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DOCTORAL DISSERTATION

A Molecular Approach to Questions in the Phylogeny of Planktonic Sarcodines

by

Linda Angela Amaral Zettler

September 1996

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Massachusetts Institute of Technology Cambridge, Massachusetts 02139

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A Molecular Approach to Questions in the Phylogeny of Planktonic Sarcodines

by

Linda Angela Amaral Zettler Sc.B. Aquatic Biology Brown University, 1990

SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF DOCTOR OF PHILOSOPHY

at the

MASSACHUSETTS INSTITUTE OF TECHNOLOGY and the WOODS HOLE OCEANOGRAPHIC INSTITUTION September, 1996

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A Molecular Approach to Questions in the Phylogeny of Planktonic Sarcodines

by

Linda Angela Amaral Zettler

Submitted to the Department of Biology in August, 1996 in Partial Fulfillment of the Requirements for the Degree of Doctor of Philosophy

Abstract

The Acantharea and the Polycystinea are two classes of sarcodines (Sarcodina) which are exclusively planktonic and occur strictly in oligotrophic marine environments. Although these protists have been the topic of research since Ernst Haeckel's systematic investigations of samples from the H. M. S. Challenger Expedition, many aspects of their phylogeny and systematics remain poorly resolved. Part of the problem is that the criteria used in systematics of these groups until now has emphasized morphological elements which may be similar due to convergence rather than common ancestry. The application of molecular biology to the field of biological oceanography offers alternative approaches to reexamining sarcodine phylogeny with the goal of producing classifications which reflect evolutionary history.

The relationships of the Acantharea and the Polycystinea (order Spumellarida) to other protists were investigated using phylogenetic analyses of small-subunit ribosomal RNA (SSU rRNA) genes. Members of these two classes have been traditionally grouped into the common superclass Actinopoda based on their specialized pseudopodia called axopodia. Sequences from two orders of Acantharea (Symphyacanthida and Chaunacanthida) and four representatives from the order Spumellarida and the class Polycystinea (one solitary and three colonial spumellaria) were aligned against 25 other eukaryotic SSU rRNA sequences extracted from a data base of more than 800 eukaryotic sequences and subjected to distance, maximum parsimony and maximum likelihood analyses. SSU rRNA-based phylogenies do not support the common ancestry of the Acantharea and the Polycystinea, implying that the superclass Actinopoda is artificial and should be discarded. The respective monophyly of the Acantharea and the Polycystinea were supported in all analyses accomplished. The origin of the sequences was confirmed by in situ hybridization experiments. SSU rRNA gene sequences for the solitary spumellarian <u>Thalassicolla nucleata</u> were compared from individuals collected from the Sargasso Sea and the Pacific Ocean. Sequences from pooled individuals showed primary structure differences which were consistent with genus-level variation reported in the literature for unrelated taxa. These results indicate that there may be different strains of this genus which are morphologically identical or that perhaps there may be allelic variation within a given individual.

The evolutionary relationships between the solitary <u>T. nucleata</u> and seven colonial spumellaria were analyzed to determine whether the two families of colonial spumellaria (Collosphaeridae and Sphaerozoidae) form a monophyletic evolutionary assemblage. Phylogenies inferred from distance and maximum likelihood methods did not support the monophyly of the colony-forming spumellaria. Parsimony methods did support the monophyly of the colonial spumellaria but with very low bootstrap support. The monophyly of members from the Collosphaeridae family was supported in all analyses with 100% bootstrap support while only distance analyses supported the monophyly of the Sphaerozoidae. The possibility that coloniality has evolved more than once in the Spumellarida has been suggested from observations of the fossil record. However, contrary conclusions have been reached from studies based on skeletal morphogenesis. The results obtained from molecular analyses question the utility of coloniality as a reliable phylogenetic marker. Sequence variation within the SSU rRNA genes of the Spumellarida appears to be sufficient enough for continued fine-scaled comparisons between existing morphospecies.

The branching patterns within three of the four orders of the Acantharea were examined using additional SSU rRNA gene sequence data from representatives of the Symphyacanthida, Chaunacanthida and Arthracanthida. The results from this analysis revealed a phylogeny which placed one representative of the Symphyacanthida (<u>Haliommatidium</u> sp.) branching among the Arthracanthida. An examination of the cytological features of <u>Haliommatidium</u> sp. in the literature revealed morphological similarities it shares with the Arthracanthida that could corroborate this result. The variability within acantharian SSU rDNA was significantly less than that observed in spumellaria, and may prove less useful in establishing relationships at taxonomic categories below the order level.

Name and Title of Thesis Advisor: David A. Caron, Associate Scientist with tenure

This dissertation is dedicated to my grandmother,

Guiseppina Quattrocchi Cavallaro

1902-1987

whose

formal education ended after

first grade, when an earthquake destroyed her school.

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I am sincerely indebted to the many people who made the work accomplished during this dissertation not only possible but also very enjoyable over the past five years. Perhaps the person who has had the most influence on my academic career has been my advisor David Caron. My first introduction to Woods Hole and WHOI were largely the result of a desire to work with Dave, a world expert on the biology of planktonic sarcodines, and learn more about a group of protists for which I had, until that point, studied only the fossil remains. I am grateful for his guidance and enthusiasm to allow me to pursue a research topic peripheral to other projects in his lab.

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Anderson also assisted in radiolarian identifications and took part in numerous e-mail and telephone conversations regarding aspects of radiolarian biology.

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Introduction

Planktonic sarcodines are a heterogeneous group of single-celled aquatic eukaryotes which include amoebae, foraminifera, and actinopods. While many planktonic sarcodines share similar ecological niches in marine and freshwater environments, it is unclear to what extent they share a common evolutionary history. Taxonomic frameworks that encompass members of the planktonic sarcodines are equivocal. This is largely because many of the morphological characters upon which these classification schemes were built are probably not phylogenetically meaningful. Some taxonomic schemes which were created at the turn of the century have seen little revision since their creation and are still in use.

Planktonic sarcodines are grouped within the subphylum Sarcodina based on the possession of pseudopodia during some part of their life cycle. The validity of this grouping has been questioned and current opinion largely regards it as an artificial taxon (Corliss 1984; Page 1987; Cavalier-Smith 1993). Further taxonomic divisions of the Sarcodina based on specialized pseudopodial structures such as axopodia, possessed by members of the superclass Actinopoda, have also come under scrutiny (Cavalier-Smith 1993). The question of the monophyly of the Actinopoda remains largely unresolved.

The application of molecular biological techniques to protistan systematics provides an independent means of examining existing systematic frameworks based on classical approaches. This thesis considers the evolutionary relationships between and among two currently-recognized actinopod classes, the Acantharea and the Polycystinea, based on sequence analysis of small-subunit ribosomal RNA genes. The reconstruction of phylogenies based on SSU rRNA genes aims to establish the relatedness of the Acantharea and Polycystinea to other eukaryotes and ultimately to provide information for further development of "natural" classification schemes within these classes.

General Background on Acantharia and Polycystine Radiolaria

Acantharea and Polycystinea are two classes of axopod-bearing protists which are strictly planktonic and found exclusively in open-ocean oligotrophic environments (see Fig.

1). Among the larger planktonic sarcodines, the acantharia and particularly the colonyforming polycystines are perhaps the most conspicuous of the zooplankton found in the open ocean owing to the bloom-like conditions often created by the Acantharea and due to the conspicuous visibility of large macroscopic colonies of spumellarian members of the Polycystinea. Acantharia range in size from 50-800 μ m in diameter, solitary spumellarians range from 10 μ m to several centimeters in diameter, and colonial spumellaria have been reported up to three meters in length. Despite an often visible presence in the plankton, sampling methods and preservation techniques have led to underestimates of living acantharian and spumellarian abundances and ultimately underestimation of their importance in marine environments (Swanberg 1979; Michaels 1988).

Although living polycystines have received limited study, their fossilized skeletons have not. Many polycystines including the colonial spumellaria considered in this thesis possess siliceous skeletons which are preserved in marine sediments. The polycystines offer the longest geological and widest biogeographical ranging microfossils available for study by micropaleontologists (Casey et al. 1983). The long fossil record left behind by shell-bearing Polycystinea has precipitated a suite of research spanning paleoclimatological, paleoecological, and evolutionary studies (e. g. Riedel and Sanfilippo 1971; Kellogg and Hays 1975; Lazarus 1983).

Unlike the Polycystinea, members of the Acantharea, which possess shells of strontium sulfate, are absent from the fossil record and have thus received far less attention than the Polycystinea. Despite a lack of geological utility, the acantharia have been the topic of various kinds of biological research. Since they possess unique non-actin myonemes, they have been intensively studied by cell biologists (Febvre 1990 and the references therein). As the sole protistan utilizers of strontium sulfate as the major structural component of their skeletons, acantharia serve an important function in the strontium cycle of the world oceans (Bernstein et al. 1987). Since members of the

Fig. 1. A schematic of hypothetical **A**. acantharian and **B**. spumellarian cells indicating cell structural features of the two different sarcodines.



Acantharea and Polycystinea often live in association with symbiotic algae, they also play a role in both primary productivity and microbial food-web dynamics (Michaels 1988; Caron and Swanberg 1990; Caron et al. 1995).

The inability to culture acantharia and polycystines through successive generations in the laboratory has been an important impediment to their study. Our inability to maintain sarcodines in laboratory culture and the care which must be taken in collecting these fragile organisms has resulted in a fragmentary understanding of their biology and more fundamentally, their relationships to other organisms. However, despite recalcitrance to laboratory culturing, acantharia and polycystines have been the objects of study for over a century and a half.

Historical Perspective: Haeckel's Radiolaria

One of the first described radiolaria (Meyen 1834) was a colonial polycystine spumellarian, belonging to the spicule-bearing genus <u>Sphaerozoum</u>. Ehrenberg (1838) erected the first classification for the radiolaria and is credited as giving the Polycystinea their name, which was derived from descriptions of spherical latticed-shells found of fossil polycystines. Earliest reports of acantharia were made by Müller (1858) who grouped the acantharia and the radiolaria together based on a shared radial disposition of the pseudopodia possessed by both groups. The highly-ordered geometrical pattern of spine orientation formed by acantharian cells has been called Müller's Law in recognition of his early observations of acantharian skeletal architecture (see Chapter 4, Fig. 1C). Thus, from the very early stages of their study, shared morphological similarities of the Acantharea and the Polycystinea united these two sarcodine groups into a common taxonomic category.

The first exhaustive accounts of both acantharian and polycystine systematics were those of Ernst Haeckel after the H. M. S. Challenger Expedition. Haeckel (1883, 1887) combined the Acantharia (modern-day Acantharea) and the Spumellaria and the Nassellaria

(now classified collectively in the class Polycystinea) along with the fourth "legion", the Phaeodaria (Phaeodarea), into the "class" Radiolaria. He further united the Acantharia and the Spumellaria (Spumellarida) into the now defunct "subclass" Porulosida based on the shared characteristics of the distribution and size of the pores in the central capsule wall. In 1909, the Acantharea and Polycystinea were grouped along with other sarcodines based on the structure of their pseudopodia into what was first created as a "class" by Calkins called the Actinopoda (Calkins 1909). The Actinopoda, still persists in modern classifications but has been elevated to a superclass (Fig. 2). The superclass Actinopoda was originally created to encompass all sarcodines which possessed microtubule-supported pseudopodia termed axopodia.

Historical Perspective: Acantharea

Following the establishment of the Actinopoda in 1909, Schewiakoff (1926) promoted the Acantharia to the level of subclass based on the differences he noted in the capsule membrane of acantharia from the radiolaria and the absence of central capsules in certain acantharia. He also revised lower level acantharian systematics to take into account cytological features. The "subclass" Acantharia was elevated to the level of superorder by Enriques (1931). He called the new superorder "Birefrangentia" based on the birefringant properties of the strontium sulfate-containing acantharian skeleton. The current status of the "class" level of organization currently given to the Acantharea was first proposed by Tregouboff (1953) and has been accepted by other specialists since that time.

Historical Perspective: Polycystinea

The remainder of the historical review will be restricted to polycystine systematics because only a limited group of spumellarian representatives from the class Polycystinea were addressed in this thesis.

Huxley (1851) further elaborated on the work of Meyen and assigned all colonial spumellaria to the species <u>Thalassicolla punctata</u>. However, Müller disagreed with the

Acrosphaera (circumtexta?) Genus: Collosphaera Collosphaera Collosphaera Collosphaera Siphonosphaera cvathina <u>Rhaphidozoum</u> acuferum Sphaerozoum punctatum **Collozoum serpentinum** Thalassicolla nucleata **Collozoum pelagicum** huxleyi Haliommatidium sp. Acanthometra sp. opoun Acantharea (acanumun) Order: Symphyacanthida Family: Pseudolithidae Genus: Haliommatidium Haliomm Genus: Siphonosphaera Genus: Rhaphidozoum Polycystmea (1) Order: Spumellarida Suborder: Sphaerocollina Family: Thalassicollidae Genus: Thalassicolla Thala Suborder: Sphaenacanthina Family: Acanthometridae Genus: Acanthometra Genus: Sphaerozoum Genus: Acrosphaera Genus: Collozoum Family: Collosphaeridae Family: Sphaerozoidae Fig. 2. Taxonomic position of the planktonic sarcodines examined in this thesis. Superclass: Actinopoda Class: Acantharea (acantharia) Order: Chaunacanthida Order: Arthracanthida Class: Based on Levine et al. (1980) and Lee et al. (1985). Phylum: Sarcomastigophora Subphylum: Sarcodina Kingdom: Protista

inclusion of the colonial radiolaria within the single genus <u>Thalassicolla</u> which was already known to contain the solitary spumellarian <u>T. nucleata</u>. Müller was the first to differentiate between the solitary and colonial spumellaria which he called the Solitaria and the Polyzoa respectively (Müller 1858; Strelkov and Reshetnyak 1971).

Haeckel was the next taxonomist to substantially revise colonial spumellarian systematics based on the presence or absence of skeletal features. He described 84 species, 17 genera and 3 families. After Haeckel's 1862-1887 systematic revisions of the spumellarian polycystines, further taxonomic revisions were largely the efforts of Brandt (1885, 1905) and his students. According to Strelkov and Reshetnyak (1971), Brandt disagreed with many aspects of Haeckel's classification, most importantly of which was his separation of the colonial spumellarian radiolaria into different orders. Brandt created a separate taxon which included all colonial radiolaria into the one group called the Sphaerozoa and reduced the number of species, genera and families proposed by Haeckel. Brandt kept the two families of colonial spumellarians recognized in modern classifications, the Collosphaeridae and the Sphaerozoidae. These two families were grouped into the suborder Polycyttaria by Haecker in 1908. Haecker also divided the Spumellaria into two additional suborders, the Sphaerellaria, which contained solitary shell-bearing forms and the Collodaria which contained either skeletonless or spicule- bearing solitary forms such as <u>Thalassicolla</u>. Further systematic revisions were carried out by Hilmers (1906), Breckner (1906), and Popofsky (1908) later by Tregouboff (1953). The latest revision of the colonial spumellaria has been carried out by Strelkov and Reshetnyak (1971).

Modern Day Classifications and Taxonomic Perspectives

Although not formally recognized, some revisions have been suggested in the recent literature to reflect a more "natural" classification scheme for the Actinopoda. Under current classification schemes recognized by the Committee in Systematics and Evolution of the Society of Protozoologists (Levine et al., 1980), the Actinopoda is a superclass

which includes four classes: the Acantharea, Polycystinea, Phaeodarea and Heliozoea. However, recognizing the diversity within the Actinopoda, Cavalier-Smith (1987) elevated the taxon Actinopoda to a "parvkingdom". He further recommended a division of the Actinopoda into the phyla "Radiozoa" and "Heliozoa" in order to account for recognized differences between the Heliozoea (Heliozoa) on the one hand and the Acantharea, Polycystinea and Phaeodarea (Radiozoa) on the other. While recognizing its diversity, Cavalier-Smith maintained the taxon Actinopoda suggesting that it might be monophyletic. More recently, Corliss (1994) adopted Cavalier-Smith's "Radiozoa" and the further divisions of the subphylum Acantharia with the class Acantharea and the subphylum Radiolaria with the classes Polycystinea and Phaeodarea.

The classification scheme used throughout this thesis does not incorporate the most recent suggestions as indicated above since no real consensus has been reached on the appropriate revisions, but instead adopts the last formally revised classification of the Protozoa made by the Committee on Systematics and Evolution of the Society of Protozoologists (Levine et al., 1980) (see Fig. 2). The Levine et al.(1980) classification scheme is used for higher level classifications wherein phyla, subphyla and superclasses end in "a"; classes end in "ea"; subclasses in "ia"; orders in "ida"; and suborders in "ina". The classification scheme of Strelkov and Reshetnyak (1971) has been used for the colonial spumellaria and that found in Lee et al. (1985) for the solitary spumellaria and the acantharia since these schemes address systematic groupings below the suborder level whereas Levine et al. (1980) stops at suborder-level classification.

As mentioned earlier, the work described herein attempts to use newly-developed molecular methods as independent tools for examining sarcodine phylogenetic relationships and producing classifications which reflect these phylogenetic relationships. There are many reasons for choosing ribosomal RNA molecules to address the phylogenetic and systematic questions posed above. These include their ubiquitous occurrence among all

living organisms, their functional uniformity, and absence of lateral gene transfer (Olsen et al. 1986; Sogin et al. 1986; Field et al. 1988). Ribosomal RNA molecules possess both very conserved and very variable regions which allow for nucleotide base pair alignments between both closely and distantly-related organisms (Gobel et al. 1987; Sogin and Gunderson 1987). In addition to these features, the current data base for rRNA gene sequences is one of the largest of its kind, and so allows for comparisons between many different organisms (Neefs et al. 1991; De Rijk et al. 1992).

Yet another advantage of rRNA-based analysis is the potential for constructing phylogenetic oligonucleotide probes based on the gene sequences of the organism of interest. Such oligonucleotide probes have been conjugated to reporter molecules and used as molecular probes in conjuction with fluorescence and transmitted light microscopy to distinguish between different kingdoms and even different species (DeLong et al. 1989; Amann et al. 1990). Ribosomal RNA probes can also provide a means of verifying sequences obtained from organisms collected from the environment (as opposed to laboratory grown cultures). Planktonic sarcodines have resisted laboratory culture through successive generations and have consequently been difficult to study. The fact that planktonic sarcodines must be collected each time more samples were needed was one of the most challenging aspects of this thesis. Since rRNA is a very abundant in the cytoplasm of cells it provides many targets for <u>in situ</u> hybridizations using rRNA probes. These probes can be a valuable tool for verifying gene sequences obtained from organisms from the environment.

This thesis is organized into four chapters which are written in manuscript form. In Chapter 1, I first present the overall phylogenetic placement of the Acantharea and Polycystinea among other eukaryotes in a broad-based SSU rRNA phylogenetic analysis. In this analysis I include two representatives from the Acantharea (one Symphyacanthid representative and one Chaunacanthid representative) and four representatives of the

Spumellarida [one solitary (<u>Thalassicolla nucleata</u>) and three colonial spumellaria (<u>Collosphaera globularis-huxleyi</u>, <u>Sphaerozoum punctatum</u> and <u>Collozoum serpentinum</u>]. In addition to phylogenetic reconstructions, data on <u>in situ</u> verification of the acantharian and spumellarian sequences is presented using acantharian and colonial spumellarianspecific oligonucleotide probes. This chapter also addresses the issue of the monophyly of the Actinopoda.

In Chapter 2, I present a comparison between the <u>Thalassicolla nucleata</u> sequence from Chapter 1 which was obtained from the Sargasso Sea with 4 additional <u>T. nucleata</u> sequences derived from Pacific samples. This chapter addresses variability within a single species and reexamines the known species in the genus <u>Thalassicolla</u> in view of the SSU rRNA sequence data obtained from specimens collected from geographically different locations.

In Chapter 3, I focus more closely on the relationships among the Spumellarida (Sphaerocollina) and more specifically, address the validity of coloniality as a legitimate phylogenetic character. In addition, to the spumellarian taxa used in Chapter 1, data from Collozoum serpentinum, Rhaphidozoum acuferum, Acrosphaera (circumtexta?) and Siphonosphaera cyathina are also utilized. Phylogenies are inferred using the same homologous positions as in the sequence alignment of Chapter 1 and using additional sites by restricting the analysis to just the colonial spumellaria.

In Chapter 4, I consider the branching patterns within the Acantharea using SSU rRNA gene sequence data from two representatives each of three orders of Acantharea, the the Symphyacanthida, the Chaunacanthida and the Arthracanthida.

In Chapter 5, I summarize the conclusions of the thesis. Appendix A includes the alignment and sequence positions used in phylogenetic analyses presented in Chapters 1, 3 and 4 along with proposed locations of the secondary structure helices.

