*** (multiple)	rRNA	1794	85.229	1981	0
Tilletiopsis pinicola	***Fungiidae*** (multiple)	rRNA	1779	85.722	2004	0
Samsoniella hepiali	***Fungia fungites***	mtDNA	1398	70.315	636	1.74E-179
Gilbertella persicaria	***Fungia fungites***	mtDNA	1254	73.046	719	0
Fonticula alba	***Fungia fungites***	mtDNA	1177	74.936	772	0
Stemonitis flavogenita	***Cycloseris costulata*** ***Danafungia horrida***	mtDNA	1032	72.868	480	2.96E-132
Rhizopus microsporus	***Fungiidae*** (multiple)	mtDNA	965	68.394	322	4.98E-85
Sympodiomycopsis kandeliae	***Cycloseris costulata***	mtDNA	959	71.324	462	7.95E-127
Arcyria cinerea	***Fungiidae*** (multiple)	mtDNA	947	73.601	563	3.15E-157
Lycogala epidendrum	***Danafungia horrida*** ***Fungia fungites***	mtDNA	885	72.316	369	3.84E-99
Turbinellus floccosus	***Ctenactis crassa*** ***Fungia fungites***	mtDNA	548	68.431	176	4.67E-41

Appendix B: Morphology

Clavaria zollingeri
inaturalist.org Observ. No. 85839910
Otago, New Zealand. © Joseph Pallante

Clavulina cinerea
inaturalist.org Observ. No. 91983918
Indiana, USA. © Stephen Russell

Clavaria zollingeri
inaturalist.org Observ. No. 260628584
Dutchess Co., New York, USA. © Christine Young

Clavulina rugosa
inaturalist.org Observ. No. 201738971
California, USA. © Taye Bright

Cycloseris explanulata.
inaturalist.org Observ. No. 105357688
Thailand. © New Heaven Reef Conservation Program.

Cycloseris cyclolites
inaturalist.org Observ. No. 262730927
New Caledonia. © Pauline Fey

Cycloseris cyclolites.
inaturalist.org Observ. No. 261920991
Ilot, New Caledonia. © Johan Bas.

Fungia fungites
inaturalist.org Observ. No. 282590514
Nord, New Caledonia. © Amaury Durbano

Heliofungia actiniformis
inaturalist.org Observ. No. 83970343
Sulawesi Utara, Indonesia. © Jean-Paul Cassez

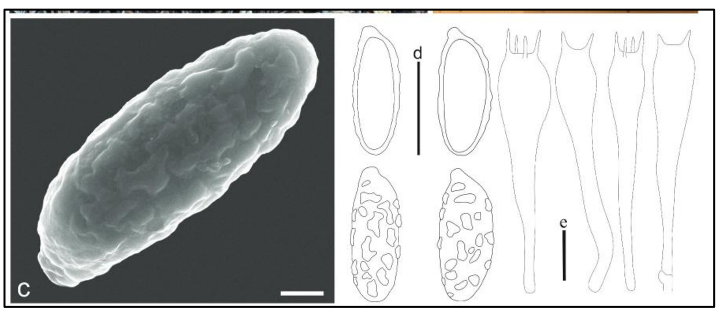
Heliofungia actiniformis
inaturalist.org Observ. No. 245031854
Romblon, Philippines. © caleidoskopable

Ramaria stricta
inaturalist.org Observ. No. 8355640
Ontario, Canada. © Ryan Hodnett

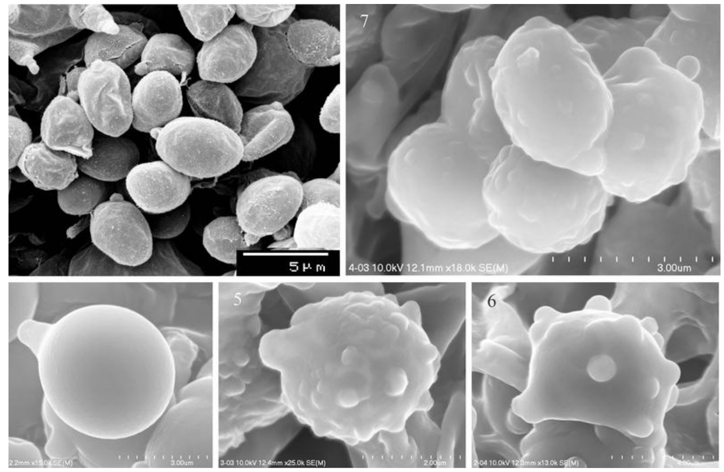
Ramaria araiospora
inaturalist.org Observ. No. 65913841
Humboldt Co., California. © David Greenberger

Ramariopsis pulchella
inaturalist.org Observ. No. 180878394
Sha Tin, Hong Kong. © Jel Lam

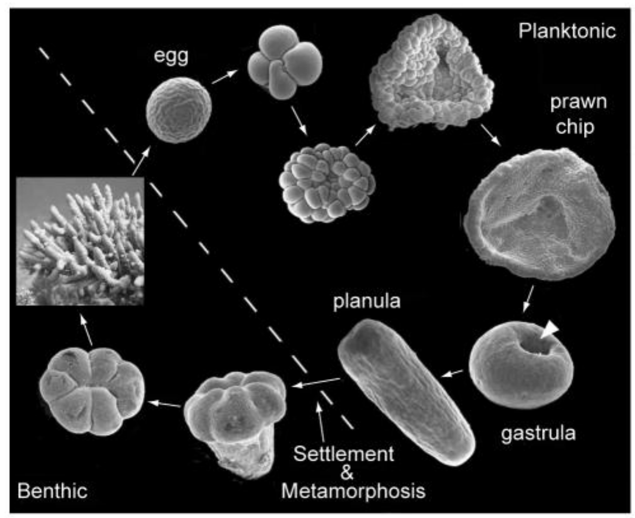
Microscopic



Ramaria obtusa, body and spores. (Li, Y. et al, 2025).



SEM pictures of ***Clavariaceae*** species spores.
Clavaria sp. and *Ramariopsis*. (Kautmanová 2011).



Coral Reproduction, NOAA
https://cdhc.noaa.gov/coral-biology/coral-reproduction/

Appendix C: NIH BLAST Web Alignments

Query: Clavulina cristata 18S ribosomal RNA gene, partial sequence ID: AF026640.1(nucleic acid) Length: 1790
RID: 5ANV7K39114 | Job Title: gb|AF026640.1| Program: BLASTN

Subject #1:Danafungia horrida partial 18S rRNA gene, specimen voucher GA133 ID: LT631153.1 Length: 1797
Subject #2:Fungia fungites partial 18S rRNA gene, specimen voucher GA018 ID: LT631154.1 Length: 1797
Subject #3:Halomitra pileus partial 18S rRNA gene, specimen voucher MAY442 ID: LT631155.1 Length: 1797
Subject #4:Herpolitha limax partial 18S rRNA gene, specimen voucher GA020 ID: LT631156.1 Length: 1797
Subject #5:Lobactis scutaria partial 18S rRNA gene, specimen voucher GA055 ID: LT631164.1 Length: 1797
Subject #6:Pleuractis paumotensis partial 18S rRNA gene, specimen voucher GA132 ID: LT631169.1 Length: 1797
Subject #7:Podabacia crustacea partial 18S rRNA gene, specimen voucher MAY435 ID: LT631170.1 Length: 1797
Subject #8:Sandalolitha robusta partial 18S rRNA gene, specimen voucher GA016 ID: LT631174.1 Length: 1797
Subject #9:Cycloseris explanulata partial 18S rRNA gene, specimen voucher BA116 ID: LT631152.1 Length: 1797
Subject #10:Fungia scutaria 18S ribosomal RNA gene, partial sequence ID: AF052884.1 Length: 1797

Sequences producing significant alignments:

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len
Lobactis scutaria partial 18S rRNA gene, specimen voucher GA055	*Lobactis scutaria*	2012	2012	99%	0.0	85.63%	1797
Herpolitha limax partial 18S rRNA gene, specimen voucher GA020	*Herpolitha limax*	2012	2012	99%	0.0	85.63%	1797
Halomitra pileus partial 18S rRNA gene, specimen voucher MAY442	*Halomitra pileus*	2012	2012	99%	0.0	85.63%	1797
Fungia fungites partial 18S rRNA gene, specimen voucher GA018	*Fungia fungites*	2012	2012	99%	0.0	85.63%	1797
Danafungia horrida partial 18S rRNA gene, specimen voucher GA133	*Danafungia horrida*	2012	2012	99%	0.0	85.63%	1797
Sandalolitha robusta partial 18S rRNA gene, specimen voucher GA016	*Sandalolitha robusta*	2007	2007	99%	0.0	85.57%	1797
Podabacia crustacea partial 18S rRNA gene, specimen voucher MAY435	*Podabacia crustacea*	2007	2007	99%	0.0	85.57%	1797
Pleuractis paumotensis partial 18S rRNA gene, specimen voucher GA132	*Pleuractis paumotensis*	2007	2007	99%	0.0	85.57%	1797
Cycloseris explanulata partial 18S rRNA gene, specimen voucher BA116	*Cycloseris explanulata*	2000	2000	99%	0.0	85.50%	1797
Fungia scutaria 18S ribosomal RNA gene, partial sequence	*Lobactis scutaria*	1998	1998	99%	0.0	85.46%	1797

Alignments:

>Lobactis scutaria partial 18S rRNA gene, specimen voucher GA055
Sequence ID: LT631164.1 Length: 1797

Range 1: 20 to 1790

Score:2012 bits(2230), Expect:0.0,
Identities:1537/1795(86%), Gaps:43/1795(2%), Strand: Plus/Plus

```
Query 15   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAACAAATTTATA  74
           ||||||||||||||||||||||||||||||||||||||||||||||||||   | ||
Sbjct 20   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAGCAC--TAGTA  77

Query 75   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTT-ACTA  133
           |||||||||||||||||||||||||||||||||| ||||||||||| ||||||| ||||
Sbjct 78   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATTGTACCTTTACTA  137

Query 134  CATGGATAACTGTGGTAATTCTAGAGCTAATACATGCTTCAAAGCCCCGACTCCTGGAAG  193
           | ||||||||| || |||||||||||||||||||||||   |||| ||||||| |||||||
Sbjct 138  CTTGGATAACCGTAGTAATTCTAGAGCTAATACATGCGA-AAAGTCCCGACTTCTGGAAG  196

Query 194  GGGTGTATTTATTAGATaaaaaayCAATGCGG-TTC-GCC--GCTCTCTTGGTGATTCAT  249
           || |||||||||||||| ||||| |||||||| ||| |||  | ||| ||||||||||||
Sbjct 197  GGATGTATTTATTAGATTAAAAACCAATGCGGGTTCTGCCCGGTTCT-TTGGTGATTCAT  255

Query 250  AATAACTTCTCGAATCGCATGGCCTTGTGCCGGTGATGCTTCATTCAAATATCTGCCCTA  309
           | ||||| |||||||||| ||||||| || || |||| ||||||||||| |||||||||
Sbjct 256  AGTAACTGATCGAATCGCACGGCCTTGCGCTGGCGATGTTTCATTCAAATTTCTGCCCTA  315

Query 310  TCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTTTCAACGGGTAACGGGGAATAAGG  369
           |||||| ||||||||| | ||| ||| |||||||||| |||||||| |||| |||| |||
Sbjct 316  TCAACTGTCGATGGTAAGGTAGTGGCTTACCATGGTTGCAACGGGTGACGGAGAATTAGG  375

Query 370  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  429
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 376  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  435

Query 430  CGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATATAGGGCTCT  489
           |||||||||||||||| ||| | ||||||||||||||| ||||||||||| |||||| |
Sbjct 436  CGCAAATTACCCAATCCTGACTCAGGGAGGTAGTGACAAGAAATAACAATACAGGGCTTT  495

Query 490  TTTGGGTCTTATAATTGGAATGAGTACAACTTAAATCCCTTAACGAGGAACAATTGGAGG  549
           |   ||||| |||||||||||||||||||||||||||||| |||||||||| | ||||||||
Sbjct 496  TCCAAGTCTTGTAATTGGAATGAGTACAACTTAAATCCTTTAACGAGGATCCATTGGAGG  555

Query 550  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  609
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 556  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  615

Query 610  GCAGTTAAAAAGCTCGTAGTTGAACTTCAGCTCTGGCCGGGCGGTCTGCCTCACGGTATG  669
           ||||||||||||||||||||| | ||| |   | |||| ||||||||| || ||||||
Sbjct 616  GCAGTTAAAAAGCTCGTAGTTGGATTTCGGGATGGCCCGGCCGGTCTGCCGCAAGGTATG  675

Query 670  T-ACTGTCTG-GCTGGGGCTTACCTT-------CTG-GTGAGCTCGCATGTCGTTCATTC  719
           | ||||| | ||||  ||| |||     ||| ||| ||||     |||| |
Sbjct 676  TTACTGGCCGAGCTGTT-CTT-CCTCGCAAAGACTGTGTGTGCTC--------TTAACTG  725

Query 720  GGTGTGTGAGGGAACCAGGACTTTTACCTTGAGAAAATTAGAGTGTTCAAAGCAGGCAAA  779
            |||||   |||  |  ||| ||||| |||| |||||||||||||||||||||| || |
Sbjct 726  AGTGTGCTCAGGATCTGCGACGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAAGCCAG  785
```

```
Query  780   TGCCCGAATACATTAGCATGGCATAATGGAATAGGACGTGCGGTTCTATTTTGTTGGTTT  839
              ||  |||||||| ||||||| ||||||||||||||| |  |||||||||||||||||||
Sbjct  786   CGCTTGAATACATAAGCATGGAATAATGGAATAGGACTTT-GGTTCTATTTTGTTGGTTT  844

Query  840   CTAGAGTCGCCGTAATGATTAATAGGGACAGTTGGGGGCATTAGTATTGAGTTGCTAGAG  899
             || ||  ||  ||||||||||| || |||||||||||||||| |||||  ||||  ||||
Sbjct  845   CTGGAACCGAAGTAATGATTAAGAGAGACAGTTGGGGGCATTCGTATTTCGTTGTCAGAG  904

Query  900   GTGAAATTCTTGGATTTACTCAAGACTAACTATTGCGAAAGCATTTGCCAAGGATGTTTT  959
             ||| |||||||||||||||  ||||| ||||| ||||||||||||||||||| |||||||
Sbjct  905   GTGGAATTCTTGGATTTACGAAAGACGAACTACTGCGAAAGCATTTGCCAAGAATGTTTT  964

Query  960   CATTAATCAAGAACGAAGGTTAGGGGATCGAAAACGATCAGATACCGTTGTAGTCTTAAC  1019
             ||||||||||||||||| ||||| |||||||| |||||||||||||||  ||||  ||||
Sbjct  965   CATTAATCAAGAACGAAAGTTAGAGGATCGAAGACGATCAGATACCGTCCTAGTTCTAAC  1024

Query  1020  AGTAAACTATGCCGACTAGGGATCGGGCAATCTCACTTTTATGTGTTGCTCGGCACCTTA  1079
               ||||| ||||| |||||||||| |    | | | ||  |||      | |||||||||
Sbjct  1025  CATAAACGATGCCAACTAGGGATCAGAGGGTGTTA-TTGGATGACCCCTTTGGCACCTTA  1083

Query  1080  CGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGG  1139
              | |||| |||||| ||||||||| ||||| |||||||| |||| |||||||||||||||
Sbjct  1084  TGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGG  1143

Query  1140  AATTGACGGAAGGGCACCACCAGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1199
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  1144  AATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1203

Query  1200  AAACTCACCAGGTCCAGACATAACTAGGATTGACAGATTGATAGCTCTTTCATGATTTTA  1259
             ||||||||||||||||||||||   |||||||||||||||| ||||||||| ||||| ||
Sbjct  1204  AAACTCACCAGGTCCAGACATAGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCTA  1263

Query  1260  TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGATA  1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1264  TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGTTA  1323

Query  1320  ACGAACGAGACCTTAACCTGCTAAATAGACAGGCCGGCTCTGGCTGGTCGCCGT---CTT  1376
             ||||||||||||||||||||||||||||  | | ||  ||  | |  |||| ||   |||
Sbjct  1324  ACGAACGAGACCTTAACCTGCTAAATAGTTACG-CGAATCCCGAT--TCGCGGTTAACTT  1380

Query  1377  CTTAGAGGGACTGTCAGTGTCTAACTGACGGAAGTTTGAGGCAATAACAGGTCTGTGATG  1436
             ||||||||||||||  || || |||  | |  ||    ||||||||||||||||||||||
Sbjct  1381  CTTAGAGGGACTGTTGGTATCCAACCAAAGTCAG--GAAGGCAATAACAGGTCTGTGATG  1438

Query  1437  CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACAGAGCCAGCGAGTTTATCACCT  1496
             ||||||||||||||||||||||||||||||||||||||   | ||| |||  | || |||
Sbjct  1439  CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACGATGTCAGAGAG--TGTCTCCT  1496

Query  1497  TGACTGAAAAGTCTGGGTAATCTTGTGAAACTTTGTCGTGCTGGGGATAGAGCATTGCAA  1556
             | || || | || ||||||||||||| |||| | ||||||||||||||||| ||||||||
Sbjct  1497  TCACCGAGAGGTGTGGGTAATCTTGT-AAACATCGTCGTGCTGGGGATAGATCATTGCAA  1555

Query  1557  TTATTGCTCTTCAACGAGGAATACCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG  1616
             |||||| |||| |||||||||| |||||||||||| ||||||||||| ||||||||||||
Sbjct  1556  TTATTGATCTTGAACGAGGAATTCCTAGTAAGCGCGAGTCATCAGCTCGCGTTGATTACG  1615

Query  1617  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGTCT  1676
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        ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||
Sbjct 1616  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGTTTAGTGAGGCCT  1675

Query 1677  CTGGATTGGCGCTGAGGAGCCGGCAACGGCAC-CTCGTTGCTGAGAAGTTGATCAAACTT  1735
          || |||||||| || |  ||||||| |  ||  | |||  | |||||| ||||||||
Sbjct 1676  TCTGACTGGCGCCGATGCTCTGGCAACAGAGCGCCGGATGCCGGAAAGTTGGTCAAACTT  1735

Query 1736  GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGA  1790
        | |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 1736  GATCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA  1790
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>Herpolitha limax partial 18S rRNA gene, specimen voucher GA020
Sequence ID: LT631156.1 Length: 1797
Range 1: 20 to 1790

Score:2012 bits(2230), Expect:0.0,
Identities:1537/1795(86%), Gaps:43/1795(2%), Strand: Plus/Plus

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Query 15   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAACAAATTTATA  74
        |||||||||||||||||||||||||||||||||||||||||||||||||| ||   |  ||
Sbjct 20   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAGCAC--TAGTA  77

Query 75   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTT-ACTA  133
        |||||||||||||||||||||||||||||||||||| |||||||||||| |||||||| ||||
Sbjct 78   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATTGTACCTTTACTA  137

Query 134  CATGGATAACTGTGGTAATTCTAGAGCTAATACATGCTTCAAAGCCCCGACTCCTGGAAG  193
        | ||||||||| || ||||||||||||||||||||||||   |||| |||||||| |||||||
Sbjct 138  CTTGGATAACCGTAGTAATTCTAGAGCTAATACATGCGA-AAAGTCCCGACTTCTGGAAG  196

Query 194  GGGTGTATTTATTAGATaaaaaayCAATGCGG-TTC-GCC--GCTCTCTTGGTGATTCAT  249
        || ||||||||||||||| ||||| ||||||||| ||| |||  | ||| |||||||||||||
Sbjct 197  GGATGTATTTATTAGATTAAAAACCAATGCGGGTTCTGCCCGGTTCT-TTGGTGATTCAT  255

Query 250  AATAACTTCTCGAATCGCATGGCCTTGTGCCGGTGATGCTTCATTCAAATATCTGCCCTA  309
        | ||||||  ||||||||||| ||||||| || || |||| |||||||||||| ||||||||||
Sbjct 256  AGTAACTGATCGAATCGCACGGCCTTGCGCTGGCGATGTTTCATTCAAATTTCTGCCCTA  315

Query 310  TCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTTTCAACGGGTAACGGGGAATAAGG  369
        |||||| ||||||||| | ||| ||| ||||||||||| |||||||| |||| |||| |||
Sbjct 316  TCAACTGTCGATGGTAAGGTAGTGGCTTACCATGGTTGCAACGGGTGACGGAGAATTAGG  375

Query 370  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  429
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 376  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  435

Query 430  CGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATATAGGGCTCT  489
        |||||||||||||||| ||| | ||||||||||||||| ||||||||||| ||||||| |
Sbjct 436  CGCAAATTACCCAATCCTGACTCAGGGAGGTAGTGACAAGAAATAACAATACAGGGCTTT  495

Query 490  TTTGGGTCTTATAATTGGAATGAGTACAACTTAAATCCCTTAACGAGGAACAATTGGAGG  549
        |   ||||| ||||||||||||||||||||||||||||| ||||||||||| | |||||||||
Sbjct 496  TCCAAGTCTTGTAATTGGAATGAGTACAACTTAAATCCTTTAACGAGGATCCATTGGAGG  555

Query 550  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  609
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct 556  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  615

Query 610  GCAGTTAAAAAGCTCGTAGTTGAACTTCAGCTCTGGCCGGGCGGTCTGCCTCACGGTATG  669
           |||||||||||||||||||||| | ||| |    | |||| ||||||||| || ||||||
Sbjct 616  GCAGTTAAAAAGCTCGTAGTTGGATTTCGGGATGGCCCGGCCGGTCTGCCGCAAGGTATG  675

Query 670  T-ACTGTCTG-GCTGGGGCTTACCTT-------CTG-GTGAGCTCGCATGTCGTTCATTC  719
           | |||| | | ||||   ||| |||        ||| ||| ||||        || | | 
Sbjct 676  TTACTGGCCGAGCTGTT-CTT-CCTCGCAAAGACTGTGTGTGCTC--------TTAACTG  725

Query 720  GGTGTGTGAGGGAACCAGGACTTTTACCTTGAGAAAATTAGAGTGTTCAAAGCAGGCAAA  779
            |||||    ||| |   ||| ||||| |||| |||||||||||||||||||| || | 
Sbjct 726  AGTGTGCTCAGGATCTGCGACGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAAGCCAG  785

Query 780  TGCCCGAATACATTAGCATGGCATAATGGAATAGGACGTGCGGTTCTATTTTGTTGGTTT  839
            ||  ||||||||| ||||||| ||||||||||||||| |  |||||||||||||||||||
Sbjct 786  CGCTTGAATACATAAGCATGGAATAATGGAATAGGACTTT-GGTTCTATTTTGTTGGTTT  844

Query 840  CTAGAGTCGCCGTAATGATTAATAGGGACAGTTGGGGGCATTAGTATTGAGTTGCTAGAG  899
           || ||  ||  ||||||||||| || ||||||||||||||| |||||  ||||  ||||
Sbjct 845  CTGGAACCGAAGTAATGATTAAGAGAGACAGTTGGGGGCATTCGTATTTCGTTGTCAGAG  904

Query 900  GTGAAATTCTTGGATTTACTCAAGACTAACTATTGCGAAAGCATTTGCCAAGGATGTTTT  959
           ||| |||||||||||||||  ||||| |||||| ||||||||||||||||||||| |||||||
Sbjct 905  GTGGAATTCTTGGATTTACGAAAGACGAACTACTGCGAAAGCATTTGCCAAGAATGTTTT  964

Query 960  CATTAATCAAGAACGAAGGTTAGGGGATCGAAAACGATCAGATACCGTTGTAGTCTTAAC  1019
           ||||||||||||||||| ||||| |||||||| |||||||||||||||  ||||  ||||
Sbjct 965  CATTAATCAAGAACGAAAGTTAGAGGATCGAAGACGATCAGATACCGTCCTAGTTCTAAC  1024

Query 1020 AGTAAACTATGCCGACTAGGGATCGGGCAATCTCACTTTTATGTGTTGCTCGGCACCTTA  1079
             ||||| ||||| |||||||||| |    | | | ||  |||      | |||||||||
Sbjct 1025 CATAAACGATGCCAACTAGGGATCAGAGGGTGTTA-TTGGATGACCCCTTTGGCACCTTA  1083

Query 1080 CGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGG  1139
            | |||| ||||||| |||||||| |||||| |||||||| |||| |||||||||||||||
Sbjct 1084 TGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGG  1143

Query 1140 AATTGACGGAAGGGCACCACCAGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1199
           |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct 1144 AATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1203

Query 1200 AAACTCACCAGGTCCAGACATAACTAGGATTGACAGATTGATAGCTCTTTCATGATTTTA  1259
           ||||||||||||||||||||||   ||||||||||||||| ||||||||||| ||||| ||
Sbjct 1204 AAACTCACCAGGTCCAGACATAGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCTA  1263

Query 1260 TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGATA  1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 1264 TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGTTA  1323

Query 1320 ACGAACGAGACCTTAACCTGCTAAATAGACAGGCCGGCTCTGGCTGGTCGCCGT---CTT  1376
           ||||||||||||||||||||||||||||  | | ||  ||       |||| ||   |||
Sbjct 1324 ACGAACGAGACCTTAACCTGCTAAATAGTTACG-CGAATCCCGAT--TCGCGGTTAACTT  1380

Query 1377 CTTAGAGGGACTGTCAGTGTCTAACTGACGGAAGTTTGAGGCAATAACAGGTCTGTGATG  1436
           ||||||||||||||  || || |||  | |  ||    ||||||||||||||||||||||
Sbjct 1381 CTTAGAGGGACTGTTGGTATCCAACCAAAGTCAG--GAAGGCAATAACAGGTCTGTGATG  1438
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Query 1437 CCCTTAGATGTTCTGGGCCGCACGCGCTACACTGACAGAGCCAGCGAGTTTATCACCT 1496
           ||||||||||||||||||||||||||||||||||||||   | ||| |||  | || |||
Sbjct 1439 CCCTTAGATGTTCTGGGCCGCACGCGCTACACTGACGATGTCAGAGAG--TGTCTCCT 1496

Query 1497 TGACTGAAAAGTCTGGGTAATCTTGTGAAACTTTGTCGTGCTGGGGATAGAGCATTGCAA 1556
           | || || | || |||||||||||||| |||| | |||||||||||||||||| |||||||||
Sbjct 1497 TCACCGAGAGGTGTGGGTAATCTTGT-AAACATCGTCGTGCTGGGGATAGATCATTGCAA 1555

Query 1557 TTATTGCTCTTCAACGAGGAATACCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG 1616
           |||||| |||| |||||||||||| |||||||||||| ||||||||||| |||||||||||||
Sbjct 1556 TTATTGATCTTGAACGAGGAATTCCTAGTAAGCGCGAGTCATCAGCTCGCGTTGATTACG 1615

Query 1617 TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGTCT 1676
           ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||
Sbjct 1616 TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGTTTAGTGAGGCCT 1675

Query 1677 CTGGATTGGCGCTGAGGAGCCGGCAACGGCAC-CTCGTTGCTGAGAAGTTGATCAAACTT 1735
             || |||||||| || |  | ||||||| |  | |  | |||| |  |||||| |||||||||
Sbjct 1676 TCTGACTGGCGCCGATGCTCTGGCAACAGAGCGCCGGATGCCGGAAAGTTGGTCAAACTT 1735

Query 1736 GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGA 1790
           | |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 1736 GATCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA 1790
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>Halomitra pileus partial 18S rRNA gene, specimen voucher MAY442
Sequence ID: LT631155.1 Length: 1797
Range 1: 20 to 1790

Score:2012 bits(2230), Expect:0.0,
Identities:1537/1795(86%), Gaps:43/1795(2%), Strand: Plus/Plus

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Query 15   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAACAAATTTATA 74
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||   |  ||
Sbjct 20   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAGCAC--TAGTA 77

Query 75   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTT-ACTA 133
           |||||||||||||||||||||||||||||||||||| ||||||||||| |||||||| ||||
Sbjct 78   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATTGTACCTTTACTA 137

Query 134  CATGGATAACTGTGGTAATTCTAGAGCTAATACATGCTTCAAAGCCCCGACTCCTGGAAG 193
           | ||||||||| || ||||||||||||||||||||||||   |||| |||||||| ||||||||
Sbjct 138  CTTGGATAACCGTAGTAATTCTAGAGCTAATACATGCGA-AAAGTCCCGACTTCTGGAAG 196

Query 194  GGGTGTATTTATTAGATaaaaaayCAATGCGG-TTC-GCC--GCTCTCTTGGTGATTCAT 249
           || |||||||||||||| ||||| ||||||||| ||| |||  | ||| |||||||||||||
Sbjct 197  GGATGTATTTATTAGATTAAAAACCAATGCGGGTTCTGCCCGGTTCT-TTGGTGATTCAT 255

Query 250  AATAACTTCTCGAATCGCATGGCCTTGTGCCGGTGATGCTTCATTCAAATATCTGCCCTA 309
           | |||||  |||||||||| ||||||| || || |||| |||||||||||| |||||||||
Sbjct 256  AGTAACTGATCGAATCGCACGGCCTTGCGCTGGCGATGTTTCATTCAAATTTCTGCCCTA 315

Query 310  TCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTTTCAACGGGTAACGGGGAATAAGG 369
           |||||| ||||||||| | ||| ||| |||||||||| |||||||| |||| |||| |||
Sbjct 316  TCAACTGTCGATGGTAAGGTAGTGGCTTACCATGGTTGCAACGGGTGACGGAGAATTAGG 375
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Query  370  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  429
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  376  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  435

Query  430  CGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATATAGGGCTCT  489
            ||||||||||||||||| ||| | ||||||||||||||| ||||||||||| |||||| |
Sbjct  436  CGCAAATTACCCAATCCTGACTCAGGGAGGTAGTGACAAGAAATAACAATACAGGGCTTT  495

Query  490  TTTGGGTCTTATAATTGGAATGAGTACAACTTAAATCCCTTAACGAGGAACAATTGGAGG  549
            |    ||||| ||||||||||||||||||||||||||| |||||||||| | ||||||||
Sbjct  496  TCCAAGTCTTGTAATTGGAATGAGTACAACTTAAATCCTTTAACGAGGATCCATTGGAGG  555

Query  550  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  609
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  556  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  615

Query  610  GCAGTTAAAAAGCTCGTAGTTGAACTTCAGCTCTGGCCGGGCGGTCTGCCTCACGGTATG  669
            |||||||||||||||||||||| | ||| |    | |||| ||||||||| || ||||||
Sbjct  616  GCAGTTAAAAAGCTCGTAGTTGGATTTCGGGATGGCCCGGCCGGTCTGCCGCAAGGTATG  675

Query  670  T-ACTGTCTG-GCTGGGGCTTACCTT-------CTG-GTGAGCTCGCATGTCGTTCATTC  719
            | |||| | | ||||   ||| |||        ||| ||| ||||        || | | 
Sbjct  676  TTACTGGCCGAGCTGTT-CTT-CCTCGCAAAGACTGTGTGTGCTC--------TTAACTG  725

Query  720  GGTGTGTGAGGGAACCAGGACTTTTACCTTGAGAAAATTAGAGTGTTCAAAGCAGGCAAA  779
             |||||    ||| |   ||| ||||| |||| ||||||||||||||||||||| || | 
Sbjct  726  AGTGTGCTCAGGATCTGCGACGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAAGCCAG  785

Query  780  TGCCCGAATACATTAGCATGGCATAATGGAATAGGACGTGCGGTTCTATTTTGTTGGTTT  839
             ||  |||||||| ||||||| ||||||||||||||| |  |||||||||||||||||||
Sbjct  786  CGCTTGAATACATAAGCATGGAATAATGGAATAGGACTTT-GGTTCTATTTTGTTGGTTT  844

Query  840  CTAGAGTCGCCGTAATGATTAATAGGGACAGTTGGGGGCATTAGTATTGAGTTGCTAGAG  899
            || ||  ||  ||||||||||| || |||||||||||||||| |||||  ||||  ||||
Sbjct  845  CTGGAACCGAAGTAATGATTAAGAGAGACAGTTGGGGGCATTCGTATTTCGTTGTCAGAG  904

Query  900  GTGAAATTCTTGGATTTACTCAAGACTAACTATTGCGAAAGCATTTGCCAAGGATGTTTT  959
            ||| |||||||||||||||  ||||| ||||| ||||||||||||||||||| |||||||
Sbjct  905  GTGGAATTCTTGGATTTACGAAAGACGAACTACTGCGAAAGCATTTGCCAAGAATGTTTT  964

Query  960  CATTAATCAAGAACGAAGGTTAGGGGATCGAAAACGATCAGATACCGTTGTAGTCTTAAC  1019
            ||||||||||||||||| ||||| |||||||| |||||||||||||||  ||||  ||||
Sbjct  965  CATTAATCAAGAACGAAAGTTAGAGGATCGAAGACGATCAGATACCGTCCTAGTTCTAAC  1024

Query  1020 AGTAAACTATGCCGACTAGGGATCGGGCAATCTCACTTTTATGTGTTGCTCGGCACCTTA  1079
              ||||| ||||| |||||||||| |    | | | ||  |||      | |||||||||
Sbjct  1025 CATAAACGATGCCAACTAGGGATCAGAGGGTGTTA-TTGGATGACCCCTTTGGCACCTTA  1083

Query  1080 CGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGG  1139
             | |||| |||||| ||||||||| ||||| |||||||| |||| |||||||||||||||
Sbjct  1084 TGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGG  1143

Query  1140 AATTGACGGAAGGGCACCACCAGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1199
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  1144 AATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1203

Query  1200 AAACTCACCAGGTCCAGACATAACTAGGATTGACAGATTGATAGCTCTTTCATGATTTTA  1259
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       ||||||||||||||||||||||  |||||||||||||||| ||||||||| ||||| ||
Sbjct 1204 AAACTCACCAGGTCCAGACATAGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCTA 1263

Query 1260 TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGATA 1319
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 1264 TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGTTA 1323

Query 1320 ACGAACGAGACCTTAACCTGCTAAATAGACAGGCCGGCTCTGGCTGGTCGCCGT---CTT 1376
       ||||||||||||||||||||||||||||  | | | ||  ||  | |  |||| ||   |||
Sbjct 1324 ACGAACGAGACCTTAACCTGCTAAATAGTTACG-CGAATCCCGAT--TCGCGGTTAACTT 1380

Query 1377 CTTAGAGGGACTGTCAGTGTCTAACTGACGGAAGTTTGAGGCAATAACAGGTCTGTGATG 1436
       ||||||||||||||  || || |||  | |  ||    ||||||||||||||||||||||
Sbjct 1381 CTTAGAGGGACTGTTGGTATCCAACCAAAGTCAG--GAAGGCAATAACAGGTCTGTGATG 1438

Query 1437 CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACAGAGCCAGCGAGTTTATCACCT 1496
       ||||||||||||||||||||||||||||||||||||||   | ||| |||  | || |||
Sbjct 1439 CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACGATGTCAGAGAG--TGTCTCCT 1496

Query 1497 TGACTGAAAAGTCTGGGTAATCTTGTGAAACTTTGTCGTGCTGGGGATAGAGCATTGCAA 1556
       | || || | || ||||||||||||| |||| | ||||||||||||||||| ||||||||
Sbjct 1497 TCACCGAGAGGTGTGGGTAATCTTGT-AAACATCGTCGTGCTGGGGATAGATCATTGCAA 1555

Query 1557 TTATTGCTCTTCAACGAGGAATACCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG 1616
       |||||| |||| |||||||||| |||||||||||| ||||||||||| ||||||||||||
Sbjct 1556 TTATTGATCTTGAACGAGGAATTCCTAGTAAGCGCGAGTCATCAGCTCGCGTTGATTACG 1615

Query 1617 TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGTCT 1676
       ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| ||
Sbjct 1616 TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGTTTAGTGAGGCCT 1675

Query 1677 CTGGATTGGCGCTGAGGAGCCGGCAACGGCAC-CTCGTTGCTGAGAAGTTGATCAAACTT 1735
          || |||||| || |  | |||||| |  | |  | ||| |  |||||| ||||||||
Sbjct 1676 TCTGACTGGCGCCGATGCTCTGGCAACAGAGCGCCGGATGCCGGAAAGTTGGTCAAACTT 1735

Query 1736 GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGA 1790
       | |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 1736 GATCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA 1790
```