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Chapter 1

Phylogenetic Relationships between the Acantharea and the Polycystinea (Spumellarida) Inferred from 16S-like Ribosomal RNA Gene Analyses: A Molecular Perspective on Haeckel's Radiolaria
ABSTRACT The evolutionary relationship of the Acantharea and the Polycystinea (Sarcodina) to other protists was investigated using comparative small-subunit ribosomal RNA (SSU rRNA) gene analyses. While current opinion regards the Acantharea as a separate class distinct from its original Haeckelian inclusion among the "Radiolaria" ("Radiolaria" sensu lato: Polcystinea, Phaeodarea and Acantharea), most investigators continue to support the hypothesis that the Acantharea and the Polycystinea share common ancestry, as revealed by their inclusion among the superclass Actinopoda (Calkins 1909). A major impediment to using a molecular approach to ascertain whether the Actinopoda represents a formal evolutionary assemblage has been an inability to culture many of these protists in the laboratory. We collected and maintained actinopods of the classes Acantharea and Polycystinea to obtain reproductive specimens highly enriched with DNA in order to facilitate DNA extraction and sequencing. The origin of the sequences described herein were confirmed by in situ hybridization experiments. The results from molecular phylogenetic analyses inferred from SSU rRNA gene sequences do not support a shared history between the Acantharea and the Polycystinea. However, the monophyly of the Acantharea and the separate monophyly of the Polycystinea (Spumellarida) are well supported by our molecular phylogenetic analyses. The acantharian lineage branches among crown organisms while the polycystine lineage diverges prior to the radiation of the crown groups. In view of our findings, we conclude that the Actinopoda does not represent a monophyletic evolutionary assemblage and recommend that this taxonomic designation be discarded.

One morphological feature which members of the Sarcodina share is the presence of a pseudopod during some part of their life cycle. Further taxonomic division is based on the structure of these pseudopodia. Even though pseudopod-bearing protists are grouped together, there are morphological and molecular data indicating that they are polyphyletic. At the morphological level, authors have argued that a lack of morphological characters (amoeboid-form) fails to provide firm support that a group of organisms shares common ancestry (Bovee and Jahn 1973; Lee et al. 1985). At the molecular level, the polyphyly of the sarcodines has been revealed by small-subunit ribosomal DNA (SSU rDNA) analyses which place various groups of the sarcodines branching at different parts of the evolutionary tree of life (Clark and Cross 1988; Hinkle and Sogin 1993).

In the superclass Actinopoda (Calkins 1909), all members possess specialized microtubule-stiffened pseudopodia called axopodia. The taxon Actinopoda has been maintained as a phylogenetic assemblage in the most recent considerations of protistan systematics with agreement that certain heliozoa should be removed (e.g. pedinellids and heliomonads) (Cavalier-Smith 1993; Corliss 1994). The classes currently represented in this superclass include the Acantharea, Polycystinea, Phaeodarea, and Heliozoea.

One of the major distinctions between the Acantharea and the Polycystinea is the composition, architecture, and symmetry of the skeleton, when present. All acantharia form skeletons composed of monocrystals of strontium sulfate which come together at the center of the cell in a symmetrical fashion known as Müller's Law (Müller 1858). Polycystine skeletons, when present, are typically siliceous and exhibit a range of morphologies from simple spicules to more elaborate latticed shells possessing radial spines. Despite these differences, the common use of radial symmetry in cell-body plan and shell architecture often gives members of the Acantharea and the polycystine order Spumellarida a superficially similar appearance.

Although the term "radiolaria" is now often reserved as an informal taxonomic descriptor for members of the Polycystinea (Spumellarida and Nassellarida) and the Phaeodarea only, the term was originally used by biologists to include members of the class Acantharea, as well. While the term "Radiolaria" was actually coined by Johannes Müller (1858), Ernst Haeckel is credited as being the first of the early taxonomists to do an extensive description of acantharian and radiolarian systematics.

Of the 4,417 species of organisms described from collections of the Challenger Expedition, 3,508 of them were new species of Radiolaria identified by Ernst Haeckel (Haeckel 1887; Anderson 1983). In his classification scheme of the class "Radiolaria", Haeckel included four legions: the Acantharia, the Spumellaria, the Nassellaria and the Phaeodaria. This classification was later modified (Deflandre 1952; Deflandre 1953; Tregouboff 1953; Goll and Merinfeld 1979) to exclude the Acantharia (Acantharea) from the Radiolaria (the Polycystinea which included Spumellarida and Nassellarida, and the Phaeodarea). Despite some taxonomic revision, many of Haeckel's original descriptions of the Challenger Radiolaria persist today. Modern systematists, while placing acantharia in a class distinct from polycystines and phaeodaria generally agree that these classes share common ancestry and should be united within the Actinopoda (Levine et al. 1980; Lee et al. 1985; Febvre 1990; Cavalier-Smith 1993; Corliss 1994).

In all phaeodaria, polycystines and members of the acantharian order Arthracanthida, the central capsule or capsular wall divides the cell into an intracapsular region and an extracapsular region. The intracapsular region includes the nucleus, mitochondria, golgi and other major cellular machinery while the extracapsular region contains the axopodial network of the cell. Phaeodarian and polycystine radiolaria possess pores in their central capsules whereas acantharia do not.

The main features which have lead taxonomists to infer the relatedness of the Acantharea and Polycystinea are the presence of axopodia and occurrence of a central capsule, although

additional cytological similarities have been noted. Most of these similarities occur between members of the Acantharea and the Polycystinea belonging to the order Spumellarida. Most acantharia are polynucleated, but the occurrence of a single nucleus in the acantharian genus <u>Haliommatidium</u> has been argued as a feature it shares with the polycystines, most of which have only one nucleus. Furthermore, some authors have observed an apparent similarity between the "gelatinous pellicle" of some Sphaerellarina, a suborder in the Spumellarida, and that of some acantharia (Hollande and Enjumet 1960; Massera Bottazzi 1978). Finally, the existence of strontium sulfate crystals (a skeletonbuilding material thought to be used only by members of the Acantharia) in some adult vegetative colonial spumellarian radiolaria and in apparently all swarmer cells of spumellaria has been suggested as potential evidence of their common ancestry (Dogel 1950; Hollande and Martoja 1974; Anderson 1981; Cavalier-Smith 1993).

Members of the Actinopoda are among the remaining protistan groups which lack any DNA sequence information with which to support or challenge the above views. We sequenced the small-subunit ribosomal RNA genes of representatives of the Acantharea and Polycystinea to determine if their assumed shared ancestry based on morphological features is supported at a molecular level. Since the taxa chosen for this study are thought to be among the most closely related of the four major classes included in the Actinopoda, this study further addresses the suitability of higher taxon-designations as Actinopoda and rekindles the debate over the best definition for "radiolaria".

MATERIALS AND METHODS

Sample Collection. All specimens were collected by divers by hand using glass or polycarbonate jars. Specimens were maintained in 0.22 µm Millipore-filtered Sargasso Sea water in glass culture tubes with brine shrimp (Artemia salina) as food until sacrificed for molecular analysis. All individuals were given sample designations prior to identification, and then order or genus-level classifications were made. All acantharia were collected off the southwestern coast of Bermuda in September 1994. Acantharian samples used in this paper were <u>Haliommatidium</u> sp. (BBSR 235: Order: Symphyacanthida, Family: Pseudolithidae) and Chaunacanthid 218 (BBSR 218: Order: Chaunacanthida). Polycystine radiolarian specimens, all from the order Spumellarida, were collected in a similar fashion off the southwestern coast of Bermuda on multiple dates. One solitary and three colonial spumellaria were used in this study. Solitary spumellarian Thalassicolla nucleata (BBS 3: Family: Thalassicollidae) was collected in May 1992, colonial spumellarian Collosphaera globularis-huxleyi (BBSR 173: Family: Collosphaeridae) was collected in May 1994, and colonial spumellarians Sphaerozoum punctatum (CR4: Family: Sphaerozoidae) and Collozoum serpentinum (CR16: Family: Sphaerozoidae) were collected in May 1995. Specimens used for in situ hybridizations were collected in September and October of 1995 in the same location.

DNA Extraction, Amplification, Cloning and Sequencing. In order to enrich for sarcodine DNA, whenever possible, reproductive acantharian and spumellarian radiolarian specimens were sacrificed at a point in their life cycle just prior to swarmer cell release from the central capsule. In the case of the acantharia, single individuals were collected upon formation of cysts that were generated prior to swarmer cell release. The rationale behind collecting the specimens at this point in their life cycle was twofold: first, there is a natural amplification of DNA which occurs within the organism at this time and second, many species of spumellarian radiolaria and acantharia either consume or expel endocytoplasmic symbiotic algae before swarmer formation, thereby reducing the potential of amplifying non-target DNA.

Individual central capsules or cysts were rinsed several times in 0.22 µm-Millipore filtered seawater followed by a final MilliQ-water rinse prior to placement in buffer solution. <u>T. nucleata</u> specimens were processed by pooling 2 central capsules, placing them in lysis buffer (40 mM EDTA, 50 mM Tris pH 8.3, 0.75 M Sucrose) and freezing at -20°C until further processed. Cells were lysed with proteinase K (10 mg/ml) and 20% SDS and then incubated at 55°C until lysis was complete. Genomic DNA was extracted with phenol, phenol/chloroform/isoamyl alcohol and chloroform/isoamyl alcohol, precipitated with ethanol and resuspended in TE buffer according to standard protocols.

The remaining samples were subjected to the following more streamlined protocols designed to minimize loss of DNA by minimizing the number of transfer steps (e.g. organic extractions and ethanol precipitation). Central capsules or individual cysts were rinsed as above, placed in modified 1X PCR Buffer (50 mM KCl, 10 mM Tris, pH 8.3, 2 mM MgCl₂, 0.001% Gelatin, 1.0% NP40 (Sigma)), stored frozen at -70°C and then heated at 95°C for 10 minutes to lyse cells and liberate DNA. Between 1 µl and 5 µl of a 20µl sample lysed in this manner was then used directly in PCR amplifications and typically yielded strong products.

<u>T. nucleata</u>, <u>C. globularis-huxleyi</u> and <u>Haliommatidium</u> sp. 16S-like rDNAs were amplified using PCR and eukaryotic primers specific to the ends of the molecule (Medlin et al. 1988). <u>T. nucleata</u> rDNA was cloned into M13 single strand phage, several clones were pooled and the resulting template was sequenced using Sequenase 2.0 (US Biochemical; Cleveland, OH) enzyme and existing rDNA primers (Elwood et al. 1985; Medlin et al. 1988). Two additional primers were designed and synthesized (Indiana University; Bloomington, IN) to obtain a full length sequence of <u>T. nucleata</u> (690FTnucl, 5'-AGAGGTGAAATTCAAG-3'; 690RTnucl, 5'- CTTGAATTTCACCTCT-3').

<u>Collosphaera globularis-huxleyi</u> and <u>Haliommatidium</u> sp. rDNA PCR products were cloned into a double-stranded TA plasmid vector pCRII (Invitrogen; San Diego, CA) and plasmid DNA for sequencing was obtained using the Magic MiniPrep system (Promega; Madison, WI). Double-stranded sequencing of both the entire forward and reverse strands of the rDNA coding regions was accomplished using the Sequenase version 2.0 kit and methods.

Oligonucleotide Probe Design. In situ whole-cell hybridizations using oligonucleotide probes complementary to the sarcodine SSU rRNA were carried out in order to verify that the sequence data was derived from the sarcodine DNA and not from a contaminating source such as algal symbionts or prey material. Oligonucleotide probes were designed which were unique to the acantharian sequence data and separate probes were designed which were unique to the colonial spumellarian sequence data. At the time of design of these probes, at least single-stranded sequence data was available representing three orders of Acantharea; Arthracanthida, Chaunacanthida and Symphyacanthida (Halionmatidium sp.), with which to search for signature sequences for designing probes (Chapter 4). For the colonial spumellarian radiolaria, at least single-stranded sequence information from <u>C. globularis-huxleyi</u> and <u>Rhaphidozoum acuferum</u> (see Chapter 3) was available.

Probes were designed which would target either the Acantharea or the colonial spumellaria (Fig. 1). Only colonial spumellarian probes were designed because it was not possible to find signature sequences which were sufficiently unique (having at least three base pair mismatches against any other SSU sequences in the RDP database) to design probes which would identify both the solitary radiolarian <u>T. nucleata</u> and the two colonials. The biotin-labeled probes designed for acantharian samples were as follows: A497bio, 5'-TCATTCCAATCAACTCAC-3'; A899bio, 5'-TCGTCATACAAAGGTCCA-3'. The probes designed for colonial spumellarian samples were as follows: R906bio, 5'-AAC-



FIG. 1. A. The locations of acantharian-specific oligonucleotide probes (in bold) A497bio and A899bio used in <u>in situ</u> hybridization experiments of acantharia. The complement of A497bio was synthesized (denoted as A497forward in the schematic) and used in combination with Primer B in PCR reactions to later specifically amplify the acantharian gene fragment approximately 1,300 bp in length. Primer A was then used in combination with A899bio to obtain an overlapping fragment to the previous one approximately 900 bp in length to obtain the rest of the gene. B. The locations of colonial spumellarian-specific oligonucleotide probes (in bold) R906bio and R1451bio used in <u>in situ</u> hybridization experiments of colonial spumellaria. The complement of R906bio was synthesized (denoted as R906forward in the schematic) and used in combination with Primer B in PCR reactions to specifically amplify the gene fragment approximately 900 bp in length. Primer A was used in combination with R1451bio to obtain an overlapping fragment to the previous one approximately 1,450 bp in length to obtain the rest of the gene.

GATAAAATACTAATA-3'; R1451bio, 5'-TATTGTAGCCCGTGCGCT-3'. All probes were analyzed by Check Probe (RDP; University of Illinois, Urbana) for potential homology to other SSU rRNA sequences in the database before syntheses were carried out. The oligonucleotide probes A899bio and R1451bio were synthesized by Eppendorf (Madison, WI) and oligonucleotide probes A497bio and R906bio were synthesized by Cruachem (Foster City, CA). The following eukaryote-specific, 5'-biotinylated probes were used as positive controls: EUK502Rbio; 5'ACCAGACTTGCCCTCC-3' (Amann et al. 1990) and EUK1209Rbio; 5'-GGGCATCACAGACCTG-3' (Giovannoni et al. 1988). These probes will hybridize with all known eukaryotic SSU rRNA.

In situ Hybridizations. In situ hybridizations were carried out using both fluorescence and colorimetric detection methods. The latter technique was necessary for the colonial spumellarian samples due to severe autofluorescence occurring in these organisms. Fluorescence in situ hybridizations on acantharia were carried out as described in Lim et al. (1993) using biotinylated probes and detection with FITC-avidin solution (20 μ g/ml in 100 mM NaHCO3-buffered saline, pH 8.2; (Vector Laboratories, Inc.; Burlingame, CA)). Acantharia were fixed for 1 hour at 4°C in 1X Histochoice (Amresco; Solon, OH) fixative diluted in 0.22 μ m-filtered Sargasso seawater. Individuals were then transferred to gel-subbed-slides, overlaid with 0.05% agarose and allowed to dry overnight. Probe was added to a final concentration of 5 ng/µl. Probe treatments consisted of a negative control (incubation in fluorescein-labeled avidin with no probe added), a positive control (biotinylated EUK 1209Rbio added), and two separate acantharian-specific probe treaments using A497bio and A899bio oligonucleotides respectively.

Hybridizations were carried out at 42°C for 6-8 hours and subsequent washes were done at 45°C. Cells were mounted in Citifluor immersion oil (Citifluor, Ltd.; London, England) and viewed on a Zeiss Axiophot equipped for epifluorescence microscopy. Epifluorescence photomicrographs were taken with an integral camera system using a

fluorescein isothiocyanate (FITC) filter set combination consisting of a 450-490 nm bandpass excitation filter; a 510 nm long-pass dichroic mirror; and a 515-565 nm band-pass emission filter. Fuji 100 ASA Provia color slide film was used for fluorescence pictures. All exposure times for a set of samples (i. e. negative control, positive control, taxonspecific probes) were kept constant so that the relative intensity was indicative of probe binding. Transmitted light photomicrographs were also taken of the same specimens using Kodak ASA 160 Tungsten film.

Colorimetric-based in situ hybridizations were carried out on colonial spumellarian samples using the Gibco BRL In Situ Hybridization and Detection System (Life Technologies; Frederick, MD) with the following modifications for use with rRNA and larger sarcodines. Colonies were preserved in 1X Histochoice with 95% ethanol added in a ratio of 4:1. Colonies were preserved for 1 hour at 4°C, transferred to 70% ethanol and held overnight at 4°C. Aliquots of preserved central capsules from a single colony were placed on silanated glass slides (Midwest Scientific; St. Louis, MO) and allowed to air dry. Slides were then baked at 65°C for 1 hour to remove endogenous alkaline phosphatase activity. Hybridizations were carried out in 50 µl-capacity Probe-Clip "Press-to-Seal" incubation chambers and holders (Midwest Scientific; St. Louis, MO). Four probe treatments were carried out using central capsules from the same colony: a negative control incubation (streptavidin-alkaline phosphatase conjugate with no probe added), a negative probe control (A899bio acantharian probe added), a positive probe control (EUK 502bio and EUK 1209bio added), and a colonial spumellarian probe treatment (R906bio and R1451bio added). All probe treatments contained final total probe concentrations of 1 ng/μl.

Hybridizations were conducted according to the manufacturer's instructions for "DNA Detection" with the above modifications and the omission of any steps specifically required for DNA targets. Slides were hybridized for 8 hours and probe detection was carried out

according to manufacturer's protocol with levamisole (Sigma; St. Louis, MO) added at 200 μ g/ml upon addition of alkaline phosphatase conjugate to further eliminate any potential endogenous alkaline phosphatase activity. Developed slides were permanently mounted in Crystal/Mount (Biomeda; Foster City, CA) and observed on a Zeiss standard microscope equipped with phase microscopy. Transmitted light photomicrographs of samples were taken with an Olympus OM4-T camera using Kodak 160 speed Tungsten film.

Direct Sequencing of PCR Products. Upon achieving successful <u>in situ</u> hybridizations, further amplifications were accomplished using group-specific probes as primers in PCR reactions to specifically amplify and sequence sarcodine rDNA. The acantharian probe A899bio was used as a reverse primer in combination with Medlin amplification-primer A (Medlin et al. 1988) to specifically amplify the first 900 base pairs of acantharian SSU rRNA genes from the chaunacanthid sample BBSR 218 (See Fig. 1). The complement of probe A497 (non-biotinylated) was synthesized (Cruachem) and used in combination with Medlin amplification primer B (Medlin et al. 1988) to amplify a gene fragment approximately 1,300 base pairs in length which overlapped the primer A/A899bio amplification fragment.

Likewise for the colonial spumellaria, the complement of probe R906bio was synthesized (Cruachem) and the primer A/R1451bio and R906/primer B primer-pair amplifications were carried out on colonial spumellarian samples CR4 and CR16 (See Fig. 1). All PCR fragments were purified using the Wizard PCR Prep system (Promega; Madison, WI). Direct sequencing of PCR products was accomplished using reagents from the Sequitherm Long Read Sequencing Kit (Epicentre Technologies; Madison, WI) along with the Sequitherm Cycle sequencing protocol developed by Li-Cor which consisted of 5 minutes of denaturation at 95°C prior to 30 cycles of 20 sec at 95°C, 30 sec at 60°C, and 1 minute at 70°C using a Perkin Elmer 2400 Thermo Cycler. Sequenced templates were run out on a Licor model 4000L sequencer. Gel images were transferred from Licor to BioImage

(Millipore Corp.; Ann Arbor, MI) and sequences were analyzed using the Millipore BioImage DNA Sequence Film Reader software.

Phylogenetic Analysis. The 16S-like rRNA sequences of acantharian and radiolarian samples were aligned against a subset of the total eukaryotic alignment data base (Olsen et al. 1992). The 31 taxa included in this study are listed in Table 1. Sequences were aligned by eye using the Olsen Multiple Sequence Alignment Editing program with regard to primary and secondary structural conservation. 1,369 positions were used in the phylogenetic analyses. A distance matrix based on pairwise distances was created for the data set and a phylogenetic tree was inferred from these data by the method of Olsen (Olsen 1988). One hundred bootstrap replicates were conducted and a consensus tree was obtained using PHYLIP 3.5 (Felsenstein 1985). Phylogenetic trees were also inferred by the maximum likelihood method in conjuction with the fastDNAml program (Olsen et al. 1994) using a generalized two parameter model of evolution (Kishino and Hasegawa 1989) and maximum parsimony method using PAUP, version 3.1.1 (Swofford 1991). The maximum parsimony tree was obtained from a consensus of 100 bootstrap replications which were conducted using a heuristic search option with random addition sequence, 10 replicates and the tree bisection-reconnection algorithm. Identical phylogenetic analyses as those described above were also performed with Phreatamoeba balamuthi removed from the data set, in order to determine stability of the relative branching of the acantharia and the polycystine radiolaria. In these analyses, the same alignment and sequence positions were used as in those analyses including Phreatamoeba balamuthi in the data set.

RESULTS

In situ hybridization experiments confirmed the origin of the acantharian and spumellarian sequences (Fig. 2). Acantharian specific probes were found to specifically hybridize to the acantharia (Fig. 2, panels F and H) and not to colonial spumellaria (Fig. 2, panel J).

	SSU rDNA	
Species	G+C (%)	Taxonomic affinity
Theileria annulata	45	Apicomplexa
Symbiodinium pilosum	45	Dinoflagellida
Oxytricha granulifera	46	Ciliophora
Blepharisma americanum	47	Ciliophora
Porphyridium aerugineum	48	Rhodophyta
Stylonema alsidii	46	Rhodophyta
<u>Emiliana huxleyi</u>	50	Haptophyta
Labyrinthuloides minuta	44	Labyrinthulid
Ochromonas danica	45	Chrysophyceae
Cafeteria roenbergensis	47	Bicosoecids
<u>Chlamydomonas</u> reinhardtii	50	Chlorophyte
<u>Oryza sativa</u>	51	Plantae
Acanthamoeba castellanii	52	Amoebida
<u>Hartmanella vermiformis</u>	49	Amoebida
Athelia bombacina	47	Fungi (Eumycota)
Blastocladiella emersonii	46	Fungi (Eumycota)
<u>Mnemiopsis leidyi</u>	47	Animalia
Diaphanoeca grandis	44	Choanoflagellate
Phreatamoeba balamuthi	47	Amoeba

Table 1. Percent G + C content and taxonomic affinities of the taxa used in this study.

Table 1. (cont.)

	SSU rDNA	
Species	G+C (%)	Taxonomic affinity
Paulinella chromatophora	48	Filosea
<u>Euglypha rotunda</u>	45	Filosea
<u>Haliommatidium</u> sp.	44	Symphyacanthida
Chaunacanthid 218	45	Chaunacanthida
Dictyostelium discoideum	42	Dictyostelida
Physarum polycephalum	52	Plasmodial Slime
		Molds
Thalassicolla nucleata	36	Spumellarida
Collosphaera globularis-huxleyi	35	Spumellarida
Sphaerozoum punctatum	37	Spumellarida
Collozoum serpentinum	38	Spumellarida
Entamoeba gingivalis	34	Amoebida
Naegleria gruberi	48	Schizopyrenida

Likewise, colonial spumellarian probes specifically hybridized with colonial spumellaria (Fig. 2, panel L).

The % G + C content of the SSU rRNA gene for <u>Haliommatidum</u> sp. and Chaunacanthid 218 were 44% and 45% respectively, which was similar to many of the other taxa used in the analyses (Table 1). However, spumellarian % G+ C content values (35% - 38%) were similar to that of <u>Entamoeba gingivalis</u> (34%) and were low relative to typical eukaryotic values which are usually around 50%. Gene lengths in base pairs (bp) for acantharian and spumellarian samples were typical for eukaryotic SSU rRNA genes. <u>Haliommatidum</u> sp. and Chaunacanthid 218 were 1788 bp and 1778 bp. Lengths of genes for spumellaria were as follows: <u>T. nucleata</u>, 1770 bp; <u>C. globularis-huxleyi</u>, 1797 bp ; <u>S. punctatum</u>, 1788 bp; <u>C. serpentinum</u>, 1798 bp.

The phylogenetic trees inferred by the distance-matrix, maximum parsimony (Fig. 3) and maximum likelihood (data not shown) methods clearly rejected a common ancestry between these two groups of actinopods. Numbers at nodes represent bootstrap values as a percentage of 100 resamplings of the data set. Only bootstrap values greater than 50% are shown and represent relative measures of confidence. Both the distance and parsimony trees placed the spumellarian radiolaria branching as a diverging lineage below the "crown" groups (Knoll 1992), those taxa representing major eukaryotic assemblages simultaneously radiating from the node labeled with a bootstrap value of 85/65. Both methods revealed a poorly resolved branching point for the acantharia (Haliommatidum sp. and Chaunacanthid 218) among the crown radiation. The relative positions of the acantharia and the polycystine radiolaria were not affected by removal of <u>Phreatamoeba balamuthi</u> (Fig. 4). Removal of <u>Phreatamoeba balamuthi</u> from the data set resulted in higher bootstrap support values for the node leading to the crown (89/98).

A low bootstrap support value of 67% was obtained for the branching of the spumellaria with <u>Entameoba gingivalis</u> in the parsimony analysis, but this support was not observed in

hybridize with all species within these orders of acantharia). Panels I through L show hybridization results for single individuals K shows the results of the positive control hybridization with eukaryote probes (EUK502R and EUK1209R) and panel L shows streptavidin-alkaline phosphatase-conjugated secondary labels. For the acantharian cells, hybridization detection was carried out phase and epifluorescence photomicrographs of the same cell. Scale bars represent 75 µm in panels A-H. Panels A and B show epifluorescence (B). Panels C and D show the positive control treatment to which a eukaryotic-specific probe designed to target all eukaryotes (EUK 1209R) was added. Panels E and F and G and H show the probing of cells with two different acantharian indolylphosphate (BCIP) substrates. Panels A-H depict four different acantharian cells of the same species with corresponding secondary label was added. Panel J shows a negative probe control treatment to which an acantharian probe was added. Panel using epifluorescence microscopy with settings specific for FITC excitation (panels B, D, F, H). Colonial spumellarian cells 16S-like (small-subunit) ribosomal RNA sequences of acantharia (A-H) and colonial spumellaria (I-L). For both acantharian FIG. 2. In situ hybridization of Histochoice-preserved specimens using oligodeoxynucleotide probes complementary to the probes (F, A497; H, A899), both designed against members of three different orders of acantharia (i.e. these probes should within the same colony. Panel I shows the negative control to which only the streptavidin-alkaline phosphatase-conjugated were viewed using phase contrast microscopy and hybridizations were detected colorimetrically using the localized, purple and colonial spumellarian cells, probes conjugated to biotin were detected by either fluoroisothiocyanate (FITC)-avidin or the negative control to which only FITC-avidin was added. Note the minimal background fluorescence of the cell under hybridization with colonial spumellarian probes (R906 and R1451). Scale bars represent 35 µm in panels I through L. precipitate of the enzymatic reaction of alkaline phosphatase on nitroblue tetrazolium (NBT) and 5-bromo-4-chloro-3-



are given above the line, whereas maximum parsimony values are below. A dash indicates that the bootstrap value for that node was below 50% in the method used for phylogeny reconstruction. The bar insert corresponds to 10 changes per 100 nucleotide nodes represent bootstrap values, given as a percentage of 100 resamplings of the data. Bootstrap values for distance analyses FIG. 3. The inferred phylogeny for the acantharia and the spumellarian radiolaria. A distance tree is shown. Numbers at the positions. Only horizontal components of the tree are measures of evolutionary distance.





reconstruction. The bar insert corresponds to 10 changes per 100 nucleotide positions. Only horizontal components of the tree FIG. 4. The inferred phylogeny for the acantharia and the spumellarian radiolaria after the removal of Phreatamoeba balamuthi resamplings of the data. Bootstrap values for distance analyses are given above the line, whereas maximum parsimony values from the data set. A distance tree is shown. Numbers at the nodes represent bootstrap values, given as a percentage of 100 are below. A dash indicates that the bootstrap value for that node was below 50% in the method used for phylogeny are measures of evolutionary distance.



10 changes per 100 nucleotides

the distance analysis nor the topology of the maximum likelihood analysis (data not shown). No other potential immediate common ancestors were indicated by these data. The position of the spumellaria relative to other groups branching below the crown varied between the distance and parsimony analyses. Therefore, the exact branching order of the spumellarian radiolaria also remains unresolved at this time. The monophyly of the acantharia and the monophyly of the spumellaria, however, were well supported (100% in all cases).

The branching patterns within the spumellaria in the distance and the parsimony analyses both showed the solitary spumellarian <u>T. nucleata</u> branching prior to the colonial spumellaria. Although the bootstrap support for this node was barely above 50% in the parsimony analysis, a higher bootstrap value was obtained (77%) with distance methods. The relationship between the solitary and colonial spumellaria has been examined using a larger suite of spumellarian taxa and additional nucleotide sites in Chapter 3.

DISCUSSION

The relative positions of the acantharia and the spumellaria in molecular phylogenetic trees indicate that the presence of axopodia, a capsule membrane and the ability to metabolize strontium sulfate should be reconsidered as reliable phylogenetic markers. Our molecular study of acantharian and spumellarian phylogeny strongly agrees with what has been speculated in the literature over the past several years: axopodia have evolved more than once and most likely represent convergent structures created in response to similar ecological constraints through evolutionary time (Merinfeld 1978; Shulman and Reshetnyak 1980; Merinfeld 1981; Reshetnyak 1981a). An independent evolution of axopodia within the chromistan Pedinellea of the Heliozoea already has been suggested on morphological grounds (Cavalier-Smith 1993). Given the results of this study, retention of the superclass Actinopoda seems inappropriate, as does the adoption of the new phylum Radiozoa, which

has been described as a modern-day Radiolaria <u>sensu lato</u> (Cavalier-Smith 1993; Corliss 1994).

The presence of a central capsule and the ability to secrete strontium sulfate have been described as two synapomorphies defining the Radiozoa (Cavalier-Smith 1993). However, the central capsule found in spumellaria and that which exists in one order of Acantharea (the Arthracanthida) have been shown to differ (Massera Bottazzi 1978; Reshetnyak 1981a). The acantharian central capsule in this order is non-perforated and of ectoplasmic origin while that of the polycystines and the phaeodaria is perforated and located between the ectoplasm and the endoplasm. Furthermore, the presence of central capsules in the Arthracanthida, which are considered to be more derived than other orders of acantharia which lack central capsules (Hollande et al. 1965; Strelkov and Reshetnyak 1974; Reshetnyak 1981a), suggests that "central capsules" may have evolved more than once.

The occurrence of strontium sulfate in both acantharia and spumellaria is another feature often cited as evidence of their common ancestry. Vegetative adults of colonial spumellaria are known to house crystals of strontium sulfate in their central capsules and the biflagellated swarmers of all spumellarian radiolaria examined thus far contain crystals of strontium sulfate in membrane bound vesicles. However, metabolism of strontium sulfate is not unique to the acantharia and spumellarian radiolaria. Crystals of strontium sulfate have been observed in the desmid alga <u>Closterium littorale</u> (Raven et al. 1986), in <u>Chara</u>, the "stonewort" freshwater plant, and in loxodid ciliates (Fenchel and Finlay 1986). The role of strontium sulfate in <u>Chara</u> and the loxodid ciliates is apparently graviperception (Fenchel and Finlay 1986; Raven et al. 1986). A similar function has been proposed in the desmid algae (Raven et al. 1986). This function apparently has never been proposed for the membrane-bound crystals found in spumellarian swarmers. Instead, Anderson (1981) has suggested that strontium sulfate crystals may serve a function in buoyancy control but

admits that silica or calcium compounds, which occur at higher concentrations in sea water, would be better candidates for this purpose. Anderson also suggested that strontium may be of some physiological importance to the spumellaria but does not elaborate on what this requirement might be. One possibility is that strontium serves a similar function in spumellaria as in some gastropods where it is required for proper shell development (Bidwell et al. 1986). A caveat to the potential importance of strontium in spumellarian skeletal development, however, is that even spumellarian species which lack skeletal material, like <u>T. nucleata</u> and <u>Collozoum</u> spp., have swarmers with crystalline strontium sulfate inclusions. Furthermore, the lack of strontium sulfate crystals in acantharian swarmer cells, seems inconsistent with the idea that strontium sulfate serves a similar function in both the Acantharea and the spumellarian polycystines.

While most of the literature has favored a common ancestry of the acantharia and the spumellaria, a series of papers published in Russian during the early 1980's argued against this idea (Shulman and Reshetnyak 1980; Reshetnyak 1981a; Reshetnyak 1981b). These papers describe several morphological features as unique to the Acantharea. These major features include the existence of a skeleton of strontium sulfate, not merely crystals of the compound as are found in some spumellaria, organized in a highly geometrical fashion according to Müller's Law. Also thought to be unique to Acantharea is the cytoplasmic feature called the calymma which, along with the ectoplasmic cortex and the non-actin containing myonemes, forms a "hydrostatic apparatus" thought to render acantharia capable of movement in the vertical direction. These authors concluded that the axopodial system was not a reliable phylogenetic marker, and defended their argument by comparison of ultrastructural studies of the axopodial systems in different groups of Actinopoda (Hollande 1953; Cachon and Cachon 1964; Febvre 1971; Cachon and Cachon 1972; Febvre 1972; Cachon et al. 1973; Febvre 1973).

In brief, the Russian authors proposed that axopodial systems evolved independently several times in evolution as amoeboid-like protists were going from benthic to pelagic modes of existence. The authors pointed out differences in the axopodial systems of various classes within the Actinopoda in support of their interpretation of the ultrastructural data provided by the French investigators cited above. They pointed out structural differences in the axoneme (the microtubular shaft which stiffens axopodia) and differences in the size and location of the axoplast (the microtubule-organizing center of the axoneme) between taxa which they say is suggestive of convergence not homology. Finally, they mention the presumed artificial grouping of actinophrid and centrohelid heliozoa (which posses very different axoneme structures) in support for their argument. For more details and diagrams comparing actinopod axopodial systems the reader is referred to the Russian literature cited above for which fairly complete translations are available from LAZ. The results from the molecular work described in this thesis support the major claims made by these Russian authors.

The absence of strontium sulfate in swarmer cells of Acantharea, as mentioned above, is noteworthy in this discussion because it suggests yet another difference between the respective requirements of acantharian and spumellarian swarmers. Given the fact that strontium sulfate crystals are thought to be involved in buoyancy control, their absence in acantharian swarmers, and the fact the acantharia are understood to reproduce at depth (Reshetnyak 1981a), the following scenario is consistent with what is currently understood about acantharian biology: Perhaps the need for strontium sulfate crystals for buoyancy control in acantharian swarmers is overcome by the ability of acantharia to regulate their depth in the water column via their "hydrostatic apparatus", allowing the acantharian to sink to the desired depth for release of its swarmer cells. In addition, many species of acantharia form cysts also composed of strontium sulfate which aid in the sinking of swarmer cells to depth. The greater density of strontium sulfate relative to silicon dioxide

may also explain why polycystine radiolaria, which can possess siliceous skeletons, utilize the heavier strontium sulfate in their swarmers. Interestingly, phaeodarian radiolaria which live deeper in the water column do not have the capacity to metabolize strontium sulfate and, like acantharia, lack strontium sulfate-containing swarmer cells. Whatever function served, the presence of strontium sulfate in these marine protists and its singular utilization as the structural compound in the skeletons of acantharia deserves further scrutiny in the evolution of this group as do their unique non-actin-containing myonemes.

Which protists, then, share most recent ancestry with the Acantharea? The branching pattern of the acantharia was strikingly shallow relative to that of the spumellarian radiolaria, possibly suggesting that the acantharia diversified more recently than the spumellaria. The most recent common ancestor of the Acantharea could possibly be found among actinopods which have been placed among the <u>incertae sedis</u>. Among them we find such specimens as <u>Podactinelius sessilis</u> (Schröder 1907), possibly the only living benthic acantharian, which was described aboard the Deutschen Südpolar-Expedition of 1901-1903. This genus was once included as a separate order Actineliida in the class Acantharea. However, since the last publication of the Committee on Systematics and Evolution of the Society of Protozoologists, it been relegated to an uncertain taxonomic affinity. This genus possesses spines of strontium sulfate (400-500) which are not arranged in the characteristic geometric pattern observed in all Acantharea.

The determination of the nearest relative of the Spumellarida remains equally challenging. If the long branches occurring in the spumellarian lineage may be interpreted as evidence of their ancient origins it may be difficult to determine the phenotype of the most recent common ancestor of the Spumellarida. Although the fossil record of spicule-bearing forms (Sphaerozoidae) extends to the Lower Oligocene (Bjørklund and Goll 1979) and that of the Collosphaeridae to the base of the Miocene (Riedel 1967), even more ancient origins are possible in view of the existence of extant skeletonless forms which would not be

preserved in the sediments. As an alternative hypotheses, the long branch lengths of the spumellaria may be explained as the result of a rapidly evolving lineage.

It is assumed that the Nassellarida which represent the second order included in the Polycystinea are closely related to the Spumellarida (Cachon et al. 1990). The molecular phylogenetic position of the Phaeodarea is also unknown and deserves consideration. As for Haeckel's Radiolaria and the definition of the Radiolaria <u>sensu lato</u> (Polcystinea, Phaeodarea and Acantharea), continued use of this definition in anything but a historical perspective, and the biological implications behind it appear unjustified in view of the results described herein.

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Chapter 2

Insights on the Diversity within a "species" of <u>Thalassicolla</u> (Spumellarida) Based on Small-Subunit Ribosomal RNA Gene Sequencing

ABSTRACT. We compared small-subunit ribosomal RNA gene sequences of samples from solitary spumellarian radiolarian <u>Thalassicolla nucleata</u> collected from the Sargasso Sea and the Pacific Ocean. Sequences derived from these separate locations showed variability in both length and base-pair composition which is consistent with genus-level variation reported in the literature for other taxa. The seven existing descriptions of <u>Thalassicolla</u> species, including <u>T. nucleata</u>, are discussed in view of these molecular findings and with reference to our current understanding of the physiology and life cycle of the spumellarian radiolaria.

Supplementary key words. Actinopoda, Polycystinea, radiolarian, sarcodine

Little systematic revision has occurred in the genus <u>Thalassicolla</u> since its first representative, <u>Thalassicolla nucleata</u> was described by Thomas Huxley in 1851. The solitary spumellarian <u>T. nucleata</u> along with many colonial spumellaria, all to which Huxley assigned the name <u>Thalassicolla punctata</u>, were among the first described living polycystine radiolaria. <u>Thalassicolla punctata</u> was later dissolved by Johannes Müller, but <u>T. nucleata</u> was retained and is still recognized as a valid species today.

The six other species of the genus <u>Thalassicolla</u> were all proposed by Ernst Haeckel primarily from specimens collected aboard the H. M. S. Challenger (Haeckel 1887). These species included the following: <u>T. pellucida</u>, <u>T. spumida</u>, <u>T. zanclea</u>, <u>T. australis</u>, <u>T. maculata</u> and <u>T. melacapsa</u>. Haeckel used qualities of the central capsule such as wall texture, color and size as the major distinguishing features upon which to separate species of <u>Thalassicolla</u>. Curiously, of the seven known species of <u>Thalassicolla</u>, only four, <u>T. pellucida</u>, <u>T. spumida</u>, <u>T. spumida</u>, <u>T. melacapsa</u> and <u>T. nucleata</u> appear to be mentioned in the literature since Haeckel's first reports, and no systematic revisions of the species of <u>Thalassicolla</u> have occurred since Haeckel's time.

As more information about the physiology and life cycle of this genus has been obtained, the validity of some of Haeckel's species descriptions have been questioned. Most of these studies have been carried out on the single species <u>T. nucleata</u>.

Since its original description, <u>T. nucleata</u> has become a model organism for research into the biology of the spumellarian radiolaria (Anderson 1978; Herring 1979; Anderson 1983). <u>Thalassicolla nucleata</u> is a large (3 - 5 mm) solitary, spumellarian polycystine found ubiquitously in tropical and subtropical surface waters of open-ocean communities including the Sargasso Sea and the Pacific Ocean, as well as other locations. <u>Thalassicolla</u> <u>nucleata</u> lacks a skeleton and represents one of the simplest examples of polycystine cell architecture: a single central capsule, usually enveloped by a dark opaque layer, which is in

turn surrounded by a matrix of highly-alveolated, symbiont filled extracapsular material (see Fig. 1A).

Given the rather simple cell-architecture of <u>T. nucleata</u>, it seems possible that the criteria used by Haeckel to distinguish between different species of <u>Thalassicolla</u> may not have been reflected on the genetic level. The morphological differences noted by Haeckel may have been the result of the physiological state of the cell, life cycle effects, or environmental influences. Ultimately it may not be possible to distinguish between species of <u>Thalassicolla</u> based on morphological criteria alone.