>Fungia fungites partial 18S rRNA gene, specimen voucher GA018
Sequence ID: LT631154.1 Length: 1797
Range 1: 20 to 1790

Score:2012 bits(2230), Expect:0.0,
Identities:1537/1795(86%), Gaps:43/1795(2%), Strand: Plus/Plus

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Query 15   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAACAAATTTATA 74
       ||||||||||||||||||||||||||||||||||||||||||||||||| ||   |  ||
Sbjct 20   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAGCAC--TAGTA 77

Query 75   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTT-ACTA 133
       ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||| ||||
Sbjct 78   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATTGTACCTTTACTA 137

Query 134  CATGGATAACTGTGGTAATTCTAGAGCTAATACATGCTTCAAAGCCCCGACTCCTGGAAG 193
       | |||||||| || |||||||||||||||||||||||  |||| ||||||| |||||||
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Sbjct 138  CTTGGATAACCGTAGTAATTCTAGAGCTAATACATGCGA-AAAGTCCCGACTTCTGGAAG 196

Query 194  GGGTGTATTTATTAGATaaaaaayCAATGCGG-TTC-GCC--GCTCTCTTGGTGATTCAT 249
           || |||||||||||||| ||||| |||||||| ||| ||| | ||| ||||||||||||
Sbjct 197  GGATGTATTTATTAGATTAAAAACCAATGCGGGTTCTGCCCGGTTCT-TTGGTGATTCAT 255

Query 250  AATAACTTCTCGAATCGCATGGCCTTGTGCCGGTGATGCTTCATTCAAATATCTGCCCTA 309
           | ||||| |||||||||| |||||| || || |||| ||||||||||| |||||||||
Sbjct 256  AGTAACTGATCGAATCGCACGGCCTTGCGCTGGCGATGTTTCATTCAAATTTCTGCCCTA 315