We approached the question of species diversity in the genus Thalassicolla by comparing gene sequences of the small subunit ribosomal RNA (SSU rRNA) in T. nucleata collected from different locations to determine if there are genetic differences which are not associated with morphological details at the species level. Two features of the life history make <u>T. nucleata</u> well-suited for molecular phylogenetic study. First, although it cannot be reared through successive generations, <u>T. nucleata</u> readily undergoes swarmer formation in the laboratory during which time the dark opaque layer surrounding the central capsular region of the cell is shed revealing a milky-white capsule beneath it (Anderson 1978). Swarmer formation marks the onset of reproduction in the cell, at which time the intracapsular DNA concentration is significantly increased and divided among swarmer cells. This "natural" amplification of DNA within the cell greatly facilitates retrieval of DNA for molecular analysis. Second, like many spumellarian radiolaria, T. nucleata lives in association with symbiotic algae which are believed to enhance survival of species in oligotrophic environments (Anderson 1978; Anderson and Botfield 1983). These algae might normally complicate separation of host DNA from symbiont DNA, but the symbionts in polycystines are physically excluded from the central capsular region by the capsular membrane. Dissection of the central capsule away from the rest of the extracapsular material which houses symbionts, along with sacrificing the cell immediately prior to

Fig. 1. A. A transmitted-light photomicrograph of a typical specimen of <u>Thalassicolla nucleata</u> showing the spherical central piece of which is only presented; a, the large alveoles; b, peculiar exoplasmatic bodies; p, black pigment in the inner zone; f, vacuoles filling up the central capsule and separated by black pigment; a, large alveoles of the calymma; k, oil globules; b, the retracted pseudopodia in the outer zone of the calymma. C. A drawing of \underline{T} . melacapsa also by Ernst Haeckel (from vacuoles filling this capsule; n, the central nucleus; l, the concentric nucleolus; g, the voluminous calymma, a small radial Haeckel 1887, Pl. 1 Fig. 5). After Haeckel: n, The large nucleus; l, numerous small nucleoli inside the nucleus; v, the capsule covered by a dark opaque layer and surrounded by an alveolated extracapsular material. Bar = 0.4 mm. B. A drawing of \underline{T} , maculata by Ernst Haeckel (from Haeckel 1887, Pl. 1 Fig.4). After Haeckel: c, The central capsule; v, exoplasmatic bodies; f, the retracted pseudopodia in the outer zone of the calymma.



swarmer release, therefore greatly enhances amplification of host DNA for further molecular analyses.

MATERIAL AND METHODS

<u>Thalassicolla nucleata</u> cells were collected in glass jars by divers. Cells were maintained in 0.22 μ m Millipore-filtered sea water in glass culture tubes and fed brine shrimp (<u>Artemia</u> <u>salina</u>) as food. <u>T. nucleata</u> samples were collected in the Sargasso Sea approximately 4 miles off the southeast coast of Bermuda and in the North Pacific Central Gyre along a transect from Portsmouth, Oregon to Honolulu, Hawaii.

Central capsules of the polycystine radiolarian cells which contain the nucleus, as well as other cellular machinery, were physically separated from extracapsular material which contained endosymbiotic algae at a time in their life cycle immediately before swarmer release. The T. nucleata sequence derived from the Sargasso Sea sample designated TnucBBS 3 was obtained from central capsules of two individuals. The Thalassicolla sequences obtained from the Pacific, designated TnW10.79, TnW10.74, TnW10.72, and TnW10.10, were four different clones derived from a single sample which contained 17 pooled central capsules. Total DNA from Sargasso Sea-collected specimens was extracted, rDNA was amplified, cloned and sequenced as described in Chapter 1. Pacific collected T. nucleata were extracted using the same protocols as the Sargasso Sea-collected specimens. However, amplified rDNA (after Saiki et al. 1988) from Pacific samples was cloned into a double-stranded TA plasmid vector pCRII (Invitrogen) and purified plasmid template DNA for sequencing was obtained using the Magic MiniPrep system (Promega). To minimize sequencing error, double stranded sequence of both the entire forward and reverse strands of the rDNA coding regions was obtained using the Sequenase version 2.0 kit and methods or Sequitherm (Epicentre) kit and Li-Cor automated sequencing methods (Li-Cor).

The 16S-like rRNA sequences of <u>Thalassicolla</u> were aligned against a larger eukaryotic data set by eye with regard to primary and secondary structural conservation using the

Olsen Multiple Sequence Alignment Editing program (Olsen et al. 1992). Absolute percent differences were calculated as a percentage of dissimilarity between pairs of the five \underline{T} . <u>nucleata</u> sequences. Percent dissimilarity values were obtained by dividing the absolute number of base pair differences between pairs of taxa by the length of the longer sequence of the pair, counting gaps and ambiguities as a single difference, and representing the resulting value as a percentage of 100.

RESULTS

The SSU rRNA sequences for five representatives of <u>T. nucleata</u> are listed in Fig. 2. Based on this alignment, <u>T. nucleata</u> sequences showed variability at 66 positions scattered over the entire length of the gene. The percent dissimilarity values of these sequences are listed in Table 1. The amount of genetic variation found among samples of <u>T. nucleata</u> small-subunit rRNA gene ranged from 0.45% to 2.54%. The largest dissimilarity values of 2.54% were seen between the sequence from the Sargasso and two sequences from the Pacific sample. The sequences derived from the Pacific sample were more similar to each other than any of the four were to the sequence derived from Sargasso. The gene lengths in base pairs (bp) for the sequences presented in this paper are as follows: TnucBBS3, 1770 bp; TnW10.79, 1771 bp; TnW10.74, 1765 bp; TnW10.72, 1771 bp.; TnW10.10, 1771 bp.

DISCUSSION

The degree of variability seen in the <u>T. nucleata</u> sequence data exceeds that expected within a given species and is comparable to that seen between different genera or within genera of other protistan taxa in the literature (Sogin et al. 1986; Manhart et al. 1995). While all the specimens used in this study fit the morphological description of <u>T. nucleata</u>, it is possible that different strains of <u>T. nucleata</u> exist which cannot be distinguished based on morphological criteria. Alternatively, the individuals collected as <u>T. nucleata</u> may have included other species indistinguishable from <u>T. nucleata</u> at the light microscope level. Yet

Sample #'s	BBS3	W10.79	W10.74	W10.72	W10.10
BBS3	0	2.37	2.32	2.54	2.54
W10.79		0	1.98	0.45	0.62
W10.74			0	1.92	2.03
W10.72				0	0.62
W10.10					0

 Table 1. Percent dissimilarity for rDNA sequences derived from different samples of

 Thalassicolla nucleata.

Fig. 2. The alignment of 16S-like rRNA sequences of Sargasso Sea-collected <u>T. nucleata</u> (TnucBBS3) and four sequences derived from a pooled sample of <u>T. nucleata</u> from the Pacific (TnW10.79, 74, 72 and 10). Sequence identity is represented by dots and nucleotide abbreviations follow the IUB code.

TnucBBS3	1	AACCUGGUUGAUCCUGCCAGUAGUCAUACGCUAACAUUAAAGAUUAAGC
TnW10.79	1	
TnW10.74	1	
TnW10.72	1	
TnW10.10	1	
TnucBBS3	50	CAUGCAUGUACGAGUAUACAAUUACCAUUUUAAACUGCGUAAAGCUCAU
TnW10.79	50	
TnW10.74	50	A
TnW10.72	50	
TnW10.10	50	A.AU
TnucBBS3	99	UAUAUCAGUUCUAACAUCUUAGGAAUACAAAAAAGAUGGAUAUUAGUGC
TnW10.79	99	GA.C
TnW10.74	97	UA.C
TnW10.72	99	GA.C
TnW10.10	99	GA.C
TnucBBS3	148	UAAUUCUACAAUCAAUACAUUUAUAACGUCUAAUUUU-UUAGACUAAAU
TnW10.79	147	UAAU
TnW10.74	145	AU
TnW10.72	147	UAAU
TnW10.10	147	
TnucBBS3	196	UACUGAGUAUCAAAAAGUACGACUAUCUGAAUUCUUAAUAUUUACUGGUU
TnW10.79	196	GG
TnW10.74	193	
TnW10.72	196	G
TnW10.10	196	G
TnucBBS3	245	ACACUACAGAGUGAUAGUUCUAUUUAGUGACUGACCCAUCAGUUGUUCU
TnW10.79	245	
TnW10.74	242	
TnW10.72	245	
TnW10.10	245	
TnucBBS3	294	AUUAUGUAGUGAAUUAUUGAGGCUGAAACGGGUAGCGGAGAAUUAGGGU
TnW10.79	294	
TnW10.74	291	
TnW10.72	294	
TnW10.10	294	
TnucBBS3	343	UCCGUUCCGGAGAAAGAGCCUGCGAAACGGCUACUACAUCUAAGGAAGG
TnW10.79	343	
TnW10.74	340	
TnW10.72	343	
TnW10.10	343	
TnucBBS3	392	CAGCAGGCGNGUAAAUUAUUCAAUUCUAAAUCAGAGAGUUAGUAACAAU
TnW10.79	392	C
TnW10.74	389	C
TnW10.72	392	C
TnW10.10	392	C

TnucBBS3	441	AUAUUACGAUGUUAAACCUUAGGGUUAAAUUAUUAUAUUGAGGAUAGAU
TnW10.79	441	
TnW10.74	438	
TnW10.72	441	
TnW10 10	441	
1111110.10	111	
TrucBBS3	490	UAUUUUAUUUAUGAUUGACUAUAGGAGGGCAAGUCUGGUGCCAGCAGC
TnW10 79	490	
$T_{\rm mw10}.79$	190	Δ
$m_{\rm pW10.74}$	107	
$\frac{11W10.72}{W}$	490	
1111110.10	490	
TnucBBS3	539	CGCGGUAAUACCAGCUCCAAUAGUGUAUGCUAACGUUGUUGCAGUUACA
TnW10.79	539	
TnW10.74	536	
$T_{\rm Tr}W10.72$	539	
$m_{\rm DW10.12}$	530	
1110.10	222	
TnucBBS3	588	AAGCUCGUAGUUGGUCUAUUAUGARUUUUAUUUAUAUAUAUAGUAUAAUUG
TnW10.79	588	АА
$T_{\rm mW10}$ 74	585	A
Trn W10 72	588	Δ
$T_{m}W10.12$	588	δ
1110010.10	200	
TnucBBS3	637	UACUAUUAUUGACAAUGCCUAAAUCUUACUUAGAACAUGUACUAUGUUG
TnW10.79	637	CUA
TnW10.74	634	CUA
TnW10.72	637	
TnW10.10	637	
TnucBBS3	686	AAAYUUACUUUUCGACAUUUCCUCAUGUUUGUUAUUACUUUGAAAAAAU
TnW10.79	686	
TnW10.74	683	
TnW10.72	686	U
TnW10.10	686	
TnucBBS3	735	UAUGUUGAUUUAAGAGAAGAAAUGAUAUUGUACUAUAGUACAGAAUAAU
TnW10.79	735	
TnW10.74	732	C
TnW10.72	735	
TnW10.10	735	C
TnucBBS3	784	ACUUGAAGAUCUCAGUAAAACUUAAACUUUUGGAUACUGGUGUARUGCU
TnW10.79	784	A
TnW10.74	781	A
TnW10.72	784	A
TnW10.10	784	A
ThucBBS3	833	CUUUAGAGUUAGCUGAAGAUAUUAAUAUUUUAGCGWUAGAGGUGAAAUU
TnW10.79	833	U
TnW10.74	830	U
TnW10.72	833	U
TnW10.10	833	U

TnucBBS3	882	CAAGAAUCGUUAUAAGAUUAACAAGUGCCAAAGCAAUUAUCUAAGAUUA
TnW10.79	882	U
TnW10.74	879	UU
TnW10.72	882	
TnW10.10	882	AA
TnucBBS3	931	AUUCAUUGAUCAAGAACGUAAGUUGAAGGAUUGAAGACGAUCAGAUACC
TnW10.79	931	
TnW10.74	928	
TnW10.72	931	· · · · · · · · · · · · · · · · · · ·
TnW10.10	931	•••••••••••••••••••••••••••••••••••••••
TnucBBS3	980	GUCGUAAUCUCAAUUGUAAACUAUAUCAACUAGGGAUUAACAACUGUUU
TnW10.79	980	
TnW10.74	977	
TnW10.72	980	•••••••••••••••••••••••••••••••••••••••
TnW10.10	980	•••••••••••••••••••••••••••••••••••••••
TnucBBS3	1029	UUUAUGACAUUGUUGGCACCUUGUGAGAAAUUAGAGUUCUCAGAUUCCG
TnW10.79	1029	
TnW10.74	1026	C
TnW10.72	1029	•••••••••••••••••••••••••••••••••••••••
TnW10.10	1029	•••••••••••••••••••••••••••••••••••••••
TnucBBS3	1078	GGGGGAGUAUGGUUGCAAGUCUGAAACUUAAAGGAAUUGACGGAAGGGC
TnW10.79	1078	
TnW10.74	1075	
TnW10.72	1078	
TnW10.10	1078	•••••••••••••••••••••••••••••••••••••••
TnucBBS3	1127	ACCACAAGUUGUGGAUACUGUGGCUUAAUUUGACUCAACACUGGAAAAC
TnW10.79	1127	
TnW10.74	1124	
TnW10.72	1127	
TnW10.10	1127	•••••••••••••••••••••••••••••••••••••••
TnucBBS3	1176	UUACCAGGUCCAGACAUAUUUAGGAUUGACAGAUUAAUAGCCCUGUCCU
TnW10.79	1176	GC
TnW10.74	1173	
TnW10.72	1176	GC
TnW10.10	1176	GC
TnucBBS3	1225	GAUUUUGUGGCUGGUGGUGCAUGGCCGUUCUUAGUUGGUGAAGUGAUUU
TnW10.79	1225	
TnW10.74	1222	
TnW10.72	1225	
TnW10.10	1225	•••••••••••••••••••••••••••••••••••••••
TnucBBS3	1274	GUCUGGUUUAUUCCGUUAACGAACGAGACUAUUACCAAUAAAUA
TnW10.79	1274	U
TnW10.74	1271	
TnW10.72	1274	•••••••••••••••••••••••••••••••••••••••
TnW10.10	1274	

TnucBBS3	1323	YACUGCAUUAGCAGUGUGAUUACUUCUUAGAGGGACUGGUGAUACAU
TnW10.79	1323	CGU.UUC
TnW10.74	1320	UUAA
TnW10.72	1323	CG. AUGUU. C.
TnW10.10	1323	CG UGUU C C
1111110.10	1545	
TnucBBS3	1370	AAGUUACUGGAGGCAAGUUGCAAUGACAGGUCUGUGAUGCCCUUAGAUG
TnW10.79	1372	
TnW10.74	1368	
TnW10.72	1372	
TnW10.10	1372	
TnucBBS3	1419	UACUGGGCCGCGCACGGGAUACAACAGGGGAGAUAAUAUGUACAUUUAA
TnW10.79	1421	
TnW10.74	1417	
TnW10.72	1421	
TnW10 10	1421	II
1111110.10	1101	
TnucBBS3	1468	ACAUAAUUUGACAAUAAUAUUGUAACCGYGAAUCUGUCUUUAAUAUGGA
TnW10.79	1469	UC
TnW10.74	1465	UC
TnW10.72	1469	UC
TnW10.10	1469	.UC
TnucBBS3	1517	AUUGCACUAUGCAAUUUUACACAUAAACUAGGAAUAUCUUGUAAGUACA
TnW10.79	1518	G
TnW10.74	1514	
TnW10.72	1518	G
TnW10.10	1518	G
TnucBBS3	1566	IIGUCAUAAUCGUGUUCUGAAUGCGUCCCUGUCCUUUGUACACACCGCCC
TnW10.79	1567	
TnW10.74	1563	С.
TnW10.72	1567	
TnW10.10	1567	
TnucBBS3	1615	GUCGCUCCUACCGAUUGGAUGAGAUGGUGAGUAAAUCUUAAUGAUUGAA
TnW10.79	1616	
TnW10.74	1612	
TnW10.72	1616	
TnW10.10	1616	C
THUCBBCS	1661	
$m_{\rm DM} 10.70$	1665	
$\frac{110010.79}{1000000000000000000000000000000000000$	1661	и с
$\frac{11010.74}{1100.72}$	1001	······································
$\frac{11010.72}{1000000000000000000000000000000000000$	1005	AUG
TUMI0.10	T002	UAG
(Thursday)	1710	
THUCBBSS	1714	AUUUAGAGGAAGAAGUUGUAACAAGGUUUUUGUAGGUGAACCUGUA
$\frac{111WIU.79}{m_{\rm r}W10.74}$	1710	тт
$\frac{110010.74}{1000000000000000000000000000000000000$	1711	U
$\frac{1100\pm0.72}{100}$	1711	
	エ / エ オ	

TnucBBS3	1762	GAAGGAUCA
TnW10.79	1763	
TnW10.74	1759	
TnW10.72	1763	
TnW10.10	1763	

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a third possibility is that <u>T. nucleata</u> possesses multiple copies of its SSU rRNA genes which differ in both length and base pair composition. The last of these three possibilities is difficult to address because individuals were pooled when samples were collected. This would make it impossible to determine the source of heterogeneity (e.g. interspecific vs. intraspecific variability). The first two possibilities require a better understanding of the criteria used in defining species of <u>Thalassicolla</u> and are addressed below.

In reviewing the original species descriptions made by Haeckel, it seems likely that at least some of Haeckel's species were probably descriptions of different physiological states of a given species or descriptions of individuals infected by parasitic dinoflagellates. For example, dinoflagellate infections are known to occur in T. nucleata (Chatton 1920; Hollande 1974) and were observed during this study in a number of <u>T. nucleata</u> specimens that were not observed to undergo swarmer formation but instead erupted with dinoflagellate parasites. In all cases, such individuals of <u>T. nucleata</u> lacked symbionts and possessed a yellowish-orange color to the central capsule which was visible beneath the dark covering of the central capsule. While all of these infected <u>T. nucleata</u> specimens (possessing yellowish-orange central capsules) were observed in the Sargasso, Haeckel makes similar references to cell-types with such yellowish-colored central capsules in T. nucleata (which is a cosmopolitan species) and also in another species in the Pacific (namely, T. maculata Fig. 1B). These details are noteworthy because of the prevalence with which we encountered specimens of this description during various trips to the Sargasso Sea. In addition, Haeckel described <u>T. maculata</u> as possessing no zooxanthellae. It seems possible that parasitism may also occur in the Pacific and that <u>T. maculata</u> is just a description of a stage in the parasitism of <u>T. nucleata</u>. Although parasitism appears to occur in Thalassicolla collected from other geographic locations, information for its frequency in the Pacific is poorly documented.

The presence or absence of an opaque layer surrounding the central capsule rendering it colorless was another criterion Haeckel used to define species of <u>Thalassicolla</u>. It is noteworthy that in two of the species descriptions of <u>Thalassicolla</u> in which Haeckel described members with colorless central capsules (<u>T. pellucida</u> and <u>T. australis</u>), he also reported an absence of zooxanthellae. This is interesting because complete loss of the extracapsular material can happen when an individual is sufficiently agitated, as might occur during ingestion, excessive wave action or excessive agitation in net tows (Verworn 1891; Gamble 1909; O. R. Anderson, personal communication). When individuals shed their dark extracapsular material, they also shed their symbionts and may require some time before regenerating the opaque layer and acquiring a new population of symbionts.

The size of the central capsule also has been used by Haeckel to delineate species of <u>Thalassicolla</u>, as in his description of <u>T. melacapsa</u> (Fig. 1C). Likewise, this feature is a questionable taxonomic criterion because of possible variability originating from non-genetic origins. For example, the diameter of the central capsule in <u>Thalassicolla</u> has been observed to change within an individual, possibly in response to physiological condition (O. R. Anderson, Amaral Zettler, personal observation). Furthermore, many of Haeckel's descriptions make reference to the "patchy" appearance of the opaque-layer surrounding the central capsule, however, this characteristic may also be attributed to nutritional status and variation in light intensity (O. R. Anderson, personal observation).

Since we lack type specimens and even drawings of all of the original species of <u>Thalassicolla</u> described by Haeckel, it is impossible to determine whether or not the above observations are important in determining the actual number of species for the genus. We do not consider this to be an exhaustive study of the species diversity of the genus <u>Thalassicolla</u>. However, we obtained notable differences at the level of the SSU rRNA gene which raises the question of what defines the species <u>T. nucleata</u>. Due to the manner in which these samples were collected it is impossible to know if these differences

represent intraspecific (multiple alleles of the rDNA gene within one species) or interspecific variability (different genes of different species). This question could be addressed by examining a single individual or preferably several individuals separately. With the current sequence information in hand, genus specific-primers could be designed to further explore the extent to which the morphological criteria used in Haeckel's species designations reflect reliable phenotypic markers for distinguishing between different species of <u>Thalassicolla</u>.

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Chapter 3

Towards a Molecular Phylogeny of Colonial Spumellarian Radiolaria¹

¹ The classification scheme of Strelkov and Reshetnyak (1971) was used for classifications at the family-level and below and that of Levine et al. (1980) for higher-level classifications. .

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ABSTRACT. Throughout their history of classification, the colonial spumellarian radiolaria have been grouped together taxonomically on the basis of their ability to form colonies. A molecular phylogenetic basis for this grouping, however, has never been explored. We used small-subunit ribosomal RNA gene sequence data to examine whether the colonial spumellarian radiolaria (Polycystinea) constitute a monophyletic evolutionary assemblage. Representatives from two spumellarian families known to form colonies, the Sphaerozoidae and the Collosphaeridae were considered in this study and included the following taxa: Sphaerozoidae: <u>Collozoum pelagicum; Collozoum serpentinum;</u> Rhaphidozoum acuferum; Sphaerozoum punctatum; and Collosphaeridae: Collosphaera globularis-huxleyi; Acrosphaera (circumtexta?); and Siphonosphaera cyathina. The results from our molecular phylogenetic analyses do not strongly support the monophyly of the colonial spumellarian radiolaria yet do not completely eliminate this possibility either. Coloniality may have arisen more than once among the Spumellarida or existing solitary Spumellarida may have once possessed colonial forms. All molecular analyses supported the monophyly of the Collosphaeridae but only distance analyses supported the monophyly of the Sphaerozoidae. The idea that coloniality appeared more than once in spumellarian evolution is contrary to current opinion based on skeletal morphogenesis studies but has been suggested from studies of the fossil record.

Supplementary key words. <u>Acrosphaera</u>, Collosphaeridae, <u>Collozoum</u>, colonial radiolaria, planktonic sarcodine, <u>Siphonosphaera</u>, Sphaerozoidae

Colonial spumellarian radiolaria are holoplanktonic sarcodines (Subphylum Sarcodina, Class Polycystinea) which occur exclusively in open ocean oligotrophic environments. As in all polycystines, each cell is physically separated into the endocytoplasm and the ectocytoplasm by a porous proteinaceous capsular wall. The capsular wall, together with the major cellular machinery it encloses, (the nucleus, mitochondria, golgi, endoplasmic reticulum, vacuoles, and oil droplets), is referred to as the central capsule. In colonial spumellarian radiolaria, thousands of individual central capsules extend their pseudopodia into a shared gelatinous extracapsular matrix which connects the cells and also typically houses numerous symbiotic algae.

As "multicellular" entities, the colonial spumellaria are macroscopic and have been reported to reach lengths of up to three meters, making them very conspicuous components of tropical and subtropical pelagic marine environments (Anderson and Swanberg 1981). Despite a visible presence in the plankton, their fragile nature and resistance to laboratory culture has left many unanswered questions regarding colonial spumellarian biology, including the reasons for colony formation. Apart from isolated reports of colony formation by phaeodaria of the family Tuscaroridae (Haecker 1908; Swanberg 1979), the spumellaria are the only other "radiolaria" sensu stricto (Polycystinea and Phaeodarea) which form colonies.

The "colonial radiolaria" are restricted to two families within the order Spumellarida; the Sphaerozoidae and the Collosphaeridae. In the Sphaerozoidae, skeletal material is either lacking or else composed of several silicate spicules of varying degrees of complexity. The most recent systematic treatment of the colonial spumellaria (Strelkov and Reshetnyak 1971) divides the Sphaerozoidae into three genera, <u>Collozoum</u>, <u>Sphaerozoum</u>, and <u>Rhaphidozoum</u>. The genus <u>Collozoum</u> possesses either simple spines (Strelkov and Reshetnyak 1971) or no skeleton. Members of the genus <u>Sphaerozoum</u> contain characteristic paired-triradiate spines, while <u>Rhaphidozoum</u> representatives have both

simple and radiate spines. Species designations are typically based on the structure of these spines, when present, or the morphology of the central capsular wall, as in the case of species within the genus <u>Collozoum</u>.

All members of the family Collosphaeridae are characterized by siliceous, spherical latticed shells having varying degrees of ornamentation. Strelkov and Reshetnyak (1971) divided the Collosphaeridae into three tribes, the Collosphaerini, the Acrosphaerini and the Siphonosphaerini, in order to maintain a more "natural" system of classification. In brief, Collosphaerini possess smooth surfaces on both the inner and outer portions of the shell, Acrosphaerini have a spine-covered outer surface of the latticed shell, and the Siphonosphaerini have latticed shells whose pores are either partially or completely elongated into tube-like projections.

It is generally assumed that the members of the colonial spumellaria were derived from a single common ancestor and that the ability to form colonies has arisen only once in their evolution (Strelkov and Reshetnyak 1971; Anderson and Swanberg 1981). Some authors have suggested that colonial spumellaria are part of a life cycle stage of solitary forms which undergo multiple binary fission of their central capsule to form colonies or perhaps that they are different stages of the same species (Brandt 1902; Hollande and Enjurnet 1953; Swanberg 1979). Solitary forms are, in fact, known for some members of the Sphaerozoidae. The genus name <u>Thalassophysa</u>, for example, is used when referring to the solitary stage of the various members of <u>Collozoum</u>. In the taxa examined in this study, <u>Thalassophysa sanguinolenta</u> is the name given to the solitary stage of the colonial <u>Collozoum pelagicum</u> (Brandt, 1902). <u>C. serpentinum</u> is also recognized as having a solitary stage (Swanberg, 1979). Solitary forms have, however, never been observed for members of the Collosphaeridae. While members of the Collosphaeridae have left behind a fossil record, only individual shells are found in the marine sediments. Therefore, it is unknown whether or not fossil collosphaeridas also produced colonies but it assumed that

they did. Likewise, we are working under the assumption that <u>Thalassicolla</u> has evolved from a solitary ancestor and that the genus is not capable of forming colonies. All available information in the literature and personal observation indicates that the genus is strictly solitary, however, the possibility that <u>Thalassicolla</u> evolved from a colonial ancestor and has now lost the character of coloniality, cannot be excluded.

Due to the application of molecular biological techniques, scientists now have a novel means of exploring the question of coloniality in spumellarian evolution. We sequenced the small-subunit ribosomal RNA (SSU rRNA) genes of representatives from both families of Spumellarida known to form colonies in order to examine the origins of coloniality and investigate the evolutionary relationships among the colonial spumellaria.

MATERIAL AND METHODS

Colonial spumellarians were collected in glass jars by divers. Colonies were maintained in 0.22 μm Millipore-filtered seawater in glass culture tubes with brine shrimp (<u>Artemia</u> <u>salina</u>) as food. All samples were collected approximately 4 miles off the southeast coast of Bermuda on the dates listed below. Samples were typically given individual sample designations prior to identification. The following samples were included in this study, with sample designation and collection date following the species identification: <u>Collozoum</u> <u>pelagicum</u> (BBSR 2, November, 1993); <u>Rhaphidozoum acuferum</u> (BBSR 7, November, 1993); <u>Collosphaera globularis-huxleyi</u> (BBSR 173, May, 1994); <u>Sphaerozoum punctatum</u> (CR 4, May, 1995); <u>Acrosphaera (circumtexta?</u>) (CR 6, May, 1995); <u>Collozoum</u> <u>serpentinum</u> (CR 16, May, 1995); <u>Siphonosphaera cyathina</u> (October, 1995). <u>C.</u> <u>pelagicum</u> consisted of a section of a vegetative (non-reproductive) colony. All other samples consisted of pooled or single central capsules from a single reproductive colony.

In all but the <u>C. pelagicum</u> sample, colonies were held until the early stages of onset of swarmer production. At that time, central capsules were physically separated from extracapsular material which contained endosymbiotic algae by repeated micropipeting.

The rationale behind sacrificing individuals at that point in their life cycle was twofold: first, a natural amplification of DNA occurs within the organism at that time as multiple copies of the genome are made in preparation for swarmer formation. Second, many species either consume or expel endocytoplasmic symbiotic algae immediately prior to swarmer formation thereby reducing the potential of amplifying non-target DNA. Individual central capsules were pipetted through several 0.22 µm-Millipore filtered seawater rinses followed by a final MilliQ-water rinse prior to placement in a modified 1X PCR buffer solution which consisted of 50 mM KCl, 10 mM Tris, pH 8.3, 2 mM MgCl₂, 0.001% Gelatin, and 1.0% NP40 (Sigma; St. Louis, MO). Samples were then stored frozen at -70°C. Samples used for molecular analyses were heated at 95°C for 10 minutes to lyse cells and liberate DNA. An aliquot of the lysed sample was used directly in PCR amplification reactions (Saiki et al. 1988). Sequences from <u>R. acuferum</u> and <u>C. globularishuxleyi</u> samples were obtained from cloned products (Chapter 1). Sequence information obtained from these two samples was then used to design "colonial spumellarian"-specific primers which were effective in amplifying SSU rRNA genes of different genera.

Sequence data from the remaining samples were obtained from directly sequencing PCR products amplified using a combination of colonial spumellarian specific primers and Medlin primers (Medlin et al. 1988). These colonial spumellarian-specific primers were synthesized as described in Chapter 1. The nucleotide sequences are: forward primer R906, 5'-TATTAGTATTTTRTCGTT-3'; reverse primer R1451bio, 5'-TATTGTAG-CCCGTGCGCT-3' (previously used as a probe in <u>in situ</u> verification experiments in Chapter 1). PCR reactions consisted of 3 minutes of denaturation at 95°C followed by 30 amplification cycles each consisting of 94°C for 1 minute, 42°C for 1 minute and 72°C for 2 minutes. Two separate 100 μ l PCR reactions typically provided enough template for sequencing reactions. PCR reactions were then pooled prior to purification using the Wizard PCR Kit (Promega; Madison, WI) to obtain purified DNA for direct sequencing.

Direct sequencing of PCR products was accomplished using IR-labeled primers and reagents from the Sequitherm Long-Read Sequencing Kit (Sequitherm; Madison, WI), along with the Sequitherm Cycle sequencing protocol developed by Li-Cor (Lincoln, NE) which consisted of 5 minutes of denaturation at 95°C prior to 30 cycles of 20 sec at 95°C (30 sec for plasmid DNA), 30 sec at 60°C, and 1 minute at 70°C using a Perkin Elmer 2400 thermo-cycler. Double stranded sequencing of the entire forward and reverse strands of the rDNA coding regions was conducted for cloned products. For directly-sequenced PCR products, double-stranded read for the all but the primer-specified ends were obtained.

The 16S-like rRNA sequences of colonial spumellaria were aligned against a subset of the total eukaryotic alignment data base (Olsen et al. 1992). Sequences were aligned by eye using the Olsen Multiple Sequence Alignment Editing program with regard to primary and secondary structural conservation. The same positions were used in this analysis as were used in the data set analyzed in Chapter 1 (1,368 total sites minus one site which became a gap when certain taxa were removed). In addition to colonial spumellaria, the alignment also included the solitary spumellarian <u>Thalassicolla nucleata</u> (Chapter 1) and acantharian outgroups <u>Haliommatidium</u> sp. and Chaunacanthid 218 (Chapter 1). In reality, however, no clearly appropriate outgroups exist for the spumellaria at the time of the writing of this manuscript since the spumellarian sequences are extremely divergent and are unrelated to any other taxa for which SSU rRNA sequence data is available.

The colonial spumellarian sequences were also analyzed independently of an outgroup (in "unrooted" networks) in order to include more sites in the analysis (an expanded number of homologous sites which included 1,635 positions). Molecular phylogenetic relationships were inferred for both data sets using distance (Olsen 1988), maximum parsimony (Swofford 1991) and maximum likelihood (Olsen et al. 1994) methods. The robustness of the tree topologies obtained were examined using 100 bootstrapping resamplings for all

three methods and additionally for the maximum parsimony method using decay analyses (Bremer 1988).

The decay analyses were accomplished by first doing an exhaustive search using PAUP 3.1.1 (Swofford, 1991) to obtain the length of the most parsimonious tree, and then sequentially adding steps to the value of the shortest tree found using the initial upper bound setting of the branch and bound search option. Resulting trees constructed at each additional step-allowance were then consensed in a strict consensus tree, and the order in which various clades "decayed" was compared.

RESULTS

Photomicrographs of the skeletal structures of spicule-bearing and skeleton-bearing colonial spumellaria used in this study are shown in Fig. 1. Species identifications were straightforward with the following two exceptions. Sample number BBSR 173 was best described as <u>Collosphaera globularis-huxleyi</u>, owing to features of the latticed shell possessed by this specimen (see Fig. 1), which appeared to exhibit qualities shared by both <u>C. globularis and C. huxleyi</u>. Haeckel (1887) asserted that these two species of <u>Collosphaera</u> formed intergrades. Therefore a combined species (globularis-huxleyi) description for this sample seemed most appropriate given the qualities of the shell morphology. Sample number CR 6 is <u>Acrosphaera</u>. The species designation was difficult to ascertain but is probably <u>A. circumtexta</u>. The length in base pairs and % G + C content of the SSU rRNA genes of spumellaria used in this study are listed in Table 1.

The results obtained from the three different phylogenetic methods used in this study did not identify a single common tree (Fig. 2). Distance methods failed to clearly segregate the solitary spumellarian <u>T. nucleata</u> from the colonial spumellaria. Maximum parsimony was the only method which segregated the colonial spumellaria from the solitary spumellarian <u>T. nucleata</u>, with low (61%) but significant bootstrap support. Weak support for the node uniting all the colonial spumellaria was also identified in the parsimony tree by the decay

Species	Length (bp)	SSU rDNA % G + C
Thalassicolla nucleata	1770	36
Rhaphidozoum acuferum	1813	39
Sphaerozoum punctatum	1788	37
Collozoum pelagicum	1792	38
Collosphaera globularis-huxleyi	1797	35
Acrosphaera (circumtexta?)	1803	35
Siphonosphaera cyathina	1791	36
Collozoum serpentinum	1798	38

Table 1. The gene lengths in base pairs (bp) and % G + C content of spumellaria used in this study.

Fig. 1. Photomicrographs of voucher sections of shell-bearing and spicule bearing colonies taken of samples used in this study. A. Acrosphaera (circumtexta?). Note the ridge-like structures often connected with thin bars. The spines, which characterize members of this genus, did not photograph well in this specimen . B. Siphonosphaera cyathina. Note the cylindrical, short tube-like projections which characterize the genus. In S. cyathina the tube-like projections are irregularly dispersed and sometimes terminate with a folded-back distal edge. C. <u>Rhaphidozoum acuferum</u>. This species is characterized by having both simple and radiate spines as the ones shown in this panel. D. Collosphaera globularis-huxleyi. A portion of the latticed-shell of this specimen reveals smooth inner and outer surfaces which characterize members of this genus. This specimen was given a species designation of <u>C. globularis-huxleyi</u> because while most of the pore and bar dimensions matched those reported for <u>C. globularis</u> a small number of specimens possessed shapes more similar to C. huxleyi. E. Sphaerozoum punctatum. This specimen shows the paired triradiate spicules possessed by this genus. The spines of S. punctatum are often barbed as seen in this photograph. Note the numerous crystal inclusions of the swarmers within the central capsule of this reproductive individual. Scale bar = $48 \,\mu m$ for all panels.


resamplings of the three respective data sets. Only bootstrap values greater than 50 % are shown. The evolutionary distances Fig. 2. Phylogenetic reconstructions for solitary and colonial spumellarians using acantharian outgroups Halionmatidium sp. and Chaunacanthid 218 inferred from: A. distance, B. maximum parsimony and C. maximum likelihood methods. There were 1,368 positions used in the phylogenetic analyses. All bootstrap values were computed separately for 100 are indicated by the bar insert (distance and maximum likelihood) which represents 10 changes per 100 nucleotides.



analysis in which collapse of this node occurred after only 3 steps. Maximum likelihood methods yielded the same topology as maximum parsimony but the branching of \underline{T} . <u>nucleata</u> separate from the colonial spumellaria was not well-supported by bootstrapping analysis. A likelihood ratio test was conducted (data not shown) but failed to find a significant difference between the distance, maximum parsimony and maximum likelihood tree topologies.

The monophyly of the Collosphaeridae was well supported in all methods for both the analyses with acantharian outgroups (Fig. 2 A - C) and the "unrooted" networks shown in Fig. 4 (A - C) (based on bootstrap values of 100% in all cases). Likewise, in both decay analyses (Figs. 3 & 5), the node leading to the Collosphaeridae was the last to collapse, implying robust support for this clade. The branching pattern within the Collosphaeridae consistently placed <u>S. cyathina</u> branching prior to the divergence of <u>C. globularis-huxleyi</u> and <u>A. (circumtexta?)</u> in all methods used. The strong support for the grouping of <u>C. globularis-huxleyi</u> and <u>A. (circumtexta?)</u> was revealed in the decay analysis of a consensus tree (Fig. 3), in which it required an additional 45 steps before the Collosphaeridae clade completely collapsed.

The separation of the remaining two families (the Sphaerozoidae and the Thalassicollidae) belonging to the suborder Sphaerocollina was not clearly supported in all cases. The bootstrap support values for these latter two families varied dramatically in the distance analysis relative to the maximum parsimony and maximum likelihood analyses (Fig. 2, A, C). The distance analysis clearly isolated the Sphaerozoidae from the Collosphaeridae and <u>T. nucleata</u> (bootstrap value of 88 on the branch leading to the Sphaerozoidae). Although the maximum parsimony and maximum likelihood methods supported a separate ancestry for the Sphaerozoidae distinct from the Collosphaeridae, the low bootstrap support for the parsimony and maximum likelihood tree topologies indicate poor support for the Sphaerozoidae as a distinct clade.

additional steps required to produce the consensus trees with progressive degrees of collapse of major nodes is shown to the Fig. 3. Results from a decay analysis of the most parsimonious tree obtained from an exhaustive search. The number of bottom left of each corresponding tree.



distances are indicated by the bar insert (distance and maximum likelihood) which represents 10 changes per 100 nucleotides. Fig. 4. Three "unrooted" trees obtained from A. distance, B. maximum parsimony and C. maximum likelihood methods using additional (1,635) positions in analyses. Only bootstrap values greater than 50 % are shown. The evolutionary



Fig. 5. Results from a decay analysis of the most parsimonious tree obtained from an exhaustive search restricting the taxa to just the colonial spumellaria. The number of additional steps required to produce the consensus trees with progressive degrees of collapse of major nodes is shown to the bottom left of each corresponding tree.



The support for branching order within the Sphaerozoidae also varied depending on the method of phylogenetic inference. In general, the branching patterns within the Sphaerozoidae were poorly resolved in the parsimony and maximum likelihood consensus trees (not shown). However, there was weak support for the grouping of <u>R. acuferum</u>, <u>C. pelagicum</u> and <u>S. punctatum</u> in the parsimony consensus tree (bootstrap value of 51%). The highest bootstrap support values were obtained from distance analyses and supported a branching order which separated the two species of <u>Collozoum</u>, placing one species branching early in the Sphaerozoidae and another sharing common ancestry with spicule-bearing genus <u>R. acuferum</u>. This tree also separated the two more commonly occurring, spicule-bearing species <u>S. punctatum</u> and <u>R. acuferum</u>.

The results from "unrooted networks" (Fig. 4, 5) provided limited additional information on the branching patterns within the Sphaerozoidae. Although the branching order was not better resolved by restricting the analysis to just the colonial spumellaria, better branching support emerged from the maximum likelihood analysis, which agreed with parsimony analysis, and placed the <u>R. acuferum</u> together with <u>S. punctatum</u> and <u>C. pelagicum</u> (bootstrap value of 95%).

DISCUSSION

Phylogenetic reconstructions based on SSU rRNA coding regions challenge existing theories regarding the evolutionary history of the colonial spumellarian radiolaria. The data from molecular phylogenetic analyses indicate that the ability to form colonies may have evolved more than once in the evolution of the spumellarian radiolaria. The distance matrix method produced a tree topology which could not resolve the branching order of <u>T</u>. <u>nucleata</u>, a solitary spumellarian, relative to the two families of colonial spumellaria examined. The maximum likelihood tree did not show strong support for the branching order of <u>T</u>. <u>nucleata</u> relative to the two colonial families. Only a bootstrap value of 61% obtained in the maximum parsimony analysis alone separated the colonial spumellaria from

<u>T. nucleata</u>. Furthermore, the weak support for the monophyly of the colonial spumellaria was identified in a decay analysis in which the most parsimonious tree collapsed the node separating <u>T. nucleata</u> from the representatives of the Sphaerozoidae after only 3 steps. All of the above indicate that the node separating the colonial spumellaria from the solitary <u>T. nucleata</u> is not very robust.

The geological records of the colonial spumellaria have been used to yield information on their evolution. Based on observations from the fossil record, Bjørklund and Goll (1979) have suggested that coloniality may have evolved independently in the Collosphaeridae and the Sphaeorozoidae. These authors argued that there is no evidence for the common ancestry of the Collosphaeridae and Sphaerozoidae in the fossil record. They state that the first occurrence of Sphaerozoidae in the fossil record is much earlier (Lower Oligocene) than the Collosphaeridae (basal Miocene) and that the distributions of the Sphaerozoidae are typically high-latitude whereas the Collosphaeridae originated and diversified from equatorial regions. More importantly, these authors assert that because the first occurrences of the Collosphaeridae in the fossil record are abrupt and characterized by fully formed lattice shells, it is probable that latticed shells were not the result of fusion of the spicules.