Query 310  TCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTTTCAACGGGTAACGGGGAATAAGG 369
           |||||| ||||||||| | ||| ||| |||||||||| |||||||| |||| |||| |||
Sbjct 316  TCAACTGTCGATGGTAAGGTAGTGGCTTACCATGGTTGCAACGGGTGACGGAGAATTAGG 375

Query 370  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG 429
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 376  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG 435

Query 430  CGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATATAGGGCTCT 489
           |||||||||||||||| ||| | ||||||||||||||| ||||||||||| ||||||| |
Sbjct 436  CGCAAATTACCCAATCCTGACTCAGGGAGGTAGTGACAAGAAATAACAATACAGGGCTTT 495

Query 490  TTTGGGTCTTATAATTGGAATGAGTACAACTTAAATCCCTTAACGAGGAACAATTGGAGG 549
           |   ||||| |||||||||||||||||||||||||||| |||||||||| | ||||||||
Sbjct 496  TCCAAGTCTTGTAATTGGAATGAGTACAACTTAAATCCTTTAACGAGGATCCATTGGAGG 555

Query 550  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT 609
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 556  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT 615

Query 610  GCAGTTAAAAAGCTCGTAGTTGAACTTCAGCTCTGGCCGGGCGGTCTGCCTCACGGTATG 669
           |||||||||||||||||||||| | ||| |   | |||| ||||||||| || ||||||
Sbjct 616  GCAGTTAAAAAGCTCGTAGTTGGATTTCGGGATGGCCCGGCCGGTCTGCCGCAAGGTATG 675

Query 670  T-ACTGTCTG-GCTGGGGCTTACCTT-------CTG-GTGAGCTCGCATGTCGTTCATTC 719
           | ||||| | ||||  ||| |||     ||| ||| ||||     |||| |
Sbjct 676  TTACTGGCCGAGCTGTT-CTT-CCTCGCAAAGACTGTGTGTGCTC--------TTAACTG 725

Query 720  GGTGTGTGAGGGAACCAGGACTTTTACCTTGAGAAAATTAGAGTGTTCAAAGCAGGCAAA 779
            |||||   ||| |  ||| ||||| |||| ||||||||||||||||||||| || |
Sbjct 726  AGTGTGCTCAGGATCTGCGACGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAAGCCAG 785

Query 780  TGCCCGAATACATTAGCATGGCATAATGGAATAGGACGTGCGGTTCTATTTTGTTGGTTT 839
            ||  |||||||| ||||||| ||||||||||||||| |  |||||||||||||||||||
Sbjct 786  CGCTTGAATACATAAGCATGGAATAATGGAATAGGACTTT-GGTTCTATTTTGTTGGTTT 844

Query 840  CTAGAGTCGCCGTAATGATTAATAGGGACAGTTGGGGGCATTAGTATTGAGTTGCTAGAG 899
           || || || ||||||||||| || ||||||||||||||||| ||||| |||| ||||
Sbjct 845  CTGGAACCGAAGTAATGATTAAGAGAGACAGTTGGGGGCATTCGTATTTCGTTGTCAGAG 904

Query 900  GTGAAATTCTTGGATTTACTCAAGACTAACTATTGCGAAAGCATTTGCCAAGGATGTTTT 959
           ||| |||||||||||||||  ||||| ||||| ||||||||||||||||||| |||||||
Sbjct 905  GTGGAATTCTTGGATTTACGAAAGACGAACTACTGCGAAAGCATTTGCCAAGAATGTTTT 964

Query 960  CATTAATCAAGAACGAAGGTTAGGGGATCGAAAACGATCAGATACCGTTGTAGTCTTAAC 1019
           ||||||||||||||||| ||||| ||||||||| ||||||||||||||| |||| ||||
Sbjct 965  CATTAATCAAGAACGAAAGTTAGAGGATCGAAGACGATCAGATACCGTCCTAGTTCTAAC 1024
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Query  1020  AGTAAACTATGCCGACTAGGGATCGGGCAATCTCACTTTTATGTGTTGCTCGGCACCTTA  1079
               ||||| ||||| |||||||||| |    | | | ||  |||      | |||||||||
Sbjct  1025  CATAAACGATGCCAACTAGGGATCAGAGGGTGTTA-TTGGATGACCCCTTTGGCACCTTA  1083

Query  1080  CGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGG  1139
              | |||| |||||| ||||||||| ||||| |||||||| |||| |||||||||||||||
Sbjct  1084  TGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGG  1143

Query  1140  AATTGACGGAAGGGCACCACCAGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1199
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  1144  AATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1203

Query  1200  AAACTCACCAGGTCCAGACATAACTAGGATTGACAGATTGATAGCTCTTTCATGATTTTA  1259
             ||||||||||||||||||||||   |||||||||||||||| ||||||||| ||||| ||
Sbjct  1204  AAACTCACCAGGTCCAGACATAGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCTA  1263

Query  1260  TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGATA  1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1264  TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGTTA  1323

Query  1320  ACGAACGAGACCTTAACCTGCTAAATAGACAGGCCGGCTCTGGCTGGTCGCCGT---CTT  1376
             ||||||||||||||||||||||||||||  | | ||  ||  | |  |||| ||   |||
Sbjct  1324  ACGAACGAGACCTTAACCTGCTAAATAGTTACG-CGAATCCCGAT--TCGCGGTTAACTT  1380

Query  1377  CTTAGAGGGACTGTCAGTGTCTAACTGACGGAAGTTTGAGGCAATAACAGGTCTGTGATG  1436
             ||||||||||||||  || || |||  | |  ||    ||||||||||||||||||||||
Sbjct  1381  CTTAGAGGGACTGTTGGTATCCAACCAAAGTCAG--GAAGGCAATAACAGGTCTGTGATG  1438

Query  1437  CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACAGAGCCAGCGAGTTTATCACCT  1496
             ||||||||||||||||||||||||||||||||||||||  | ||| |||  | || |||
Sbjct  1439  CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACGATGTCAGAGAG--TGTCTCCT  1496

Query  1497  TGACTGAAAAGTCTGGGTAATCTTGTGAAACTTTGTCGTGCTGGGGATAGAGCATTGCAA  1556
             | || || | || ||||||||||||| |||| | ||||||||||||||||| ||||||||
Sbjct  1497  TCACCGAGAGGTGTGGGTAATCTTGT-AAACATCGTCGTGCTGGGGATAGATCATTGCAA  1555

Query  1557  TTATTGCTCTTCAACGAGGAATACCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG  1616
             |||||| |||| |||||||||| |||||||||||| ||||||||||| ||||||||||||
Sbjct  1556  TTATTGATCTTGAACGAGGAATTCCTAGTAAGCGCGAGTCATCAGCTCGCGTTGATTACG  1615

Query  1617  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGTCT  1676
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| ||
Sbjct  1616  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGTTTAGTGAGGCCT  1675

Query  1677  CTGGATTGGCGCTGAGGAGCCGGCAACGGCAC-CTCGTTGCTGAGAAGTTGATCAAACTT  1735
                || |||||| || |  | |||||| |  | |  | ||| |  |||||| ||||||||
Sbjct  1676  TCTGACTGGCGCCGATGCTCTGGCAACAGAGCGCCGGATGCCGGAAAGTTGGTCAAACTT  1735

Query  1736  GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGA  1790
             | |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1736  GATCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA  1790
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>Danafungia horrida partial 18S rRNA gene, specimen voucher GA133

Sequence ID: LT631153.1 Length: 1797
Range 1: 20 to 1790

Score:2012 bits(2230), Expect:0.0,
Identities:1537/1795(86%), Gaps:43/1795(2%), Strand: Plus/Plus

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Query  15   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAACAAATTTATA  74
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||   |  ||
Sbjct  20   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAGCAC--TAGTA  77

Query  75   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTT-ACTA  133
            ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||| ||||
Sbjct  78   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATTGTACCTTTACTA  137

Query  134  CATGGATAACTGTGGTAATTCTAGAGCTAATACATGCTTCAAAGCCCCGACTCCTGGAAG  193
            | |||||||| || ||||||||||||||||||||||||   |||| ||||||| |||||||
Sbjct  138  CTTGGATAACCGTAGTAATTCTAGAGCTAATACATGCGA-AAAGTCCCGACTTCTGGAAG  196

Query  194  GGGTGTATTTATTAGATaaaaaayCAATGCGG-TTC-GCC--GCTCTCTTGGTGATTCAT  249
            || |||||||||||||| ||||| |||||||| ||| |||   | ||| ||||||||||||
Sbjct  197  GGATGTATTTATTAGATTAAAAACCAATGCGGGTTCTGCCCGGTTCT-TTGGTGATTCAT  255

Query  250  AATAACTTCTCGAATCGCATGGCCTTGTGCCGGTGATGCTTCATTCAAATATCTGCCCTA  309
            | |||||  |||||||||| ||||||| || || |||| ||||||||||| |||||||||
Sbjct  256  AGTAACTGATCGAATCGCACGGCCTTGCGCTGGCGATGTTTCATTCAAATTTCTGCCCTA  315

Query  310  TCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTTTCAACGGGTAACGGGGAATAAGG  369
            |||||| |||||||||| | ||| ||| ||||||||||| |||||||||| |||| |||| |||
Sbjct  316  TCAACTGTCGATGGTAAGGTAGTGGCTTACCATGGTTGCAACGGGTGACGGAGAATTAGG  375

Query  370  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  429
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  376  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  435

Query  430  CGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATATAGGGCTCT  489
            ||||||||||||||||| ||| | ||||||||||||||| ||||||||||| |||||| |
Sbjct  436  CGCAAATTACCCAATCCTGACTCAGGGAGGTAGTGACAAGAAATAACAATACAGGGCTTT  495

Query  490  TTTGGGTCTTATAATTGGAATGAGTACAACTTAAATCCCTTAACGAGGAACAATTGGAGG  549
            |    ||||| ||||||||||||||||||||||||||| |||||||||| | ||||||||
Sbjct  496  TCCAAGTCTTGTAATTGGAATGAGTACAACTTAAATCCTTTAACGAGGATCCATTGGAGG  555

Query  550  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  609
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  556  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  615

Query  610  GCAGTTAAAAAGCTCGTAGTTGAACTTCAGCTCTGGCCGGGCGGTCTGCCTCACGGTATG  669
            |||||||||||||||||||||| | ||| |    | ||||| |||||||| || ||||||
Sbjct  616  GCAGTTAAAAAGCTCGTAGTTGGATTTCGGGATGGCCCGGCCGGTCTGCCGCAAGGTATG  675

Query  670  T-ACTGTCTG-GCTGGGGCTTACCTT-------CTG-GTGAGCTCGCATGTCGTTCATTC  719
            | |||| | | ||||   ||| |||        ||| ||| ||||        || | |
Sbjct  676  TTACTGGCCGAGCTGTT-CTT-CCTCGCAAAGACTGTGTGTGCTC--------TTAACTG  725

Query  720  GGTGTGTGAGGGAACCAGGACTTTTACCTTGAGAAAATTAGAGTGTTCAAAGCAGGCAAA  779
             |||||    ||| |   ||| ||||| |||| |||||||||||||||||||||| || |
Sbjct  726  AGTGTGCTCAGGATCTGCGACGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAAGCCAG  785
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Query  780  TGCCCGAATACATTAGCATGGCATAATGGAATAGGACGTGCGGTTCTATTTTGTTGGTTT  839
             ||  |||||||| ||||||| ||||||||||||||| |  |||||||||||||||||||
Sbjct  786  CGCTTGAATACATAAGCATGGAATAATGGAATAGGACTTT-GGTTCTATTTTGTTGGTTT  844

Query  840  CTAGAGTCGCCGTAATGATTAATAGGGACAGTTGGGGGCATTAGTATTGAGTTGCTAGAG  899
            || ||  ||  ||||||||||| || ||||||||||||||||| ||||| |||| ||||
Sbjct  845  CTGGAACCGAAGTAATGATTAAGAGAGACAGTTGGGGGCATTCGTATTCGTTGTCAGAG  904

Query  900  GTGAAATTCTTGGATTTACTCAAGACTAACTATTGCGAAAGCATTTGCCAAGGATGTTTT  959
            ||| |||||||||||||||  ||||| ||||| ||||||||||||||||||| |||||||
Sbjct  905  GTGGAATTCTTGGATTTACGAAAGACGAACTACTGCGAAAGCATTTGCCAAGAATGTTTT  964

Query  960  CATTAATCAAGAACGAAGGTTAGGGGATCGAAAACGATCAGATACCGTTGTAGTCTTAAC  1019
            ||||||||||||||||| ||||| ||||||||| |||||||||||||||  |||| ||||
Sbjct  965  CATTAATCAAGAACGAAAGTTAGAGGATCGAAGACGATCAGATACCGTCCTAGTTCTAAC  1024