The conclusions made by the above authors based on the fossil record, however, appear to be difficult to test rigorously. Since skeleton-forming colonial spumellaria are not preserved in their colonial form in the fossil record, it is impossible to know which fossil forms actually produced colonies. In fact, this very problem lead Haeckel to give different species names to some shell-bearing fossil forms which were later found to be synonyms of colony-forming spumellaria. Furthermore, the existence of solitary-stages of Sphaerozoidae and the occurrence of spicule-bearing spumellaria which have never been observed to form colonies brings into question the phylogenetic importance of colony formation. For example it has been suggested that the genus <u>Collozoum</u> may have

members which all have solitary stages (Swanberg, 1979). Given the relative phylogenetic positions obtained in the distance analysis for the two <u>Collozoum</u> species, both of which have been cited as having solitary stages, we might conclude that coloniality may not be a definitive phylogenetic character. Likewise, while <u>T. nucleata</u> has never been observed to form colonies, we have to consider the possibility that its exclusively solitary habit may be a secondarily derived characteristic. If this is the case, similar arguments could be used for the existence of other exclusively solitary spumellaria so it is unclear that this question can be easily resolved even with additional sequence data from solitary forms.

The absence of solitary forms in the Collosphaeridae, however, is noteworthy. Strelkov and Reshetnyak (1971) hypothesized that the skeleton of the Collosphaeridae is derived from an ancestor with spines which merged to form a skeletal structure. A similar perspective on the possible phylogenetic relationships of the colonial spumellaria was reached by Anderson and Swanberg (1981) in their analysis of skeletal morphogenesis in representatives from the Collosphaeridae. These authors proposed a mechanism for shell deposition in colonial spumellaria which involved the precursory production of "cytokalymma" (differentiated extracapsular cytoplasm), followed by deposition of "organic nucleation centers" which serve as the matrix for the developing silicate shell. The authors described two methods of shell morphogenesis (bridge-growth and rim-growth) which they submitted could account for the variations in pore characteristics and shell ornamentation such as spines and tubules. Like Strelkov and Reshetnyak, these authors suggested that shell-bearing forms evolved from a spicule-bearing ancestor and that lattice shells are the result of the fusion of bar-like elements.

The phylogenetic reconstructions carried out in this study unanimously supported the monophyly of shell-bearing colonial spumellaria belonging to the family Collosphaeridae. Strong support was identified by both high bootstrap values (100% in all cases) and robust Bremer (decay analysis) support. Branching patterns within the Collosphaeridae indicate

that <u>Siphonosphaera</u> diverged prior to the split of <u>Collosphaera</u> and <u>Acrosphaera</u>. Evidence from physiological and electron microscopy studies indicates that the tubelike-projections seen in members of the genus <u>Siphonosphaera</u> may be the result of silicification after cytoplasmic streaming which is exhibited by all members of the spumellaria, as well as many other protista (Cachon and Cachon 1972; Anderson and Swanberg 1981; Anderson 1981). While the tube-like projections displayed by <u>S. cyathina</u> are very symmetrical, other species of the genus possess tubular ornamentation which is irregular and bears a striking resemblance to cytoplasmic shapes created during cytoplasmic streaming (Anderson and Swanberg 1981).

The observed divergence of <u>Siphonosphaera</u> prior to <u>Collosphaera</u> and <u>Acrosphaera</u> is contrary to an hypothesis presented by Strelkov and Reshetnyak (1971). These authors speculated that members of the genus <u>Collosphaera</u> represent a more primitive line of decent and that <u>Acrosphaera</u> and <u>Siphonosphaera</u> represent more derived forms. They argued that the smooth latticed skeletons possessed by the members of the genus <u>Collosphaera</u> represent more primitive features than the more elaborate skeletons of the genus <u>Acrosphaera</u>, which have a spiny appearance or those of <u>Siphonosphaera</u> which possess tube-like projections. Anderson and Swanberg (1981) also stated that spines and tubule ornamentation are most likely more derived features. However, if cytoplasmic streaming is fundamental in the formation of the tube-like projections possessed by <u>Siphonosphaera</u>, one can imagine that these structures may have arisen any time in evolution and possibly even more than once.

The monophyly of the Sphaerozoidae was well-supported in the distance analysis (bootstrap value of 88% leading to this family) however parsimony and maximum likelihood methods generated tree topologies which were in general poorly supported by the bootstrapping method. A well-supported branching pattern was also identified within the Sphaerozoidae using distance methods. The branching pattern for the distance analysis separated the two <u>Collozoum</u> species indicating a separate ancestry for the two <u>Collozoum</u> taxa. This pattern indicates that a secondary loss of skeletal material (i.e. spicules) occurred within <u>C. pelagicum</u>.

A similar conclusion about secondary skeletal loss was reached by Strelkov and Reshetnyak (1971). These authors proposed that the absence of skeletal elements is a secondary phenomenon and that the common ancestor of the Sphaerozoidae was spiculebearing. They apparently attributed the secondary loss of skeletal elements to the fact that members of genus <u>Collozoum</u>, which are typically free of any skeletal material, are very infrequently found to possess simple spicules in their cytoplasm. These authors fail to consider that the occurrence of these spicules may be due to ingestion of other spumellaria or other spicule-bearing protists (Anderson, personal communication). Therefore, absence of skeletal features (which largely defines the genus <u>Collozoum</u>) may not be a reliable phylogenetic marker.

<u>Collozoum serpentinum</u> differs most noticeably from <u>C. pelagicum</u> by the characteristics of its central capsule. The central capsule in <u>C. serpentinum</u> is elongated and often forms twisted loops whereas in <u>C. pelagicum</u> it is characterized by digitform apophyses which are often branching at the ends. Interestingly, in maximum parsimony and maximum likelihood analyses of the "unrooted" network phylogenies, <u>C. pelagicum</u> was observed to branch with <u>R. acuferum</u> and <u>S. punctatum</u>, both spicule-bearing colonials. Although perhaps only coincidental, the shape of the apophyses on the central capsule of <u>C.</u> <u>pelagicum</u> bears a crude resemblance to the spicules of <u>R. acuferum</u> and <u>S. punctatum</u> suggesting a possible evolutionary connection between these apophyses and the radiate spicules possessed by <u>Rhaphidozoum</u> and <u>Sphaerozoum</u>.

Based on our molecular results, the diversity within the Spumellarida, both solitary and colonial forms, should not be understated. Molecular phylogenetic analyses of the SSU rRNA genes in this study revealed diversity within the colonial and solitary spumellaria that

rivals that observed in many other protist groups analyzed to date. An explanation for such divergence within this order is wanting given our incomplete understanding of generation times and other factors which would affect the rate at which these protists evolved.

Other questions remain concerning the degree of variability within an individual colony. In a recent study, Petrushevskaya and Swanberg (1990) examined the morphological variability in the Collosphaeridae. These authors concluded that much of the variability seen within a colony is due to environmental differences and that sexual reproduction is probably absent in colonial radiolaria. However, geologists have reported "hybridizations" in Collosphaeridae which they believe are attributable to sexual reproduction (Bjørklund and Goll 1979). The question of whether or not colonial spumellarians are indeed entirely clonal can now be examined by comparing the SSU rRNA genes from several individuals from the same colony.

While this molecular study has not resolved of the issue of the evolution of coloniality among the spumellaria, it has raised the question of the importance of this character in determining relationships among the Spumellarida. This analysis, while far from a complete molecular diagnosis, has revealed potential avenues for further exploration into colonial spumellarian evolution. We believe that the molecular tools designed during this work will be helpful in determining the extent to which morphological variability seen in colonial spumellarians is reflected at the genetic level. Such studies as this will hopefully provide much-needed insights into the life history of these morphologically and genetically diverse protists.

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Chapter 4

Phylogenetic Relationships among Three Orders of Acantharea Based on SSU rRNA Gene Sequencing

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SUMMARY

The phylogeny of the Acantharea was examined using small-subunit ribosomal RNA (SSU rRNA) gene sequence analysis of two previously sequenced (Chapter 1) acantharia along with additional representatives from the Symphyacanthida, Chaunacanthida and the Arthracanthida. Our previous studies showed that Acantharea form a monophyletic group branching as an independent protist lineage among crown groups but not directly related to any of them. The results from this more in-depth molecular analysis of the branching patterns within the Acantharea revealed a phylogeny which is not entirely consistent with morphology-based phylogenies. In particular, the phylogenetic placement of <u>Haliommatidium</u> sp. was in disagreement with its current taxonomic placement among the Symphyacanthida. In molecular analyses described herein, <u>Haliommatidium</u> clustered with members of the order Arthracanthida. Apart from cyst formation and number of axopodial exit pores, <u>Haliommatidium</u> sp. shares several morphological features with the Arthracanthida which support these molecular results.

Key words: Acantharea, evolution, molecular phylogeny, small-subunit ribosomal RNA

INTRODUCTION

Members of the class Acantharea are heterotrophic planktonic sarcodines which are common components of open ocean environments. In addition to their role as consumers, acantharia also contribute to primary productivity in the ocean via their symbioses with eukaryotic algae. Acantharia typically occur at densities of 10 cells l⁻¹ (Caron and Swanberg 1990), however, they have occasionally been found to dominate the biomass of microzooplankton during "bloom-like" conditions (Merinfeld 1969; Massera Bottazzi and Andreoli 1981; Febvre 1990) where densities from 30-35 cells l⁻¹ have been reported (Michaels 1988). While acantharian abundances in the world oceans have been underestimated in the past improved methods of sampling and preservation (Michaels 1988) are revealing their abundances in the plankton.

Acantharian cells are divided into the endoplasm and the ectoplasm (see Fig. 1 A, B), which are separated by a capsular wall in one order of acantharia, the Arthracanthida. The ectoplasm is encompassed by the periplasmic cortex or outer pellicle, and also the outermost layer, the calymma. The calymma houses the characteristic acantharian non-actin-filaments called myonemes. The myonemes are contractile bundles located around the tips of the skeletal spines and are postulated to contribute to active vertical motion in the acantharia (Febvre 1981; Reshetnyak 1981; Febvre and Febvre-Chevalier 1982).

Acantharia are further distinguished from other protists on the basis of the Müllerianarrangement of spines and their skeletal composition. The acantharian skeleton is organized in a highly symmetrical fashion known as Müller's law, in which 10 diametric or 20 radial spines come together at the center of the cell to form a characteristic geometric pattern (see Fig. 1C). The acantharia are the only protists known to construct skeletons of monocrystals of strontium sulfate (Schröder 1907; Hollande and Cachon-Enjumet 1963; Massera-Bottazzi and Vinci 1965), although other protistan groups are known to metabolize strontium sulfate or similar alkaline earth compounds (Fenchel and Finlay 1986; Fig. 1. A. An unidentified acantharian specimen. B. Schematic diagram showing the location of the myonemes (m), endoplasm (en), ectoplasm (ec) and spines (sp). C.
Müllerian arrangement of spines (after Febvre, 1990). (p) polar spine; (t) tropical spine; (e) equatorial spine.



Raven et al. 1986). As such, acantharia play a role in the cycling of strontium in the ocean (Bernstein et al. 1987) and some attempts have been made to use the levels of Sr ⁹⁰ incorporated into acantharian skeletons as a means of measuring radioactivity in the oceans (Schreiber and Ortalli 1964; Strelkov and Reshetnyak 1974).

Like other skeleton-bearing sarcodines, the acantharia were first classified on the basis of their skeletal morphology (Müller 1858; Hertwig 1879; Haeckel 1888). These authors all considered Acantharia as members of the "Radiolaria", a now defunct formal taxonomic term whose original definition encompassed them (see Chapter 1 for a more in-depth discussion of the differences between Acantharea and Polycystinea). Schewiakoff (1926) is credited with establishing a classification scheme which incorporated aspects of acantharia as distinct from the "radiolaria" (Polycystinea and Phaeodarea) and still serves as the foundation of modern-day classifications. Despite the need for systematic revision noted in the latest protistology reviews of the acantharia (Cachon and Cachon 1985; Febvre 1990) the past decade has seen very little systematic revision within the Acantharea. The latest treatments of the group include Trebougoff (1953) and Reshetnyak (1981) (in Russian).

There are 150 species, 50 genera, 20 families and 4 orders of acantharia reported in the most recent literature (Febvre 1990). Morphology-based systematic work requires the labor-intensive and time-consuming techniques of treatment of specimens with sulfuric acid prior to observation under the light microscope or use of electron-microscopy to determine species-level identifications. Furthermore, the phylogenetic significance of the some of the criteria used in distinguishing between different taxa (such as nature of the central juncture of the spines (after treatment with sulfuric acid)) have not been challenged. Since the acantharia lack a fossil record, there are few alternative methods available for comparing how well existing systematic schemes reflect phylogenetic relationships.

Ribosomal RNA-based phylogenetic approaches offer an alternative means of inferring relationships within the Acantharea. Recent cloning and sequencing efforts of small-subunit ribosomal RNA genes (Chapter 1) show a branching of Acantharea among crown groups. In this paper, we examine more closely the branching pattern of three orders of Acantharia in an effort to compare existing taxonomic frameworks with the results from this study.

MATERIALS AND METHODS

One very practical problem with the methods used in making accurate identifications of acantharia is that they typically destroy cytoplasmic material in the process. This makes microscopic identification at the light-microscope level difficult and in some cases only allows for order or family-level identifications with confidence. However, in certain groups, especially within the Arthracanthida, as well as, the Symphyacanthida (such as <u>Haliommatidium</u>), there are representatives which can be identified live to genus-level due to very distinctive features.

Individuals were given sample numbers prior to identification. In this study, all identifications were made by Dr. A. F. Michaels (Bermuda Biological Station for Research, Inc., Bermuda) who is a specialist in acantharian biology. Acantharian samples used in this paper were: Arthracanthid 205 (Order: Arthracanthida, Suborder: Sphaenacanthina, Family: Acanthometridae, <u>Acanthometra</u> sp.), Arthracanthid 206, (Order: Arthracanthida), Symphyacanthid 211 (Order: Symphyacanthida), Chaunacanthid 217 (Order: Chaunacanthida), and Chaunacanthid 218 (Order: Chaunacanthida), and Symphyacanthid 218 (Order: Chaunacanthida), and Symphyacanthid 235 (Order: Symphyacanthida, Family: Pseudolithidae, <u>Haliommatidium</u> sp.).

All specimens were collected in glass or polycarbonate jars by divers off the southwestern coast of Bermuda in September 1994. Specimens were maintained in 0.22 µm Millipore-filtered Sargasso Sea water in glass culture tubes with brine shrimp (<u>Artemia salina</u>) as food until sacrificed for molecular analysis. Whenever possible, reproductive

acantharia, which are often characterized by cyst-formation, were sacrificed for molecular analyses. The rationale for using reproductive individuals was to obtain samples that were highly enriched with sarcodine DNA over non-target DNA's such as prey or symbiotic algal DNA which may be present in the sample.

Individual central capsules or cysts were passed through several 0.22 μ m-Millipore filtered seawater rinses followed by a final MilliQ (distilled, deionized)-water rinse. Specimens were then placed in a modified 1X PCR buffer solution which consisted of 50 mM KCl, 10 mM Tris, pH 8.3, 2 mM MgCl₂, 0.001% Gelatin, and 1.0% NP40 (Sigma; St. Louis, MO). Cells were then stored frozen at either -20°C or -70°C. Samples for molecular analyses were heated at 95°C for 10 minutes to lyse cells and liberate DNA. An aliquot of the lysed sample was used directly in PCR amplification reactions (Saiki et al. 1988). Typically anywhere between 1 and 5 μ l of a 20 μ l sample lysed in this manner yielded strong PCR amplifications.

Arthracanthid 206, Chaunacanthid 217 and Symphyacanthid 235 (<u>Haliommatidium sp.</u>) 16S-like rDNAs were amplified using PCR and eukaryotic primers specific to the ends of the molecule (Medlin, 1988) and subsequently cloned into a double-stranded TA plasmid vector pCRII (Invitrogen; San Diego, CA). Plasmid DNA was purified using Promega Wizard Midiprep (Promega; Madison. WI) kit and methods. Remaining samples, Arthracanthid 205 (<u>Acanthometra</u> sp.), Symphyacanthid 211, and Chaunacanthid 218 SSU rRNA genes were PCR-amplified in two overlapping fragments using one acantharianspecified primer in combination with either the forward or reverse Medlin primer to yield a final full length product. These acantharian-specific primers were synthesized as described in Chapter 1 and consisted of the forward primer A497, 5'GTGAGTTGATTGGAATGA-3' and the reverse primer A899, 5'-TCGTCATACAAAGGTCCA-3'.

All PCR fragments were purified using the Wizard PCR Prep system (Promega; Madison, WI). Direct sequencing of PCR products as well as cloned plasmid DNA was accomplished using reagents from the Sequitherm Long Read Sequencing Kit (Epicentre Technologies; Madison, WI) along with the Sequitherm Cycle sequencing protocol developed by Li-Cor which consisted of 5 minutes of denaturation at 95°C prior to 30 cycles of 20 sec at 95°C (30 sec for plasmid DNA), 30 sec at 60°C, and 1 minute at 70°C using a Perkin Elmer 2400 Thermo Cycler. Sequenced templates were run out on a Licor model 4000L sequencing machine.

Gel images were transferred from Licor to BioImage (Millipore Corp; Ann Arbor, MI) and sequences were analyzed using the BioImage DNA Sequence Film Reader software. The 16S-like rRNA sequences of acantharian samples were aligned against a subset of the total eukaryotic alignment data base (Olsen et al. 1992). Sequences were aligned by eye using the Olsen Multiple Sequence Alignment Editing program with regard to primary and secondary structural conservation. Phylogenetic analyses employed distance (Olsen 1988), maximum parsimony (Swofford 1991) and maximum likelihood (Olsen et al. 1994) methods. The sites used in this analysis included 1,368 positions and was identical to the one used in the analyses to infer the phylogenetic placement of acantharia relative to the polycystine radiolaria (Chapter 1). The 1 base pair difference (e.g. 1,369 positions used in Chapter 1 compared with 1,368 positions used in this study) is due to one site becoming a gap when the data set was restricted to the acantharian and two polycystine spumellarian sequences. <u>Thalassicolla nucleata</u> and <u>Collosphaera globularis-huxleyi</u> were used as outgroups in the analyses. Bootstrap (Felsenstein 1985) and decay (Bremer 1988) analyses were conducted to provide a means of relative branch support.

RESULTS

All phylogenetic reconstructions accomplished yielded identical tree topologies. However, bootstrap values obtained for the three methods differed and are indicated on the nodes of the consensus parsimony tree shown in Fig. 2. Distance bootstrap values are listed on top, parsimony in the middle, and maximum likelihood on the bottom. In general,

all analyses favored the branching of the Symphyacanthida with the Chaunacanthida and segregated these two orders from the Arthracanthida. <u>Haliommatidium</u> sp., currently classified as a symphyacanthid, was observed to branch with the Arthracanthida in all analyses. <u>Haliommatidium</u> sp. branched with <u>Acanthometra</u> sp. with moderate support in all analyses but the distance analysis, wherein the branch order between <u>Acanthometra</u> sp., <u>Haliommatidium</u> sp. and Arthracanthid 206 was poorly resolved.

In addition to bootstrapping, the stability of branching was tested further in a decay analysis depicted in Fig. 3. The decay analysis was accomplished by first performing an exhaustive search using PAUP 3.1.1 to obtain the length of the most parsimonious tree, and then sequentially adding steps to the value of the shortest tree found using the initial upper bound setting of the branch and bound search option. Resulting trees constructed at each additional step-allowance were then consensed in a strict consensus tree, and the order in which various clades "decayed" was compared.

The trees depicted in Fig. 3 show the single most parsimonious tree obtained which was 608 steps long, followed by the strict-consensus trees from 609, 614, 615 and 621 steps respectively. After 1 additional step (608-609), the node joining <u>Haliommatidium</u> sp. and <u>Acanthometra</u> sp. collapsed. Six steps (608-614) were required for the collapse of the chaunacanthid clade. After 7 steps (608-615) the connection between the chaunacanthid clade and Symphyacanthid 211 was lost. Complete loss of structure in the acantharian lineage resulted after 13 steps (608-621) with the collapse of the "arthracanthid" clade (including <u>Haliommatidium</u> sp.).

Fig. 2. The most parsimonious tree inferred from of an exhaustive search using maximum parsimony. Distance and maximum likelihood analyses yielded the same tree topology. Three sets of bootstrap values are given for each method as follows: distance (top value), maximum parsimony (middle value), maximum likelihood (bottom value). Only values greater than 50% are shown, the dash for the node leading to Arthracanthid 205 and Symphyacanthid 235 indicates a distance bootstrap value which was less than 50%. Acantharian sequences are indicated in bold.



Fig. 3. The results of a decay analysis conducted using the most parsimonious tree from an exhaustive PAUP search. Strict consensus trees obtained after 1 step (608-609), 6 steps (608-614), 7 steps (608-615), and 13 steps (608-621) indicate the order of decay of the major clades in the acantharian lineage. Acantharian sequences are represented in bold.




DISCUSSION

The current classification scheme for the Acantharea, based on morphological criteria established by Schewiakoff in his 1926 monograph, has been accepted with little formal systematic revision since that time (Reshetnyak 1981; Febvre 1990). Some specialists acknowledge that members of the symphyacanthid family Pseudolithidae, of which <u>Haliommatidium</u> is a member, require taxonomic reevaluation (Cachon and Cachon 1982; Cachon and Cachon 1985) but no formal revisions have been suggested to date. The results from this study found the placement of members of the Arthracanthida and the Chaunacanthida to be consistent with the systematic scheme proposed by the above authors. However, the results for the Symphyacanthida indicate that some of the morphological criteria used in defining the symphyacanthid clade are not reliable phylogenetic markers.

One of the major results of this study was the branching of Symphyacanthid 235 (<u>Haliommatidium</u> sp.) with Arthracanthid 205 (<u>Acanthometra</u> sp.) and an unidentified arthracanthid, Arthracanthid 206 within the arthracanthid clade. This result was well-supported by both the bootstrapping and decay analysis results. Reexamination of the literature available on the morphology and cytology of <u>Haliommatidium</u>, however, reveals some salient features shared by <u>Haliommatidium</u> and members of the Arthracanthida which substantiate this result.

The features which distinguish members of the Arthracanthida from other orders of acantharia include the following: the existence of a central capsule; a well-defined body plan possessing latticed or armored shells; the presence of a small number of apertures in the calymma for the axopodia to exit, and an increase in the number of myonemes compared to other orders (from 24-40). In considering these criteria, there are several morphological features of <u>Halionmatidum</u> which might place it among the Arthracanthida.

When we compare the above features to those found in Halionmatidium we see that

Febvre (1990) makes note of a very conspicuous central capsular wall in <u>Haliommatidium</u> as is seen in most Arthracanthida. In addition, <u>Haliommatidium</u> forms a latticed shell through the fusion of the apophyses on its spines, similar to those that can be seen in members of the Arthracanthida. Furthermore, Haliommatidium is known to possess 23-34 myonemes as compared with the 8-12 myonemes possessed by other members of the order Symphyacanthida (Strelkov and Reshetnyak 1974).

One difference between <u>Haliommatidium</u> and members of the Arthracanthida lies in the number of apertures for the exit of axonemes which number between 30-40 in the family Pseudolithidae whereas there are many fewer in the Arthracanthida. Another difference between <u>Haliommatidium</u> and members of the Arthracanthida is that <u>Haliommatidium</u> forms a cyst prior to swarmer formation, whereas no members of the Arthracanthida form cysts. The cysts formed by <u>Haliommatidium</u>, however, develop differently than those of other cyst-forming Symphyacanthida such as members of the Astrolithiidae.

Other differences exist between <u>Haliommatidium</u> and other Symphyacanthida members. For example, one of the distinguishing features of the Symphyacanthida is the inability of the central skeletal mass to be dissociated with sulfuric acid treatment. The central body of members of the genus <u>Haliommatidium</u> can be dissociated by sulfuric acid treatment whereas dissociation does not occur in most other Symphyacanthida. Finally, another striking difference found in <u>Haliommatidium</u> that is not seen in any other acantharian let alone symphyacanthid, is a single large nucleus during the trophic stage of the organism instead of the many nuclei observed in all other types of vegetative acantharia. The evolutionary significance of this mononuclear condition seen in <u>Haliommatidium</u> remains enigmatic. In any event, many morphological features possessed by <u>Haliommatidium</u> set it apart from other symphyacanthids.

The branching of Symphyacanthid 211 relative to the chaunacanthid clade is also noteworthy. The data indicate that the Symphyacanthida diverged prior to the

Chaunacanthida. This hypothesis is contrary to what has been suggested based on the morphological data alone (Schewiakoff 1926; Strelkov and Reshetnyak 1974; Reshetnyak 1981). These authors suggest that based on myoneme number and skeletal complexity, the Symphyacanthida are probably more derived than the Chaunacanthida. However, given that the Symphyacanthida (as it is currently defined) was shown to be polyphyletic in this analysis, the branching order of the Symphyacanthida relative to the Chaunacanthida is best determined only after the analysis of additional symphyacanthid sequence data.

The results from this study revealed that analysis of SSU rRNA genes may prove useful in future taxonomic revision within the Acantharea, at least at the order level of taxonomic organization. The additional acantharian order the Plegmacanthida (Reshetnyak 1981) (not yet formally recognized) along with representatives from the Holacanthida and representatives of a once proposed fifth order, the Actineliida (Levine et al. 1980) await molecular investigation.

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Chapter 5 Conclusions

The work described in this thesis is significant for its contribution to eukaryotic molecular phylogeny and to the field of acantharian and polycystine biology. The sequence data obtained are the first SSU rRNA genes to be obtained from the Acantharea and Polycystinea respectively. They represent the first molecular genetic work to be accomplished on representatives of either of these two classes. The writing of this thesis and subsequent publication of the contents of its chapters as manuscripts in scientific journals will hopefully instigate further applications of molecular approaches to answering questions in the biology of these understudied protists.

The most significant result from this thesis comes with the finding that based on SSU rRNA gene-based phylogenies, the Acantharea and the Polycystinea do not share common ancestry (Chapter 1). These results imply that the taxon Actinopoda (as well as any other taxon uniting Acantharea and Polycystinea such as Cavalier-Smith's newly proposed "Radiozoa") is not monophyletic and should be discarded in future systematic revisions of the Sarcodina. These results are actually in agreement with speculations made by a variety of authors who have submitted that axopodia are convergent structures which are probably the result of ecological constraints placed on organisms possessing a common planktonic mode of existence (Cachon and Balamuth 1977; Merinfeld 1978; Shulman and Reshetnyak 1980; Merinfeld 1981; Reshetnyak 1981). The results from Chapter 1 also support the monophyly of the Acantharea and at least the separate monophyly of the order Spumellarida of the Polycystinea.

The extent to which SSU rRNA genes differ within a given species of <u>Thalassicolla</u> <u>nucleata</u> was the focus of Chapter 2. The amount of variation observed within a species of this genus collected from the Sargasso Sea and the Pacific Ocean was higher than one might expect for a single species, with the highest values falling at levels observed at the genus level in other taxa. Perhaps given the amount of divergence displayed within the

spumellarian SSU rRNA genes sequenced during this thesis, these values should not be surprising.

Whether this degree of genetic variation warrants new species or strain designations in the <u>Thalassicolla</u> genus is unclear but raises the important question of what defines a species in <u>Thalassicolla</u>. The existing species designations made by Haeckel for <u>Thalassicolla</u> are suspect because they occur so infrequently in the literature following their initial descriptions, and also because they include a total of seven species, four of which are lacking in symbionts. Given our present understanding of the feeding behavior within <u>Thalassicolla</u> and the importance of symbiont-derived nutrition, it seems that some of these species may not be valid. These facts in combination with morphological changes associated with parasitism, differences in physiological condition, and external factors such as excessive wave agitation, may have contributed to the morphological features used by Haeckel to describe different species of this genus.

The third chapter examined the phylogeny of the colonial spumellaria and attempted to determine whether or not the colonial radiolaria represent a monophyletic evolutionary assemblage. One robust conclusion drawn from this chapter was the monophyly of the Collosphaeridae, which is comprised of shell-bearing colonial forms. Representatives of three genera from this family grouped together with bootstrap values of 100% in all analyses accomplished. These results are exciting because they suggest a potential for determining further relationships between the Collosphaeridae and comparing them to phylogenies derived from the polycystine fossil record. These results also suggest a potential for establishing a phylogeny based classification for the Collosphaeridae.

Representatives of the two families of Spumellarida known to form colonies used in these analyses indicated that the colonial spumellaria may not be monophyletic. Because the different methods employed in reconstructing phylogenies did not yield the same answer, I cannot be fully confident of this result. The monophyly of the colonial

spumellaria was supported in only one of the methods (maximum parsimony) and with low bootstrap support (61%). Given these results, it appears that coloniality may not serve as a reliable phylogenetic marker.

All of these results come with the overwhelming revelation of the high sequence divergence exhibited by the Spumellarida. However, Hillis et al. (1996) discuss several possibilities that might account for the observed differences in heterogeneity rates seen within a given gene. Among them are differences in DNA repair efficiency and differences in exposure to mutagens, both of which may explain some of the source of this variability. It may be that the spumellaria, as planktonic organisms, are subjected to high levels of UV damage since they typically occur in the surface portions of water column. If spumellaria lack a means of protecting themselves from UV or else do not possess adequate DNA repair mechanisms to efficiently repair damaged DNA, this might explain some of the observed sequence divergence.

Furthermore, the low % G + C content found in the spumellarian sequences may make them more susceptible to thymine-dimer formations created during exposure to UV which may be difficult to repair with existing DNA Repair mechanisms. However, if UV radiation is acting as a selective force in the % G + C content of these organisms, we would expect to see high % G + C content not the low values observed thus far in the Spumellarida. This scenario has been proposed by Singer and Ames (1970) to account for the high % G + C content in bacteria inhabiting high UV-exposed environments. It seems equally likely that members of the Spumellarida may have evolved mechanisms to deal with UV and that the long branch lengths observed in the spumellarian phylogenies are attributable to other reasons such as long divergence times or fast organismal generation times.

The final chapter of this thesis examined the evolutionary relationships between three orders of Acantharea. The results from this work were consistent with the

morphology-based systematics in that they supported the monophyly of the Chaunacanthida and the Arthracanthida. The exception was in the phylogenetic placement of <u>Haliommatidium</u> sp. with the Arthracanthida. While this result is contrary to its current taxonomic position among the Symphyacanthida, it is less surprising when one reexamines the morphological features that <u>Haliommatidium</u> sp. shares with the Arthracanthida. Given this result, the formation of cysts (an ability possessed by <u>Haliommatidium</u> sp. but not members of the Arthracanthida) may not be a reliable phylogenetic marker whereas myoneme number and presence of a central capsule wall may be. In any event, it appears that the Acantharia are a more recently divergent lineage that are not closely related to any known protistan group for which there is currently SSU rRNA sequence information.

The molecular approach using an SSU rRNA-based method for reconstructing phylogenies of the Acantharea and the Polycystinea has proven to be a fruitful one. Within the spumellaria, especially, there appears to be sufficient sequence variation to make fine-scaled comparisons between existing morphospecies. The variability within the acantharian SSU rDNA was significantly less that of the spumellaria, and may prove less useful in establishing differences at the species level. The design of acantharian and colonial spumellarian oligonucleotide probes and primers accomplished during this thesis, will assist in further efforts to establish a phylogeny-based systematic framework for both of these protistan groups. The application of the oligonucleotide probes also holds potential for addressing ecological questions surrounding the life cycle and distributions of these elusive protists.

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APPENDIX A: SEQUENCE ALIGNMENT

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Thalassicolla nucleata (BBS3) from the Sargasso Sea Thalassicolla "nucleata" clone number 79 collected from the Facific sample W10 Thalassicolla "nucleata" clone number 74 collected from the Facific sample W10 Thalassicolla "nucleata" clone number 72 collected from the Pacific sample W10 Thalassicolla "nucleata" clone number 10 collected from the Pacific sample W10 M88518:Symbiodinium pilosum:dinoflagellate:Zooxanthellales M32703:Chlamydomonas reinhardtii:Chlorophyte:Volvocales X00755:Oryza sativa (rice):chlorophyte L27635:Porphyridium aerugineum:rhodophyte:Bangiophycideae L27634:Labyrinthuloides minuta:stramenopile:labyrinthulid M64243: Theileria annulata: apicomplexa: Coccidia piroplasm 1,369 homologous sites included in phylogenetic analyses L27633:Cafeteria roenbergensis:stramenopile:bicosoecid X13160:Physarum polycephalum:physarids M18732:Naegleria gruberi:schizopyrenids:vahlkampfiids possible secondary structure helices M11435:Acanthamoeba castellanii: Amoebida 123799:Phreatamoeba balamuthi 128204:Stylonema alsidii:Rhodophyte:Porphyridiaceae X53486:OXYTricha granulifera:ciliate:hypotrich M97909:Blepharisma americanum:ciliate:heterotrich M95168:Hartmanella vermiformis:"Lobosa" M32704:Ochromonas danica:stramenopile:chrysophyte M55638:Athelia bombacina:fungus:basidiomycete X77692:Euglypha rotunda CCAP 1520/1:Sarcodina K02641:Dictyostelium discoideum:dictyostelids L10824:Diaphanoeca grandis:Choanoflagellate Paulinella chromatophora SSU rRNA, X81811 Symphyacanthid 235 (Haliommatidium sp.) Arthracanthid 205 (Acanthometra sp.) Entamoeba gingivalis (st.ATCC30927) L10826:Mnemiopsis leidyi:Ctenophore L04957:Emiliana huxleyi:Haptophyte M54937:Blastocladiella emersonii Collosphaera globularis-huxleyi Acrosphaera (circumtexta?) Siphonophaera cyathina Rhaphidozoum acuferum Sphaerozoum punctatum Collozoum vermiformi Collozoum pelagicum Symphyacanthid 211 Arthracanthid 206 Chaunacanthid 218 Chaunacanthid 217 (ZBBSR206): (ZBBSR235): 1 (1369mask): (SYMPILO1): : (ENIDOLNE) (NAEGRUBE) : (THEANNUL): (ZBBSR205): (EUGROTUN): (ZBBSR173): (siphcyan): (ZBBSR2): : (рихрогус) (euk heli): (MNELEIDY): (HARVERMI): (Pchroma): (DICDISCO): ~ ~ Ä (ZBBSR7): ï (ZBBSR218): (ZBBSR217): (ATHBOMBA) (ORYSATIV) (PORAERUG) (ZBBSR211) (BLEAMERI) (DIAGRAND) (BLAEMERS) (ACACAST1) (PHRBALAM) (OCHDANIC) (OXYGRANU) (CHLREINH) (STYALSID) (EMIHUXLE) (CAFROENB) (LABMINUT) (W10274 (W10272 (W10210 (W10279 (ZTnucl (ZCR16 (ZCR6A (ZCR4 (rad

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27 Pchroma	AACcugguUGAuccggccagUaguCauaugcuUGUcucaAAGAUUAAgccAugcaUGUAAguauaagCAAC	3 Pchroma
28 EUGROTUN	AACcugguUGAuccugccagUa-aCauaugcuUGUcucaAAGACUAAgccAugcAUGUCUAAguauaaaCAACuuuauacugc	G EUGROTUN
29 ENTOGING	auaugcuGAUGuuaAAGAUUAAgccAugcAUGUGUAAGuAuAAGACCAAGaaGG-	G ENTOGING
30 DICDISCO	UAAcugguUGAuccugccagUaguCauaugcuUGUCucaAAGAUUAAgccAugcAUGUCUAAguauaaAUUC	G DICDISCO
31 ZTnucl	CAACcugguUGAuccugccagUaguCauacgcUAACAuuaAAGAUUAAgccAugcAUGUACGAguaUACAAUuaccAU	U ZTRUCI
32 W10Z79	AACcugguUGAuccugccagUaguCauacgcUAACAuuaAAGAUUAAgccAugcaUGuACGAgUaaAAAAuuUccAU	U W10279
33 W10Z74	AACcugguUGAuccugccagUaguCauacgcUAACAuuaAAGAUUAAgccAugcaUGUACGAguaaAAuuaccAU	U W10274
34 W10Z72	AACcugguUGAuccugccagUaguCauacgcUAACAuuaAAGAUUAAgccAugcAUGUACGAgUaaAAAAuuUccAU	U W10272
35 W10Z10	AACcugguUGAuccugccagUaguCauacgcUAACAuuaAAGAUUAAgccAugcaUGUACGAGUaaAAAAuuUccAU	U WICZIO
36 ZBBSR7	AACcugguUGAuccugccagUaguCauacacUUACUuuaAAGAUUAAgccAugcAUGUCUUAaugCuuugUUUUuqUaacau	U ZBBSR7
37 ZBBSR173	AACcugguUGAuccugccagUaguCauauacUUGUCuuUAAGaUUAAgccAugcaUGUCCAquuCuUuaAUUUuuCQaaac	U ZBBSR173
38 Siphcyan	CcugguUGAgccugccagUaguCauaUVcUUgUCuuaAAGAUUAAgccAugcAUGUCUCAgUucGAUGGAUC	U Siphevan
39 ZBBSR2	AACcugguUGAgecugccagUaguCauacacUUGUCuuaAAGAUUAAgecAugeAUGUUAAauoCuUuGUUUaUaUaIBaau	U ZBBSR2
40 ZCR4	AACcugguUGACccugccagUaguCauacacUUGUCuuaAAGAUUAAgccAugcAUGUCUCAaugCuuUgUUUAUUUU3agc	U ZCR4
41 ZCR16	AACcugguUGAgccugccagUaguCauacacUUGUCuaaAAGAUUAAgccAuguAUGUCUAUqUaCUUcGAUA	U ZCR16
42 ZCR6A	aaCcugguUQAgccugccagUaguCauauacUUGUCucaAAGAUUAAgccAugcAUGUCUCAguuCuUACacUUguAUAUAA	U ZCR6A
43 PHYPOLYC	UACcugguUGAuccugccagUagu-guaugcuUCUccuaAGACUAAgccAugcAUGUCUCCGAAUAGAGCAAGU-CUCU-	DYLOUYC
44 NAEGRUBE	UACcugguUGAuccugccagUaCu-auaugcuUGUCucaAAGCCUAAgccAugcAAUGUAAGauCAAUCauaugcgguuUCggccguguaUAau-	U NAEGRUBE
45 euk hell	1 2 1 3 4 5 6	euk heli
46 rad		rađ
	 2 ANNELELDY 2 ANNELELDY 3 CACRARIDY 4 ATHRORAND 4 ATHRORAND 6 CHLREINH 7 CONYSATIV 8 PORASATIV 8 PORASATIL 10 CNYSATIL 11 STYALSID 12 CAFRORND 15 CAFRORND 16 CAFRORND 17 BLEAMERI 18 CAFRORND 10 CAFROND 10 CAFROND 11 CAFROND 12 CAFROND 14 CAFROND 14 CAFROND 15 CAFROND 15 CAFROND 16 CAFROND 17 CAFROND 18 CAFROND 18 CAFROND 19 CAFROND 10 CAFROND 10 CAFROND 11 CAFROND 12 CAFROND 14 CAFROND 14 CAFROND 15 CAFROND 15 CAFROND 16 CAFROND 17 CAFROND 18 CAFROND 18 CAFROND 19 CAFROND 10 CAFROND 11 CAFROND 11 CAFROND 12 CAFROND 13 CAFROND 14 CAFROND 14 CAFROND 14 CAFROND 14 CAFROND 	 TRRZERJAN ACCUOPTIONALCENDER OF ACTIONAL STATUS CONSTRUCTORY ACTIONATION AND ALL ACTIONATION AND ALL ACTIONATION AND ALL ACTIONATIONAL ACTIONAL ACTI