Query  1020 AGTAAACTATGCCGACTAGGGATCGGGCAATCTCACTTTTATGTGTTGCTCGGCACCTTA  1079
              ||||| ||||| |||||||||| |    | | | ||  |||      | |||||||||
Sbjct  1025 CATAAACGATGCCAACTAGGGATCAGAGGGTGTTA-TTGGATGACCCCTTTGGCACCTTA  1083

Query  1080 CGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGG  1139
             | |||| |||||| ||||||||| ||||| |||||||| |||| |||||||||||||||
Sbjct  1084 TGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGG  1143

Query  1140 AATTGACGGAAGGGCACCACCAGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1199
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  1144 AATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1203

Query  1200 AAACTCACCAGGTCCAGACATAACTAGGATTGACAGATTGATAGCTCTTTCATGATTTTA  1259
            ||||||||||||||||||||||   |||||||||||||||| ||||||||| ||||| ||
Sbjct  1204 AAACTCACCAGGTCCAGACATAGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCTA  1263

Query  1260 TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGATA  1319
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1264 TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGTTA  1323

Query  1320 ACGAACGAGACCTTAACCTGCTAAATAGACAGGCCGGCTCTGGCTGGTCGCCGT---CTT  1376
            ||||||||||||||||||||||||||||  | | ||  ||  | |  |||| ||   |||
Sbjct  1324 ACGAACGAGACCTTAACCTGCTAAATAGTTACG-CGAATCCCGAT--TCGCGGTTAACTT  1380

Query  1377 CTTAGAGGGACTGTCAGTGTCTAACTGACGGAAGTTTGAGGCAATAACAGGTCTGTGATG  1436
            ||||||||||||||  || || |||  | |  ||    ||||||||||||||||||||||
Sbjct  1381 CTTAGAGGGACTGTTGGTATCCAACCAAAGTCAG--GAAGGCAATAACAGGTCTGTGATG  1438

Query  1437 CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACAGAGCCAGCGAGTTTATCACCT  1496
            ||||||||||||||||||||||||||||||||||||||   | ||| |||  | || |||
Sbjct  1439 CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACGATGTCAGAGAG--TGTCTCCT  1496

Query  1497 TGACTGAAAAGTCTGGGTAATCTTGTGAAACTTTGTCGTGCTGGGGATAGAGCATTGCAA  1556
            | || || | || ||||||||||||| |||| | ||||||||||||||||| ||||||||
Sbjct  1497 TCACCGAGAGGTGTGGGTAATCTTGT-AAACATCGTCGTGCTGGGGATAGATCATTGCAA  1555

Query  1557 TTATTGCTCTTCAACGAGGAATACCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG  1616
            |||||| |||| |||||||||| |||||||||||| ||||||||||| ||||||||||||
Sbjct  1556 TTATTGATCTTGAACGAGGAATTCCTAGTAAGCGCGAGTCATCAGCTCGCGTTGATTACG  1615

Query  1617 TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGTCT  1676
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           |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||
Sbjct  1616  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGTTTAGTGAGGCCT  1675

Query  1677  CTGGATTGGCGCTGAGGAGCCGGCAACGGCAC-CTCGTTGCTGAGAAGTTGATCAAACTT  1735
                || |||||| || |  | ||||||  | |  | |||| | ||||| ||||||||
Sbjct  1676  TCTGACTGGCGCCGATGCTCTGGCAACAGAGCGCCGGATGCCGGAAAGTTGGTCAAACTT  1735

Query  1736  GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGA  1790
             | |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1736  GATCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA  1790
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>Sandalolitha robusta partial 18S rRNA gene, specimen voucher GA016
Sequence ID: LT631174.1 Length: 1797
Range 1: 20 to 1790

Score:2007 bits(2225), Expect:0.0,
Identities:1536/1795(86%), Gaps:43/1795(2%), Strand: Plus/Plus

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Query  15   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAACAAATTTATA  74
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||   |  ||
Sbjct  20   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAGCAC--TAGTA  77

Query  75   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTT-ACTA  133
            ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||| ||||
Sbjct  78   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATTGTACCTTTACTA  137

Query  134  CATGGATAACTGTGGTAATTCTAGAGCTAATACATGCTTCAAAGCCCCGACTCCTGGAAG  193
            | |||||||| || |||||||||||||||||||||||   |||| ||||||| |||||||
Sbjct  138  CTTGGATAACCGTAGTAATTCTAGAGCTAATACATGCGA-AAAGTCCCGACTTCTGGAAG  196

Query  194  GGGTGTATTTATTAGATaaaaaayCAATGCGG-TTC-GCC--GCTCTCTTGGTGATTCAT  249
            || |||||||||||||| ||||| |||||||| ||| |||  | ||| ||||||||||||
Sbjct  197  GGATGTATTTATTAGATTAAAAACCAATGCGGGTTCTGCCCGGTTCT-TTGGTGATTCAT  255

Query  250  AATAACTTCTCGAATCGCATGGCCTTGTGCCGGTGATGCTTCATTCAAATATCTGCCCTA  309
            | |||||  |||||||||| ||||||| || || |||| ||||||||||| |||||||||
Sbjct  256  AGTAACTGATCGAATCGCACGGCCTTGCGCTGGCGATGTTTCATTCAAATTTCTGCCCTA  315

Query  310  TCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTTTCAACGGGTAACGGGGAATAAGG  369
            |||||| ||||||||| | ||| ||| |||||||||| |||||||| |||| |||| |||
Sbjct  316  TCAACTGTCGATGGTAAGGTAGTGGCTTACCATGGTTGCAACGGGTGACGGAGAATTAGG  375

Query  370  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  429
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  376  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  435

Query  430  CGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATATAGGGCTCT  489
            ||||||||||||||||| ||| | ||||||||||||||| ||||||||||| |||||| |
Sbjct  436  CGCAAATTACCCAATCCTGACTCAGGGAGGTAGTGACAAGAAATAACAATACAGGGCTTT  495

Query  490  TTTGGGTCTTATAATTGGAATGAGTACAACTTAAATCCCTTAACGAGGAACAATTGGAGG  549
            |    ||||| ||||||||||||||||||||||||||| |||||||||| | ||||||||
Sbjct  496  TCCAAGTCTTGTAATTGGAATGAGTACAACTTAAATCCTTTAACGAGGATCCATTGGAGG  555

Query  550  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  609
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 556   GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  615

Query 610   GCAGTTAAAAAGCTCGTAGTTGAACTTCAGCTCTGGCCGGGCGGTCTGCCTCACGGTATG  669
            |||||||||||||||||||||| | ||| |    | |||| ||||||||| || ||||||
Sbjct 616   GCAGTTAAAAAGCTCGTAGTTGGATTTCGGGATGGCCCGGCCGGTCTGCCGCAAGGTATG  675

Query 670   T-ACTGTCTG-GCTGGGGCTTACCTT-------CTG-GTGAGCTCGCATGTCGTTCATTC  719
            | |||| | | ||||   ||| |||        ||| ||| ||||        || | |
Sbjct 676   TTACTGGCCGAGCTGTT-CTT-CCTCGCAAAGACTGTGTGTGCTC--------TTAACTG  725

Query 720   GGTGTGTGAGGGAACCAGGACTTTTACCTTGAGAAAATTAGAGTGTTCAAAGCAGGCAAA  779
             |||||    ||| |  ||| ||||| |||| ||||||||||||||||||||| || |
Sbjct 726   AGTGTGCTCAGGATCTGCGACGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAAGCCAG  785

Query 780   TGCCCGAATACATTAGCATGGCATAATGGAATAGGACGTGCGGTTCTATTTTGTTGGTTT  839
             ||  |||||||| ||||||| ||||||||||||||| |  |||||||||||||||||||
Sbjct 786   CGCTTGAATACATAAGCATGGAATAATGGAATAGGACTTT-GGTTCTATTTTGTTGGTTT  844

Query 840   CTAGAGTCGCCGTAATGATTAATAGGGACAGTTGGGGGCATTAGTATTGAGTTGCTAGAG  899
            || ||  ||  ||||||||||| || |||||||||||||||| |||||  ||||  ||||
Sbjct 845   CTGGAACCGAAGTAATGATTAAGAGAGACAGTTGGGGGCATTCGTATTTCGTTGTCAGAG  904

Query 900   GTGAAATTCTTGGATTTACTCAAGACTAACTATTGCGAAAGCATTTGCCAAGGATGTTTT  959
            ||| |||||||||||||||  ||||| ||||| ||||||||||||||||||| |||||||
Sbjct 905   GTGGAATTCTTGGATTTACGAAAGACGAACTACTGCGAAAGCATTTGCCAAGAATGTTTT  964

Query 960   CATTAATCAAGAACGAAGGTTAGGGGATCGAAAACGATCAGATACCGTTGTAGTCTTAAC  1019
            ||||||||||||||||| ||||| |||||||| |||||||||||||||  ||||  ||||
Sbjct 965   CATTAATCAAGAACGAAAGTTAGAGGATCGAAGACGATCAGATACCGTCCTAGTTCTAAC  1024

Query 1020  AGTAAACTATGCCGACTAGGGATCGGGCAATCTCACTTTTATGTGTTGCTCGGCACCTTA  1079
              ||||| ||||| |||||||||| |    | | | ||  |||      | |||||||||
Sbjct 1025  CATAAACGATGCCAACTAGGGATCAGAGGGTGTTA-TTGGATGACCCCTTTGGCACCTTA  1083

Query 1080  CGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGG  1139
             | |||| |||||| ||||||||| ||||| |||||||| |||| |||||||||||||||
Sbjct 1084  TGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGG  1143

Query 1140  AATTGACGGAAGGGCACCACCAGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1199
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct 1144  AATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1203

Query 1200  AAACTCACCAGGTCCAGACATAACTAGGATTGACAGATTGATAGCTCTTTCATGATTTTA  1259
            ||||||||||||||||||||||   |||||||||||||||| ||||||||| ||||| ||
Sbjct 1204  AAACTCACCAGGTCCAGACATAGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCTA  1263

Query 1260  TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGATA  1319
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 1264  TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGTTA  1323

Query 1320  ACGAACGAGACCTTAACCTGCTAAATAGACAGGCCGGCTCTGGCTGGTCGCCGT---CTT  1376
            ||||||||||||||||||||||||||||  | | ||  ||  | |  |||| ||   |||
Sbjct 1324  ACGAACGAGACCTTAACCTGCTAAATAGTTACG-CGAATCCCGAT--TCGCGGTTAACTT  1380

Query 1377  CTTAGAGGGACTGTCAGTGTCTAACTGACGGAAGTTTGAGGCAATAACAGGTCTGTGATG  1436
            ||||||||||||||  || || |||  | |  ||    ||||||||||||||||||||||
Sbjct 1381  CTTAGAGGGACTGTTGGTATCCAACCAAAGTCAG--GAAGGCAATAACAGGTCTGTGATG  1438
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Query  1437  CCCTTAGATGTTCTGGCCGCACGCGCTACACTGACAGAGCCAGCGAGTTTATCACCT  1496
             |||||||||||||||||||||||||||||||||||   | ||| |||  | || |||
Sbjct  1439  CCCTTAGATGTTCTGGCCGCACGCGCTACACTGACGATGTCAGAGAG--TGTCTCCT  1496

Query  1497  TGACTGAAAAGTCTGGGTAATCTTGTGAAACTTTGTCGTGCTGGGGATAGAGCATTGCAA  1556
             | || || | || ||||||||||| | |||| | ||||||||||||||||| ||||||||
Sbjct  1497  TCACCGAGAGGTGTGGGTAATCTT-TTAAACATCGTCGTGCTGGGGATAGATCATTGCAA  1555

Query  1557  TTATTGCTCTTCAACGAGGAATACCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG  1616
             |||||| |||| |||||||||| |||||||||||| ||||||||||| ||||||||||||
Sbjct  1556  TTATTGATCTTGAACGAGGAATTCCTAGTAAGCGCGAGTCATCAGCTCGCGTTGATTACG  1615

Query  1617  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGTCT  1676
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| ||
Sbjct  1616  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGTTTAGTGAGGCCT  1675

Query  1677  CTGGATTGGCGCTGAGGAGCCGGCAACGGCAC-CTCGTTGCTGAGAAGTTGATCAAACTT  1735
                || |||||| || |  | |||||| |  | | |  | |||    |||||| ||||||||
Sbjct  1676  TCTGACTGGCGCCGATGCTCTGGCAACAGAGCGCCGGATGCCGGAAAGTTGGTCAAACTT  1735

Query  1736  GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGA  1790
             | |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1736  GATCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA  1790
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>Podabacia crustacea partial 18S rRNA gene, specimen voucher MAY435
Sequence ID: LT631170.1 Length: 1797
Range 1: 20 to 1790

Score:2007 bits(2225), Expect:0.0,
Identities:1536/1795(86%), Gaps:43/1795(2%), Strand: Plus/Plus

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Query  15    GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAACAAATTTATA  74
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||   |  ||
Sbjct  20    GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAGCAC--TAGTA  77

Query  75    CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTT-ACTA  133
             ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||| ||||
Sbjct  78    CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATTGTACCTTTACTA  137

Query  134   CATGGATAACTGTGGTAATTCTAGAGCTAATACATGCTTCAAAGCCCCGACTCCTGGAAG  193
             | |||||||| || |||||||||||||||||||||||   |||| ||||||| |||||||
Sbjct  138   CTTGGATAACCGTAGTAATTCTAGAGCTAATACATGCGA-AAAGTCCCGACTTCTGGAAG  196

Query  194   GGGTGTATTTATTAGATaaaaaayCAATGCGG-TTC-GCC--GCTCTCTTGGTGATTCAT  249
             || |||||||||||||| ||||| |||||||| ||| |||  | ||| ||||||||||||
Sbjct  197   GGATGTATTTATTAGATTAAAAACCAATGCGGGTTCTGCCCGGTTCT-TTGGTGATTCAT  255

Query  250   AATAACTTCTCGAATCGCATGGCCTTGTGCCGGTGATGCTTCATTCAAATATCTGCCCTA  309
             | |||||  |||||||||| ||||||| || || |||| ||||||||||| |||||||||
Sbjct  256   AGTAACTGATCGAATCGCACGGCCTTGCGCTGGCGATGTTTCATTCAAATTTCTGCCCTA  315

Query  310   TCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTTTCAACGGGTAACGGGGAATAAGG  369
             |||||| ||||||||| | ||| ||| |||||||||| |||||||| |||| |||| |||
Sbjct  316   TCAACTGTCGATGGTAAGGTAGTGGCTTACCATGGTTGCAACGGGTGACGGAGAATTAGG  375
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Query 370  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  429
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 376  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  435

Query 430  CGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATATAGGGCTCT  489
           ||||||||||||||||| ||| | ||||||||||||||| ||||||||||| |||||| |
Sbjct 436  CGCAAATTACCCAATCCTGACTCAGGGAGGTAGTGACAAGAAATAACAATACAGGGCTTT  495

Query 490  TTTGGGTCTTATAATTGGAATGAGTACAACTTAAATCCCTTAACGAGGAACAATTGGAGG  549
           |    ||||| ||||||||||||||||||||||||||| |||||||||| | ||||||||
Sbjct 496  TCCAAGTCTTGTAATTGGAATGAGTACAACTTAAATCCTTTAACGAGGATCCATTGGAGG  555

Query 550  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  609
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 556  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  615

Query 610  GCAGTTAAAAAGCTCGTAGTTGAACTTCAGCTCTGGCCGGGCGGTCTGCCTCACGGTATG  669
           |||||||||||||||||||||| | ||||   | |||| ||||||||| || ||||||
Sbjct 616  GCAGTTAAAAAGCTCGTAGTTGGATTTCGGGATGGCCCGGCCGGTCTGCCGCAAGGTATG  675

Query 670  T-ACTGTCTG-GCTGGGGCTTACCTT-------CTG-GTGAGCTCGCATGTCGTTCATTC  719
           | ||||| | ||||  ||| |||     ||| ||| ||||     || | |
Sbjct 676  TTACTGGCCGAGCTGTT-CTT-CCTCGCAAAGACTGTGTGTGCTC--------TTAACTG  725

Query 720  GGTGTGTGAGGGAACCAGGACTTTTACCTTGAGAAAATTAGAGTGTTCAAAGCAGGCAAA  779
           |||||   ||| |  ||| ||||| |||| ||||||||||||||||||||| || |
Sbjct 726  AGTGTGCTCAGGATCTGCGACGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAAGCCAG  785

Query 780  TGCCCGAATACATTAGCATGGCATAATGGAATAGGACGTGCGGTTCTATTTTGTTGGTTT  839
           || |||||||| ||||||| ||||||||||||||| | ||||||||||||||||||
Sbjct 786  CGCTTGAATACATAAGCATGGAATAATGGAATAGGACTTT-GGTTCTATTTTGTTGGTTT  844

Query 840  CTAGAGTCGCCGTAATGATTAATAGGGACAGTTGGGGGCATTAGTATTGAGTTGCTAGAG  899
           || ||  || ||||||||||| || |||||||||||||||| ||||| |||| ||||
Sbjct 845  CTGGAACCGAAGTAATGATTAAGAGAGACAGTTGGGGGCATTCGTATTTCGTTGTCAGAG  904

Query 900  GTGAAATTCTTGGATTTACTCAAGACTAACTATTGCGAAAGCATTTGCCAAGGATGTTTT  959
           ||| |||||||||||||| ||||| ||||| ||||||||||||||||||| |||||||
Sbjct 905  GTGGAATTCTTGGATTTACGAAAGACGAACTACTGCGAAAGCATTTGCCAAGAATGTTTT  964

Query 960  CATTAATCAAGAACGAAGGTTAGGGGATCGAAAACGATCAGATACCGTTGTAGTCTTAAC  1019
           ||||||||||||||||| ||||| ||||||||| |||||||||||||| |||| ||||
Sbjct 965  CATTAATCAAGAACGAAAGTTAGAGGATCGAAGACGATCAGATACCGTCCTAGTTCTAAC  1024

Query 1020 AGTAAACTATGCCGACTAGGGATCGGGCAATCTCACTTTTATGTGTTGCTCGGCACCTTA  1079
            ||||| ||||| |||||||||| |  | | | || |||   | |||||||||
Sbjct 1025 CATAAACGATGCCAACTAGGGATCAGAGGGTGTTA-TTGGATGACCCCTTTGGCACCTTA  1083

Query 1080 CGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGG  1139
           | |||| |||||| ||||||||| ||||| |||||||| |||| |||||||||||||||
Sbjct 1084 TGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGG  1143

Query 1140 AATTGACGGAAGGGCACCACCAGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1199
           ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 1144 AATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1203

Query 1200 AAACTCACCAGGTCCAGACATAACTAGGATTGACAGATTGATAGCTCTTTCATGATTTTA  1259
           |||||||||||||||||||||  |||||||||||||||| |||||||||| |||||| ||
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Sbjct  1204  AAACTCACCAGGTCCAGACATAGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCTA  1263

Query  1260  TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGATA  1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1264  TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGTTA  1323

Query  1320  ACGAACGAGACCTTAACCTGCTAAATAGACAGGCCGGCTCTGGCTGGTCGCCGT---CTT  1376
             ||||||||||||||||||||||||||||  | | ||  ||  | |  |||| ||   |||
Sbjct  1324  ACGAACGAGACCTTAACCTGCTAAATAGTTACG-CGAATCCCGAT--TCGCGGTTAACTT  1380

Query  1377  CTTAGAGGGACTGTCAGTGTCTAACTGACGGAAGTTTGAGGCAATAACAGGTCTGTGATG  1436
             ||||||||||||||  || || |||  | |  ||    ||||||||||||||||||||||
Sbjct  1381  CTTAGAGGGACTGTTGGTATCCAACCAAAGTCAG--GAAGGCAATAACAGGTCTGTGATG  1438

Query  1437  CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACAGAGCCAGCGAGTTTATCACCT  1496
             ||||||||||||||||||||||||||||||||||||||   | ||| |||  | || |||
Sbjct  1439  CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACGATGTCAGAGAG--TGTCTCCT  1496

Query  1497  TGACTGAAAAGTCTGGGTAATCTTGTGAAACTTTGTCGTGCTGGGGATAGAGCATTGCAA  1556
             | || || | || ||||||||||| | |||| | ||||||||||||||||| ||||||||
Sbjct  1497  TCACCGAGAGGTGTGGGTAATCTT-TTAAACATCGTCGTGCTGGGGATAGATCATTGCAA  1555

Query  1557  TTATTGCTCTTCAACGAGGAATACCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG  1616
             |||||| |||| |||||||||| |||||||||||| ||||||||||| ||||||||||||
Sbjct  1556  TTATTGATCTTGAACGAGGAATTCCTAGTAAGCGCGAGTCATCAGCTCGCGTTGATTACG  1615

Query  1617  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGTCT  1676
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| ||
Sbjct  1616  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGTTTAGTGAGGCCT  1675

Query  1677  CTGGATTGGCGCTGAGGAGCCGGCAACGGCAC-CTCGTTGCTGAGAAGTTGATCAAACTT  1735
                || |||||| || |  | |||||| |  | |  | ||| |  |||||| ||||||||
Sbjct  1676  TCTGACTGGCGCCGATGCTCTGGCAACAGAGCGCCGGATGCCGGAAAGTTGGTCAAACTT  1735

Query  1736  GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGA  1790
             | |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1736  GATCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA  1790
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>Pleuractis paumotensis partial 18S rRNA gene, specimen voucher GA132
Sequence ID: LT631169.1 Length: 1797
Range 1: 20 to 1790

Score:2007 bits(2225), Expect:0.0,
Identities:1536/1795(86%), Gaps:43/1795(2%), Strand: Plus/Plus

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Query  15    GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAACAAATTTATA  74
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||   |  ||
Sbjct  20    GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAGCAC--TAGTA  77

Query  75    CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTT-ACTA  133
             ||||||||||||||||||||||||||||||||||| ||||||||||| ||||||| ||||
Sbjct  78    CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATTGTACCTTTACTA  137

Query  134   CATGGATAACTGTGGTAATTCTAGAGCTAATACATGCTTCAAAGCCCCGACTCCTGGAAG  193
             | |||||||| || |||||||||||||||||||||||   |||| ||||||| |||||||
Sbjct  138   CTTGGATAACCGTAGTAATTCTAGAGCTAATACATGCGA-AAAGTCCCGACTTCTGGAAG  196
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Query 194  GGGTGTATTTATTAGATaaaaaayCAATGCGG-TTC-GCC--GCTCTCTTGGTGATTCAT  249
           || |||||||||||||| ||||| |||||||| ||| |||  | ||| ||||||||||||
Sbjct 197  GGATGTATTTATTAGATTAAAAACCAATGCGGGTTCTGCCCGGTTCT-TTGGTGATTCAT  255

Query 250  AATAACTTCTCGAATCGCATGGCCTTGTGCCGGTGATGCTTCATTCAAATATCTGCCCTA  309
           | |||||  |||||||||| ||||||| || || |||| ||||||||||| |||||||||
Sbjct 256  AGTAACTGATCGAATCGCACGGCCTTGCGCTGGCGATGTTTCATTCAAATTTCTGCCCTA  315

Query 310  TCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTTTCAACGGGTAACGGGGAATAAGG  369
           |||||| ||||||||| | ||| ||| |||||||||| |||||||| |||| |||| |||
Sbjct 316  TCAACTGTCGATGGTAAGGTAGTGGCTTACCATGGTTGCAACGGGTGACGGAGAATTAGG  375

Query 370  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  429
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 376  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  435

Query 430  CGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATATAGGGCTCT  489
           ||||||||||||||||| ||| | ||||||||||||||| ||||||||||| |||||| |
Sbjct 436  CGCAAATTACCCAATCCTGACTCAGGGAGGTAGTGACAAGAAATAACAATACAGGGCTTT  495

Query 490  TTTGGGTCTTATAATTGGAATGAGTACAACTTAAATCCCTTAACGAGGAACAATTGGAGG  549
           |    ||||| ||||||||||||||||||||||||||| |||||||||| | ||||||||
Sbjct 496  TCCAAGTCTTGTAATTGGAATGAGTACAACTTAAATCCTTTAACGAGGATCCATTGGAGG  555

Query 550  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  609
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 556  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  615

Query 610  GCAGTTAAAAAGCTCGTAGTTGAACTTCAGCTCTGGCCGGGCGGTCTGCCTCACGGTATG  669
           |||||||||||||||||||||| | ||| |    | |||| ||||||||| || ||||||
Sbjct 616  GCAGTTAAAAAGCTCGTAGTTGGATTTCGGGATGGCCCGGCCGGTCTGCCGCAAGGTATG  675

Query 670  T-ACTGTCTG-GCTGGGGCTTACCTT-------CTG-GTGAGCTCGCATGTCGTTCATTC  719
           | |||| | | ||||   ||| |||        ||| ||| ||||        || | |
Sbjct 676  TTACTGGCCGAGCTGTT-CTT-CCTCGCAAAGACTGTGTGTGCTC--------TTAACTG  725

Query 720  GGTGTGTGAGGGAACCAGGACTTTTACCTTGAGAAAATTAGAGTGTTCAAAGCAGGCAAA  779
            |||||    ||| |   ||| ||||| |||| ||||||||||||||||||||| || |
Sbjct 726  AGTGTGCTCAGGATCTGCGACGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAAGCCAG  785

Query 780  TGCCCGAATACATTAGCATGGCATAATGGAATAGGACGTGCGGTTCTATTTTGTTGGTTT  839
            ||  |||||||| ||||||| ||||||||||||||| |  |||||||||||||||||||
Sbjct 786  CGCTTGAATACATAAGCATGGAATAATGGAATAGGACTTT-GGTTCTATTTTGTTGGTTT  844

Query 840  CTAGAGTCGCCGTAATGATTAATAGGGACAGTTGGGGGCATTAGTATTGAGTTGCTAGAG  899
           || ||  ||  ||||||||||| || |||||||||||||||| |||||  ||||  ||||
Sbjct 845  CTGGAACCGAAGTAATGATTAAGAGAGACAGTTGGGGGCATTCGTATTTCGTTGTCAGAG  904

Query 900  GTGAAATTCTTGGATTTACTCAAGACTAACTATTGCGAAAGCATTTGCCAAGGATGTTTT  959
           ||| |||||||||||||||  ||||| ||||| ||||||||||||||||||| |||||||
Sbjct 905  GTGGAATTCTTGGATTTACGAAAGACGAACTACTGCGAAAGCATTTGCCAAGAATGTTTT  964

Query 960  CATTAATCAAGAACGAAGGTTAGGGGATCGAAAACGATCAGATACCGTTGTAGTCTTAAC  1019
           ||||||||||||||||| ||||| |||||||| |||||||||||||||  ||||  ||||
Sbjct 965  CATTAATCAAGAACGAAAGTTAGAGGATCGAAGACGATCAGATACCGTCCTAGTTCTAAC  1024

Query 1020 AGTAAACTATGCCGACTAGGGATCGGGCAATCTCACTTTTATGTGTTGCTCGGCACCTTA  1079
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          ||||| ||||| ||||||||||| |   | | | || |||    | |||||||||
Sbjct 1025 CATAAACGATGCCAACTAGGGATCAGAGGGTGTTA-TTGGATGACCCCTTTGGCACCTTA 1083

Query 1080 CGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGG 1139
           | |||| |||||| ||||||||| ||||| |||||||| |||| |||||||||||||||
Sbjct 1084 TGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGG 1143

Query 1140 AATTGACGGAAGGGCACCACCAGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG 1199
           |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct 1144 AATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG 1203

Query 1200 AAACTCACCAGGTCCAGACATAACTAGGATTGACAGATTGATAGCTCTTTCATGATTTTA 1259
           ||||||||||||||||||||||  |||||||||||||||| ||||||||| |||||| ||
Sbjct 1204 AAACTCACCAGGTCCAGACATAGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCTA 1263

Query 1260 TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGATA 1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 1264 TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGTTA 1323

Query 1320 ACGAACGAGACCTTAACCTGCTAAATAGACAGGCCGGCTCTGGCTGGTCGCCGT---CTT 1376
           |||||||||||||||||||||||||||| | | || || | | |||| ||   |||
Sbjct 1324 ACGAACGAGACCTTAACCTGCTAAATAGTTACG-CGAATCCCGAT--TCGCGGTTAACTT 1380

Query 1377 CTTAGAGGGACTGTCAGTGTCTAACTGACGGAAGTTTGAGGCAATAACAGGTCTGTGATG 1436
           |||||||||||||| || || ||| | | ||   |||||||||||||||||||||
Sbjct 1381 CTTAGAGGGACTGTTGGTATCCAACCAAAGTCAG--GAAGGCAATAACAGGTCTGTGATG 1438

Query 1437 CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACAGAGCCAGCGAGTTTATCACCT 1496
           ||||||||||||||||||||||||| |||||||||||||   | |||| |||  | || |||
Sbjct 1439 CCCTTAGATGTTCTGGGCCGCACGCTCGCTACACTGACGATGTCAGAGAG--TGTCTCCT 1496

Query 1497 TGACTGAAAAGTCTGGGTAATCTTGTGAAACTTTGTCGTGCTGGGGATAGAGCATTGCAA 1556
           | || || | || |||||||||||||| |||| | ||||||||||||||||| |||||||||
Sbjct 1497 TCACCGAGAGGTGTGGGTAATCTTGT-AAACATCGTCGTGCTGGGGATAGATCATTGCAA 1555

Query 1557 TTATTGCTCTTCAACGAGGAATACCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG 1616
           |||||| |||| ||||||||||| |||||||||||| ||||||||||| ||||||||||||
Sbjct 1556 TTATTGATCTTGAACGAGGAATTCCTAGTAAGCGCGAGTCATCAGCTCGCGTTGATTACG 1615

Query 1617 TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGTCT 1676
           |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||
Sbjct 1616 TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGTTTAGTGAGGCCT 1675

Query 1677 CTGGATTGGCGCTGAGGAGCCGGCAACGGCAC-CTCGTTGCTGAGAAGTTGATCAAACTT 1735
             || |||||| || |  | ||||||| |  | | | |||| |  |||||| ||||||||
Sbjct 1676 TCTGACTGGCGCCGATGCTCTGGCAACAGAGCGCCGGATGCCGGAAAGTTGGTCAAACTT 1735

Query 1736 GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGA 1790
           | |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 1736 GATCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA 1790
```

>Cycloseris explanulata partial 18S rRNA gene, specimen voucher BA116
Sequence ID: LT631152.1 Length: 1797
Range 1: 20 to 1790

Score:2000 bits(2217), Expect:0.0,

Identities:1533/1793(85%), Gaps:39/1793(2%), Strand: Plus/Plus

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Query  15   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAACAAATTTATA  74
            ||||||||||||||||||||||||||||||||||||||||||||||||||||   |  ||
Sbjct  20   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAACAC--TAGTA  77

Query  75   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACC-TTACTA  133
            ||||||||||||||||||||||||||||||||||| ||||||||||| ||||| ||||||
Sbjct  78   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATTGTACCATTACTA  137

Query  134  CATGGATAACTGTGGTAATTCTAGAGCTAATACATGCTTCAAAGCCCCGACTCCTGGAAG  193
            | |||||||| || |||||||||||||||||||||||   |||| ||||||| |||||||
Sbjct  138  CTTGGATAACCGTAGTAATTCTAGAGCTAATACATGCGA-AAAGTCCCGACTTCTGGAAG  196

Query  194  GGGTGTATTTATTAGATaaaaaayCAATGCGG-TTC-GCC--GCTCTCTTGGTGATTCAT  249
            || |||||||||||||| ||||| |||||||| ||| |||  | ||| ||||||||||||
Sbjct  197  GGATGTATTTATTAGATTAAAAACCAATGCGGGTTCTGCCCGGTTCT-TTGGTGATTCAT  255

Query  250  AATAACTTCTCGAATCGCATGGCCTTGTGCCGGTGATGCTTCATTCAAATATCTGCCCTA  309
            | |||||  |||||||||| ||||||| || || |||| ||||||||||| |||||||||
Sbjct  256  AGTAACTGATCGAATCGCACGGCCTTGCGCTGGCGATGTTTCATTCAAATTTCTGCCCTA  315

Query  310  TCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTTTCAACGGGTAACGGGGAATAAGG  369
            |||||| ||||||||| | ||| ||| |||||||||| |||||||| |||| |||| |||
Sbjct  316  TCAACTGTCGATGGTAAGGTAGTGGCTTACCATGGTTGCAACGGGTGACGGAGAATTAGG  375

Query  370  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  429
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  376  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG  435

Query  430  CGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATATAGGGCTCT  489
            ||||||||||||||||| ||| | ||||||||||||||| ||||||||||| |||||| |
Sbjct  436  CGCAAATTACCCAATCCTGACTCAGGGAGGTAGTGACAAGAAATAACAATACAGGGCTTT  495

Query  490  TTTGGGTCTTATAATTGGAATGAGTACAACTTAAATCCCTTAACGAGGAACAATTGGAGG  549
            |    ||||| ||||||||||||||||||||||||||| |||||||||| | ||||||||
Sbjct  496  TCCAAGTCTTGTAATTGGAATGAGTACAACTTAAATCCTTTAACGAGGATCCATTGGAGG  555

Query  550  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  609
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  556  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT  615

Query  610  GCAGTTAAAAAGCTCGTAGTTGAACTTCAGCTCTGGC-CGGGCGGTCTGCCTCACGGTAT  668
            |||||||||||||||||||||| | ||| |   |||| ||| ||||||||| || |||||
Sbjct  616  GCAGTTAAAAAGCTCGTAGTTGGATTTC-GGGATGGCTCGGCCGGTCTGCCGCAAGGTAT  674

Query  669  G-TACTGTCTGGCTGGGGCTTACCT-------TCTG-GTGAGCTCGCATGTCGTTCATTC  719
            | ||||| | ||   |  ||| |||       | || ||| ||||        || | |
Sbjct  675  GTTACTGGCCGGGCTGTTCTT-CCTCGCAAAGACTGTGTGTGCTC--------TTAACTG  725

Query  720  GGTGTGTGAGGGAACCAGGACTTTTACCTTGAGAAAATTAGAGTGTTCAAAGCAGGCAAA  779
             ||||| |  ||| |   ||| ||||| |||| ||||||||||||||||||||| || |
Sbjct  726  AGTGTGCGCAGGATCTGCGACGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAAGCCAG  785

Query  780  TGCCCGAATACATTAGCATGGCATAATGGAATAGGACGTGCGGTTCTATTTTGTTGGTTT  839
             ||  |||||||| ||||||| ||||||||||||||| |  |||||||||||||||||||
Sbjct  786  CGCTTGAATACATAAGCATGGAATAATGGAATAGGAC-TTTGGTTCTATTTTGTTGGTTT  844
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Query  840   CTAGAGTCGCCGTAATGATTAATAGGGACAGTTGGGGGCATTAGTATTGAGTTGCTAGAG  899
             || ||  ||  ||||||||||| || |||||||||||||||| |||||  ||||  ||||
Sbjct  845   CTGGAACCGAAGTAATGATTAAGAGAGACAGTTGGGGGCATTCGTATTTCGTTGTCAGAG  904

Query  900   GTGAAATTCTTGGATTTACTCAAGACTAACTATTGCGAAAGCATTTGCCAAGGATGTTTT  959
             |||||||||||||||||||  ||||| ||||| ||||||||||||||||||| |||||||
Sbjct  905   GTGAAATTCTTGGATTTACGAAAGACGAACTACTGCGAAAGCATTTGCCAAGAATGTTTT  964

Query  960   CATTAATCAAGAACGAAGGTTAGGGGATCGAAAACGATCAGATACCGTTGTAGTCTTAAC  1019
             ||||||||||||||||| ||||| |||||||| |||||||||||||||  ||||  ||||
Sbjct  965   CATTAATCAAGAACGAAAGTTAGAGGATCGAAGACGATCAGATACCGTCCTAGTTCTAAC  1024

Query  1020  AGTAAACTATGCCGACTAGGGATCGGGCAATCTCACTTTTATGTGTTGCTCGGCACCTTA  1079
               ||||| ||||| |||||||||| |    | | | | ||  |||      | |||||||||
Sbjct  1025  CATAAACGATGCCAACTAGGGATCAGAGGGTGTTA-TTGGATGACCCCTTTGGCACCTTA  1083

Query  1080  CGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGG  1139
              | |||| |||||| ||||||||| ||||| |||||||| |||| |||||||||||||||
Sbjct  1084  TGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGG  1143

Query  1140  AATTGACGGAAGGGCACCACCAGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1199
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  1144  AATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG  1203

Query  1200  AAACTCACCAGGTCCAGACATAACTAGGATTGACAGATTGATAGCTCTTTCATGATTTTA  1259
             ||||||||||||||||||||||   |||||||||||||||| ||||||||| ||||| ||
Sbjct  1204  AAACTCACCAGGTCCAGACATAGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCTA  1263

Query  1260  TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGATA  1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1264  TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGTTA  1323

Query  1320  ACGAACGAGACCTTAACCTGCTAAATAGACAGGCCGGCTCTGGCTGGTCGCCGTCTTCTT  1379
             ||||||||||||||||||||||||||||  | |||    | |  |||  |    ||||||
Sbjct  1324  ACGAACGAGACCTTAACCTGCTAAATAGTTACGCCAATCCCGATTGGCGGTTAACTTCTT  1383

Query  1380  AGAGGGACTGTCAGTGTCTAACTGACGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCC  1439
             |||||||||||  || || |||  | |  ||    |||||||||||||||||||||||||
Sbjct  1384  AGAGGGACTGTTGGTATCCAACCAAAGTCAG--GAAGGCAATAACAGGTCTGTGATGCCC  1441

Query  1440  TTAGATGTTCTGGGCCGCACGCGCGCTACACTGACAGAGCCAGCGAGTTTATCACCTTGA  1499
             |||||||||||||||||||||||||||||||||||   | ||| |||  | || |||| |
Sbjct  1442  TTAGATGTTCTGGGCCGCACGCGCGCTACACTGACGATGTCAGAGAG--TGTCTCCTTCA  1499

Query  1500  CTGAAAAGTCTGGGTAATCTTGTGAAACTTTGTCGTGCTGGGGATAGAGCATTGCAATTA  1559
             | || | || |||||||||||   |||| | |||||||||||||||| ||||||||||| 
Sbjct  1500  CCGAGAGGTGTGGGTAATCTT-ACAAACATCGTCGTGCTGGGGATAGATCATTGCAATTT  1558

Query  1560  TTGCTCTTCAACGAGGAATACCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACGTCC  1619
             ||| |||| |||||||||| |||||||||||| ||||||||||| |||||||||||||||
Sbjct  1559  TTGATCTTGAACGAGGAATTCCTAGTAAGCGCGAGTCATCAGCTCGCGTTGATTACGTCC  1618

Query  1620  CTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGG-TCTCT  1678
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||| | |||
Sbjct  1619  CTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGTTTAGTGAGGCTTTCT  1678

Query  1679  GGATTGGCGCTGAGGAGCCGGCAACGGCAC-CTCGTTGCTGAGAAGTTGATCAAACTTGG  1737
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        || |||| | ||   | ||||||| | || | |||| | |||||| |||||||||
Sbjct 1679 -GACTGGCACCGATACTCTGGCAACAGAGCGCCGGATGCCGGAAAGTTGGTCAAACTTGA 1737

Query 1738 TCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGA 1790
        |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 1738 TCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA 1790
```

>Fungia scutaria 18S ribosomal RNA gene, partial sequence
Sequence ID: AF052884.1 Length: 1797
Range 1: 20 to 1790

Score:1998 bits(2215), Expect:0.0,
Identities:1534/1795(85%), Gaps:43/1795(2%), Strand: Plus/Plus

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Query 15   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAACAAATTTATA 74
        |||||||||||||||||||||||||||||||||||||||||||||||||| ||   | ||
Sbjct 20   GTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAGCAC--TAGTA 77

Query 75   CTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTATTTGATGGTACCTT-ACTA 133
        |||||||||||||||||| ||||||||||||||| ||||||||||| ||||||| ||||
Sbjct 78   CTGTGAAACTGCGAATGGCCCATTAAATCAGTTATCGTTTATTTGATTGTACCTTTACTA 137

Query 134  CATGGATAACTGTGGTAATTCTAGAGCTAATACATGCTTCAAAGCCCCGACTCCTGGAAG 193
        | ||||||||| || |||||||||||||||||||||||   |||| ||||||| |||||||
Sbjct 138  CTTGGATAACCGTAGTAATTCTAGAGCTAATACATGCGA-AAAGTCCCGACTTCTGGAAG 196

Query 194  GGGTGTATTTATTAGATaaaaaayCAATGCGG-TTC-GCC--GCTCTCTTGGTGATTCAT 249
        || |||||||||||||| ||||| |||||||| ||| |||  | ||| |||||||||||||
Sbjct 197  GGATGTATTTATTAGATTAAAAACCAATGCGGGTTCTGCCCGGTTCT-TTGGTGATTCAT 255

Query 250  AATAACTTCTCGAATCGCATGGCCTTGTGCCGGTGATGCTTCATTCAAATATCTGCCCTA 309
        | |||||  |||||||||| ||||||| || || |||| |||||||||||| |||||||||
Sbjct 256  AGTAACTGATCGAATCGCACGGCCTTGCGCTGGCGATGTTTCATTCAAATTTCTGCCCTA 315

Query 310  TCAACTTTCGATGGTAGGATAGAGGCCTACCATGGTTTCAACGGGTAACGGGGAATAAGG 369
        |||||| ||||||||| | ||| ||| ||||||||||| |||||||| |||| |||| |||
Sbjct 316  TCAACTGTCGATGGTAAGGTAGTGGCTTACCATGGTTGCAACGGGTGACGGAGAATTAGG 375

Query 370  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG 429
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 376  GTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCG 435

Query 430  CGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACAATATAGGGCTCT 489
        ||||||| ||||||||| ||| | ||||||||||||||| ||||||||||| ||||||| |
Sbjct 436  CGCAAATCACCCAATCCTGACTCAGGGAGGTAGTGACAAGAAATAACAATACAGGGCTTT 495

Query 490  TTTGGGTCTTATAATTGGAATGAGTACAACTTAAATCCCTTAACGAGGAACAATTGGAGG 549
        |   ||||| |||||||||||||||||||||||||||| |||||||||| | ||||||||
Sbjct 496  TCCAAGTCTTGTAATTGGAATGAGTACAACTTAAATCCTTTAACGAGGATCCATTGGAGG 555

Query 550  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT 609
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 556  GCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTT 615

Query 610  GCAGTTAAAAAGCTCGTAGTTGAACTTCAGCTCTGGCCGGGCGGTCTGCCTCACGGTATG 669
        ||||||||||||||||||||| |||| |    | |||| ||||||||| || ||||||
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Sbjct 616  GCAGTTAAAAAGCTCGTAGTTGGATTTCGGGATGGCCCGGCCGGTCTGCCGCAAGGTATG 675

Query 670  T-ACTGTCTG-GCTGGGGCTTACCTT-------CTG-GTGAGCTCGCATGTCGTTCATTC 719
           | |||| | | ||||  ||| |||     ||| ||| ||||     || | |
Sbjct 676  TTACTGGCCGAGCTGTT-CTT-CCTCGCAAAGACTGTGTGTGCTC--------TTAACTG 725

Query 720  GGTGTGTGAGGGAACCAGGACTTTTACCTTGAGAAAATTAGAGTGTTCAAAGCAGGCAAA 779
            |||||  ||| |  ||| ||||| |||| ||||||||||||||||||||| || |
Sbjct 726  AGTGTGCTCAGGATCTGCGACGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAAGCCAG 785

Query 780  TGCCCGAATACATTAGCATGGCATAATGGAATAGGACGTGCGGTTCTATTTTGTTGGTTT 839
            || |||||||| ||||||| ||||||||||||||| | ||||||||| |||||||||
Sbjct 786  CGCTTGAATACATAAGCATGGAATAATGGAATAGGACTTT-GGTTCTATTCTGTTGGTTT 844

Query 840  CTAGAGTCGCCGTAATGATTAATAGGGACAGTTGGGGGCATTAGTATTGAGTTGCTAGAG 899
           || || || ||||||||||| || |||||||||||||||| ||||| |||| ||||
Sbjct 845  CTGGAACCGAAGTAATGATTAAGAGAGACAGTTGGGGGCATTCGTATTTCGTTGTCAGAG 904

Query 900  GTGAAATTCTTGGATTTACTCAAGACTAACTATTGCGAAAGCATTTGCCAAGGATGTTTT 959
           ||| ||||||||||||||| ||||| ||||| ||||||||||||||||||| |||||||
Sbjct 905  GTGGAATTCTTGGATTTACGAAAGACGAACTACTGCGAAAGCATTTGCCAAGAATGTTTT 964

Query 960  CATTAATCAAGAACGAAGGTTAGGGGATCGAAAACGATCAGATACCGTTGTAGTCTTAAC 1019
           ||||||||||||||||| ||||| ||||||||| ||||||||||||||| |||| ||||
Sbjct 965  CATTAATCAAGAACGAAAGTTAGAGGATCGAAGACGATCAGATACCGTCCTAGTTCTAAC 1024

Query 1020 AGTAAACTATGCCGACTAGGGATCGGGCAATCTCACTTTTATGTGTTGCTCGGCACCTTA 1079
             ||||| ||||| |||||||||| |   | | | || |||    | |||||||||
Sbjct 1025 CATAAACGATGCCAACTAGGGATCAGAGGGTGTTA-TTGGATGACCCCTTTGGCACCTTA 1083

Query 1080 CGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGG 1139
            | |||| |||||| ||||||||| ||||| ||||||||| |||| |||||||||||||||
Sbjct 1084 TGGGAAACCAAAGTTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGG 1143

Query 1140 AATTGACGGAAGGGCACCACCAGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG 1199
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 1144 AATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGG 1203

Query 1200 AAACTCACCAGGTCCAGACATAACTAGGATTGACAGATTGATAGCTCTTTCATGATTTTA 1259
           ||||||||||||||||||||||  |||||||||||||||| |||||||||| |||||| ||
Sbjct 1204 AAACTCACCAGGTCCAGACATAGTAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCTA 1263

Query 1260 TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGATA 1319
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 1264 TGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCCGTTA 1323

Query 1320 ACGAACGAGACCTTAACCTGCTAAATAGACAGGCCGGCTCTGGCTGGTCGCCGT---CTT 1376
           |||||||||||||||||||||||||||| | ||| || | | |||| ||  |||
Sbjct 1324 ACGAACGAGACCTTAACCTGCTAAATAGTTACG-CGAATCCCGAT--TCGCGGTTAACTT 1380

Query 1377 CTTAGAGGGACTGTCAGTGTCTAACTGACGGAAGTTTGAGGCAATAACAGGTCTGTGATG 1436
           |||||||||||||| || || ||| | | ||   |||||||||||||||||||||
Sbjct 1381 CTTAGAGGGACTGTTGGTATCCAACCAAAGTCAG--GAAGGCAATAACAGGTCTGTGATG 1438

Query 1437 CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACAGAGCCAGCGAGTTTATCACCT 1496
           ||||||||||||||||||||||||||||||||||||||  | ||| ||| | || |||
Sbjct 1439 CCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGACGATGTCAGAGAG--TGTCTCCT 1496
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Query 1497 TGACTGAAAAGTCTGGGTAATCTTGTGAAACTTTGTCGTGCTGGGGATAGAGCATTGCAA 1556
           | || || | || ||||||||||||| |||| | |||||||||||||||||| |||||||||
Sbjct 1497 TCACCGAGAGGTGTGGGTAATCTTGT-AAACATCGTCGTGCTGGGGATAGATCATTGCAA 1555

Query 1557 TTATTGCTCTTCAACGAGGAATACCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG 1616
           |||||| |||| |||||||||| |||||||||||| ||||||||||| ||||||||||||
Sbjct 1556 TTATTGATCTTGAACGAGGAATTCCTAGTAAGCGCGAGTCATCAGCTCGCGTTGATTACG 1615

Query 1617 TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGTCT 1676
           |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||
Sbjct 1616 TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGTTTAGTGAGGCCT 1675

Query 1677 CTGGATTGGCGCTGAGGAGCCGGCAACGGCAC-CTCGTTGCTGAGAAGTTGATCAAACTT 1735
             || |||||| || | ||||||| | || | |||| | |||||| |||||||||
Sbjct 1676 TCTGACTGGCGCCGATGCTCTGGCAACAGAGCGCCGGATGCCGGAAAGTTGGTCAAACTT 1735

Query 1736 GGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGA 1790
           | ||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 1736 GATCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA 1790
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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	Lobactis scutaria partial 18S rRNA gene, specimen voucher GA055	Lobactis scutaria	2012	2012	99%	0.0	85.63%	1797	LT631164.1
☑	Herpolitha limax partial 18S rRNA gene, specimen voucher GA020	Herpolitha limax	2012	2012	99%	0.0	85.63%	1797	LT631156.1
☑	Halomitra pileus partial 18S rRNA gene, specimen voucher MAY442	Halomitra pileus	2012	2012	99%	0.0	85.63%	1797	LT631155.1
☑	Fungia fungites partial 18S rRNA gene, specimen voucher GA018	Fungia fungites	2012	2012	99%	0.0	85.63%	1797	LT631154.1
☑	Danafungia horrida partial 18S rRNA gene, specimen voucher GA133	Danafungia horrida	2012	2012	99%	0.0	85.63%	1797	LT631153.1
☑	Sandalolitha robusta partial 18S rRNA gene, specimen voucher GA016	Sandalolitha robusta	2007	2007	99%	0.0	85.57%	1797	LT631174.1
☑	Podabacia crustacea partial 18S rRNA gene, specimen voucher MAY435	Podabacia crustacea	2007	2007	99%	0.0	85.57%	1797	LT631170.1
☑	Pleuractis paumotensis partial 18S rRNA gene, specimen voucher GA132	Pleuractis paumotensis	2007	2007	99%	0.0	85.57%	1797	LT631169.1
☑	Cycloseris explanulata partial 18S rRNA gene, specimen voucher BA116	Cycloseris explanulata	2000	2000	99%	0.0	85.50%	1797	LT631152.1
☑	Fungia scutaria 18S ribosomal RNA gene, partial sequence	Lobactis scutaria	1998	1998	99%	0.0	85.46%	1797	AF052884.1