Posi- Sequence

tion:	identity:	Data:		
104	1 1369mask			1369mask
104	2 MNELEIDY	AAACUGCGAAUGGcucAUUARAUcagUUAUCguCuAUUugaUUGCCC	UVACUAcaudG-AuaAcCGuadUAA	MUELEIDY
104	3 DIAGRAND	AAACUGCGAAUGGcucAUUAAAUcagUUAUAguuuAUUugaUAGUAC		DIAGRAND
104	4 ATHBOMBA	AAACUGCGAAUGGcucAUUAAAUcagUUAUAguuuAUUugaUgAUACC	UUACUAcaugG-AuaAcuGuggUAA	ATHBOMBA
104	5 BLAEMERS	AAACUGCGAAUGGcucAUUAAAUcagUUAUAauuuAUUugauAGUACCCC	AUVACUACUUGG-AUAACCGuggUAA	BLAEMERS
104	6 CHLREINH	AAACUGCGAAUGGcucAUUAAAUcagUUAUAguuuAUUugaUgGUACC	UACUACUCGG-AuaAcCGuagUAA	CHLREINH
104	7 ORYSATIV	AAACUGCGAAUGGcucAUUAAAUcagUUAUAguuugUUugaugGUACG	UGCUACUCgG-AuaAcCGuagUAA	ORYSATIV
104	8 PORAERUG	AAACUGCGRAUGGcucAUUAAAAcagUCAUAauuuACUygaUaGUACC	uuuuacuuge-AuaCeCeuagUAA	PORAERUG
104	9 ACACAST1	AGACUGCGGAUGGCucAUUAAAUcagUUAUAguuuAUUugauGGUCUCUUUUGUCUU	UUUUUACCUAcUugG-AuaAcCGuggUAA	ACACAST1
104	10 PHRBALAM	AAACUGCGGACGGcucCAUAGAUcagUAAUAguucgUUcagugAUUUGAA	AAAGUAcUugG-AuaAcCcuguUAA	PHRBALAM
104	11 STYALSID	AAACUGCGAAUGGcucAUUAAAAcagUUAUAauuuAUUugauAGUACC	UACUAcUugG-AuaAcCGuagUAA	STYALSID
104	12 EMIHUXLE	AAACUGCGAAUGGcucAUUAAAUcagUUAUGguuuAUUugaUGGUACCU	UGCUAcUugG-AuaAcCGuagUAA	EMIHUXLE
104	13 OCHDANIC	AAACUGCGAAUGGcucAUUAUAUcagUUAUAguuuCUUugaugGUCCU	ugcuAcUugg-AuaAcCGuagUAA	OCHDANIC
104	14 CAFROENB	AAACUGCGAAUGGcucAUVAUCagUUAUAguuuAUUugaUAGUUU	UCCUAuAugg-AuaAcCGurgUAA	CAFROENB
104	15 LABMINUT	AAACUGCGAAUGGcucAUUAUAUCagUUAUAguuuAUUugauAGAUUUC	UACUAcUugg-AuaAcCGuagUAA	LABMINUT
104	16 OXYGRANU	AAACUGCGAAUGGcucAUDAAAAcagUDAUAguuuAUDugauAAUCGA	AUUVAcaugG-AuaAcCGuggUAA	OXYGRANU
104	17 BLEAMERI	AGACUGCGAAUGGcucAUUAAAAcagUUAUAguuuAUUugcuAGACG	UUUAuaugG-AuaAcCGuagUAA	BLEAMERI
104	18 HARVERMI	AAACUGCGAAUGGcucAUUAAAUcagUUAUAguCuACUugaucGUAUC	UUCUUAcAugG-AuaAcCGuagUAA	HARVERMI
104	19 THEANNUL	AAACUGCGAAUGGcucAUVACAAcagUUAUAguuuAUUugauGUUCG	UUUCUAcaugG-AuaAccGugcUAA	THEANNUL
104	20 SYMPILO1	AAACUGCGAAUGGcucAUUAAAGcagUUAUAauuuAUUUgaugGUCA	CUGCUACAugG-AuaAcuGuggUAA	SYMPILO1
104	21 ZBBSR205	AGACUGCGGACGGcucAUVAUCagUUAUAgUuuAUUugaUGGUCGA	UUACUAcaagg-AuaACCGuagGAA	ZBBSR205
104	22 ZBBSR206	AGACUGCGGACGGcucAUVAUCagUUAUAGUuuAUUugaUGGUCGA	UUACUAcaagg-AuaACCGuagGAA	ZBBSR206
104	23 ZBBSR235	AGACUGCGGACGGcucAUVAUAUCagUUAUAgUuuAUUugaUGGUCGA	UUACUAcaagg-AuaACCGuagGAA	ZBBSR235
104	24 ZBBSR218	AGACUGCGGACGGcucAUVAUAUCagUUAUAGUuuAUUugaUGGUCGA	UUACUAcaagG-AuaACCGuagUAA	ZBBSR218
104	25 ZBBSR217	AGACUGCGGACGGcucAUUAUAUcagUUAUAgUuuAUUugaUGGUCGA	UUACUAcaagG-AuaACCGuagUAA	ZBBSR217
104	26 ZBBSR211	AGACUGCGGACGGcucAUVAUAUCagUUAUAgUuuAUUugaUGGUCGA	UCACUAcaagg-AuaACCGuagUAA	ZBBSR211
104	27 Pchroma	AAACUGCGUACAGeucAUUAUAUCagCAAUAauuuAUUugaUGGUUUC	UUACUAcUugG-AuaAcCGuagUAA	Pchroma
104	28 EUGROTUN	AAACUGCGUACAGcucAUUAUAUCagCAAUUauuuAUUugaUGGUACC	UUACUAcaugG-AuaAcCGuggUAA	EUGROTUN
104	29 ENTOGING	AAACUGCGGACGGcucAUUAGAAcagUUAUaAuuucUuugauuAGUAC	CAUAcaagGAAuaGcuuuguGAA	ENTOGING
104	30 DICDISCO	AAACUGCAGACGGcucAUVACAAcagUGAUaAacUAAuagacuuUCGGGUU	UUACCU-uUugG-AuaAccGcAgUAA	DICDISCO
104	31 ZTnucl	AAACUGCGUAAAGcucAUUAUAUCagUUCUAacA-UCUuaggaauaCA	AAAAgaugG-AuAUuAgugCUAA	ZTnucl
104	32 W10Z79	AAACUGCGUAAAGcucAUUAUCagUUCUAacA-UCUuaggaauaCG	AAAaaaCgG-AuAUuAgugCUAA	W10Z79
104	33 W10274	AAACUGCGUAAAGcucAUUAUAUCagUUCUAacA-UCUuaggaauaCU	AAAaaaCgG-AuAUuAgugCUAA	W10274
104	34 W10Z72	AAACUGCGUAAAGcucAUUAUAUCagUUCUAacA-UCUuaggaauaCG	AAAaaaCgG-AuAUuAgugCUAA	W10272
104	35 W10Z10	AAACUGCGUAAAGcucAUUAUAUcagUUCUAacA-UCUuaggaauaCG	AAAaaaCgG-AuAUuAgugCUAA	W10210
104	36 ZBBSR7	AGAUUGCGGACGGcucAUUAUAAcagUUUUUauuuaaUUgauauuaU	UUUUUAGgugG-AuaCGCGuggUAA	ZBBSR7
104	37 ZBBSR173	AGAUUGCGAAUGGcucAGUAUAAcagUUACCauuuGUUugaauGACU	AUUUAugugG-AuaAcuUUggAAU	ZBBSR173
104	38 Siphcyan	AGAUUGCGAAUGGuuuAGUAUAAcagBUUCUauAuUCUugaauAANU	uucuugugg-AuaAcugCggGAA	Siphcyan
104	39 ZBBSR2	AGAUUGCGGACGGcucAUUAUAAcagUUAUUguAuUaUugaGAuUAC	uwguaggugg-AuaCcuGuggUAA	ZBBSR2
104	40 ZCR4	AGAUUGCAAAUGGcucAUUAUAAcagUUAUUauAuUAUugagauuAU	UUUAUAGgugG-AuACuUaugaGAA	ZCR4
104	41 ZCR16	AGACUGCAGAUGGcucAUUAUAucagUUUUUguAugCUugacAUUAU	CUUAUAugugG-AuaCcuGuggAAA	ZCR16
104	42 ZCR6A	AGAUUGCAAAUUGcucAGUAUAAcagUUACCauuGGUUugaauAAUA	GUUIAugugG-AuaAcuUIggAAU	ZCR6A
104	43 PHYPOLYC	AAUCUGCGAACGGcucCGCAUACcagUUGUAAACCAUAGCAAGCAAGCGGGUUGUUGCCGCAAG	3CGACGGCGCGGUUCAcAGgG-AuaAccCuggUAA	PHYPOLYC
104	44 NAEGRUBE	AGUCUGUGGAAGGcucAUUAUAACagUUAUacucc-uAgcCAcuggAAAG	UUUAcaagG-AuaCcAcCguUAA	NAEGRUBE
104	45 euk heli	7 8 9	10	euk heli
104	46 rad	A A	A = = = = = = = = = = = = = = = = = = =	rad

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tion:	identity:	Data:		
204	1 1369mask			1369maak
204	2 MNELEIDY	UUcuaGAaCuaAUAcauaCGAAAAQueeee-GACuurtit==================================	101	VOTE TEL
204	3 DIAGRAND	UUcuaGAgCuaAUAcattocCGAAAAGGcccc-GACuiGktIII.		TURADATO TO
204	4 ATHBOMBA			INPUGATO
204	5 BLAEMERS	UJcuaGaocuaAUAcattocActifcAAmiccuGACcorritatio		Admodula Admodula
204	6 CHLREINH	UUcuaGAgCuaAUAceUgCGCACA-accc-GACuucU		HNIGATHO
204	7 ORYSATIV	UUcuaGAgCuaAUAcoUoCAACAAAcccc-GACUIICC		INTENED OF
204	8 PORAERUG	UUcuadAccuaAUAcatterCignCiaAraucr-GaCuceC		ATTER FOOD
204	9 ACACAST1			PUNARNUS
204	10 PHERALAM	accangeservesservesservesservesservesservesservesservesservesservesservesservesservesservesservesservesservesse fillfminarabetisenservesservesservesservesservesservesservesservesservesservesservesservesservesservesservesserv	cucecaugegeada-gggauguau-uuauuagguu	ACACASTI
	11 CHARTER TO		GACCGBGB-GGGUCGCAC-UUGUCUUAAU	PHRBALAM
	DISTRICT TT	-ccuaeAgcuaAUAcrugccUAAAcgccc-GACUCAC	GAA-gggugGUAU-uuauuAGAUA	STYALSID
507	ALXUNTRA 21	UucuadAgcuaAUAcaUgCAGGAGUuccc-GAcuCAC	······································	EMIHUXLE
402	11 OCHDANIC	Uucua@AgcuaAUAcaUgCAGCAAUcccu-GAcuUA	·········ggÅÅ-agggUGUAC-uuauuagaUA	OCHDANIC
204	14 CAFROENB	UUcuaGAgCuaAUAcaUgCACGAAGuccG-GAucccUC	gggaRA-AggaUGCGU-uuauuagauA	CAFROENB
204	15 LABMINUT	UUcuaGAgCuaAUAcaUgCAACAAAgccc-aUU	u-gggcUGUAU-uuauuagauA	LABMINUT
204	16 OXYGRANU	UUcuaGAgCuaAUAcaugCUGGUVagecu-GACuuuU	GUggaA-gggcuGUAU-uuauuAgaUA	OXYGRANU
204	17 BLEAMERI	UUcuaGAgCuaAUAcaugCUGGUua+cgc-U	GU-gcguaGUAU-uuauuAgauA	BLEAMERI
204	18 HARVERMI	AUcuaGAgCuaAUAcaUgCUAAAAAuccuGGAcgcgGC	AcgcgGAA-gggaCGAGU-uuauuAGAU-	HARVERMI
204	19 THEANNUL	UUguaGggCuaAUAcaugUUCGAG-gcca-UUUU-serververververververververververververve	uggcGGCGu-uuauuagaCC	THEANNUL
204	20 SYMPILO1	UUcuaGagCuaAUAcaUgCACCAAaaccc-AACuucG	CAgaa-ggguuGUAU-uuauuAgaUA	SYMPILO1
204	21 ZBBSR205	UUcuaGAGCuaAUAcuugCACUUcaAggu-gacUU-+++++++++++++++++++++++++++++++++++	AAAUgu-uaccugCAC-uuauuagaUU	ZBBSR205
204	22 ZBBSR206	UUcuaGAGCuaAUAcuugCACUUcaAAcu-gaUUU		ZBBSR206
204	23 ZBBSR235	UUcuaGAGCuaAUAcuugCACUUcaAggu-gauUU	AAACau-caucudCAC-uuauuagaUU	ZBBSR235
204	24 ZBBSR218	UUcuaGAGCuaAUAcuugCACUUcaAaac-acUUU		ZBBSR218
204	25 ZBBSR217	WcuaGAGCuaAVAcuugCACW0caAaac-acWW		ZBRSR017
204	26 ZBBSR211	UUcuaGAGCuaAUAcuuoCACUCcaAaaa-caIII		1100000
204	27 Pchroma	UdeuaGAgeuaAUAcatteeceCAAA-AccineGACileniite==================================		TTTVCGG7
204	2.8 BUIGROTITM			FCULOMA
107	20 ENTROTING	vocuatory/cuatory/cauge/changlacee-AAeueuoge=================================	ggggA-gggauGUAU-uuauuagaUA	EUGROTUN
	DNIDOINA CZ	vaaaaaagaaaavocuugode=seeduccuguucuoluokuote====================================	AUAGGCGCAU-UUCgaacagg	ENTOGING
		AUC-GGGGCUAAUACAUACAUACAUGGGUGACUGGC **********************************	·····AAcggAA-gcucAGCGA-uuauuagCau	DICDISCO
102	TONULZ IS	UUCUACAAUGAAUACAUUUAUAACgucuaaUUUUU	aaauUACu	ZTNUCL
107	6/20TM 75	UUCUACAAUACAUUUAUAUAACgucuauuUUU	aauagau-U-aaauUACu	67201W
204	71 MI02/4	UUCuacAaUCaAUAcAuuuAUAACgucuaAUUU	nAuagau-U-aaauUACu	W10Z74
204	34 W10Z72	UUCuacAaUCaAUAcAuuuAUAACgucuauuUUU	มสลุบสฐลุน-บ-ลลลูนบิลิCบ	W10272
204	35 W10Z10	UUCuacAaUCaAUAcAuuuAUAACgucuauuUUU~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		W10210
204	36 ZBBSR7	UUcuaGAGCuaAUAcauGUCAUAAAaauUguauaCUUUUUUAUAUGAU	Uuduu-U-uuguuauauuuu	ZBBSR7
204	37 ZBBSR173	UGcuUCagCuaAUAcaugGU-ACUuAuauuuaaAUCUAUUAUUUUGAU	uugUaUaUauaGaU-UUGauUUuu	ZBBSR173
204	38 Siphcyan	UUuuUcagCuaAUAcaugGU-Acuau-guauaAAUAUAUAUUUGAU	Auguauau-ggCUGUuaUuUuu	Siphevan
204	39 ZBBSR2	UUcuaGagCuaAUAcauGUC-GCUAaug-GUauaUUUUUAUU	uauti-GAGcautitauuuguu	ZBBSR2
204	40 ZCR4	AAuuauUaAAaAUAuauGAUUUUAaaauAuuUaUU	UAUu-UggCauuuauugcu	2CR4
204	41 ZCR16	UCcuaGagCuaAUAcaugCC-AG-aaauAAuauUUCUAUUUGUA	UaUu-gGGCauuuAUuu-Cu	ZCR16
204	42 ZCR6A	UUcuUUagCuaAUAcaugGU-ACAauauauaua-uaccU-AUAAAUGUAUUAUAUUAU	CAuauguauaude-CAUUUuu	ZCR6A
204	43 PHYPOLYC	UUcugAggCuaAUAcAAgAACGUACCAcc-cgcuuCGACCCGUAA	GGGGAggggggggg	DATOTAC
204	44 NAEGRUBE	CUgeAgCgAua-UAeuugUUCCCUUCGgg-guGG	uaauaguAu-uugUGCugaa	NAEGRUBE
204	45 euk heii	10 11	1-1 1	euk heli
204	46 rad	<pre></pre>		rađ

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304	1 1369mask		1369mask
304	2 MNELEIDY	. AAAA-accAaUgcguu-UAAC	MNELEIDY
304	3 DIAGRANE	AAAA-accaaCAUUAUU	DIAGRAND
304	4 ATHBOMBA	. AAAA-accaaCgcgggcUC	ATHBOMBA
304	5 BLAEMERS	CAAA-accagGGCAcccggGGCA	BLAEMERS
304	6 CHLREINH	AAAG-gccAGCcggggcUCU	CHLREINH
304	7 ORYSATIV	. AAAG-gCugACgcggggcUCC	ORYSATIV
304	8 PORAERUG	CGCA-accadCcgggcUUgg	PORAERUG
304	9 ACACAST1	AAA-accagGG-gcaggggucaGC	ACACAST1
304	10 PHRBALAN	UCAC-AgugccccGgAACUGAGGCUGUUCGACGUGGUAGGGGAGGAGGACGCUGAAUGGGGGCUGGUAGAAACAACuGggggguauAAAACCAAGGAGGAAGGAAGCAA	PHRBALAM
304	11 STYALSII	CAAA-accaaCcggcW	STYALSID
304	12 EMIHUXLE	AGAA-ACcaa-ACCGGU	EMIHUXLE
304	13 OCHDANIC	-GAA-ACCaauggggG	OCHDANIC
304	14 CAFROENE	-CAACCUUC	CAFROENB
304	15 LABMINUT	-GAA-ACcaaugcaggggUUU	LABMINUT
304	16 OXYGRANU	ACAA-ACcaauaUUCCCCG	OXYGRANU
304	17 BLEAMERI		BLEAMERI
304	18 HARVERMI	UAAAaccGACaccucuccGCaccucuccGC	HARVERMI
304	19 THEANNUL	UAA-accAA-accgcUU	THEANNUL
304	20 SYMPILO1	CAGA-accaUCGcaggCUC	SYMPILO1
304	21 ZBBSR205	UACC-aucaAugCU-CUUC	ZBBSR205
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304	23 ZBBSR235	UACC-aCcaAugCU-CUUC	ZBBSR235
304	24 ZBBSR218	cccc-accaAugcc-uuu	ZBBSR218
304	25 ZBBSR217	CCCC-aCcaAugCC-UUU	ZBBSR217
304	26 ZBBSR211	CCCC-aCcaAugCC-CAU	ZBBSR211
304	27 Pchroma	AAA-accaaCGcguccuC	Pchroma
304	28 EUGROTUN	CAAA-accaauaccaccUC	EUGROTUN
304	29 ENTOGING	aurguagaadade	ENTOGING
304	30 DICDISCC	uCUAccaaUgccUU	DICDISCO
304	31 ZTnucl	gagu-aucaAAAGUÀ	ZTnucl
304	32 W10279	gagu-aucaAAAGug	W10Z79
304	33 W10Z74	gagu-aucaAAAGuA	W10274
304	34 W10272	gagu-aucaAAAgug	W10272
304	35 W10Z10	gagu-aucaAAAGug	01201M
304	36 ZBBSR7	gAAa-aucaACA+UGUVACG	ZBBSR7
304	37 ZBBSR173	aucaaacuAAAA-UGUG	ZBBSR173
304	38 Siphcyan	a00aaau0AAA000A	Siphcyan
304	39 ZBBSR2	auCaaAcCAAAA-UGUU	ZBBSR2
304	40 ZCR4	UuCaaAcCAAAA-UGUU	ZCR4
304	41 ZCR16	auuàaGccAgAG-UGAG	ZCR16
304	42 ZCR6A	aucaaaccAAAA-UGUG	2CR6A
304	43 PHYPOLYC	CAGG-UCGCAAA-UAJUUAACUG	PHYPOLYC
304	44 NAEGRUBE	GCCUAgeuauugUAaceuAgUUUUuc	NAEGRUBE
304	45 euk heli	2	euk heli
304	46 rad	A11444141	rad

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tion:		identity:	Data:	
404	-	1369mask		1369mask
404	2	MNELEIDY		MNELETDY
404	m	DIAGRAND		DIAGRAND
404	4	ATHBOMBA		ATHBOMBA
404	ŝ	BLAEMERS		BLAEMERS
404	9	CHLREINH		CHLREINH
404	5	ORYSATIV		ORYSATIV
404	eo ·	PORAERUG		PORAERUG
404	σ	ACACAST1		ACACAST1
404	25	PHRBALAM	\AAAGCCAUAACCCGGGCGAUGGCcuugguGgAAACCUCUGGGCUCAAgguuguuAuUAuGuUcauuguGgccuuCUCGGGGUUAUUUGAAUGUAGUAAU A	PHRBALAM
	1:	STALSTD		STYALSID
404	4 6	OCHDANTC		EMIHUXLE
404	4	CAFROENB		OCHDAN IC
404	15	LABMINUT		LAPMININ I
404	16	OXYGRANU		TUNE OVYO
404	5	BLEAMERI		PL.FAMFRT
404	18	HARVERMI		HARVERMT
404	19	THEANNUL		THEANNIT.
404	20	SYMPIL01		SYMPTLO1
404	21	ZBBSR205		ZARSR205
404	22	ZBBSR206		ZBBSR206
404	23	ZBBSR235		ZBBSR235
404	24	ZBBSR218		ZBBSR218
404	25	ZBBSR217		ZBBSR217
404	26	ZBBSR211		ZBBSR211
404	27	Pchroma		Pchroma
404	28	EUGROTUN		EUGROTUN
404	29	ENTOGING		ENTOGING
404	30	DICDISCO		DICDISCO
404	H:	ZTDUC1		ZTnucl
404	2 2 2	W10279		W10279
404		M10274		W10274
404	4 1	Z/ZOTM		W10Z72
	2 4	DTZOTM		W10210
		/ Yeaan		ZBBSR7
404	2	5/TYSHAZ		ZBBSR173
		nayondi e		Siphcyan
		70007		ZBBSR2
404	41	2CR16		ZCR4
404	42	ZCR6A		0TUD7
404	4	PHYPOLYC		PHYPOLYC
404	44	NAEGRUBE		NAEGRUBE
404	45	euk heli		euk heli
404	46	rad		rađ

"Sept4aln" on 5-SEP-96 15:33:41

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tion:	identity:	Data:		
604	1 1369mask			1369maat
604	2 MNELEIDY	gu UrgaAuegeA - uggeccu		MNPT. FTDV
604	3 DIAGRAND	UGGCGAAucgeAUGAAucgeAUGAAucgeAGUgeCgGGGGGGUGUUC	accountered accountered	DTAGRAND
604	4 ATHBOMBA	UCUCGAAucgeAuggeCUU	accenticae	ATHROMBA
604	5 BLAEMERS	UUGCGGAucgcAuagcCUUU	acceuAUCAac	BLAEMERS
604	6 CHLREINH	UCACGAAucguaugggCUC	ICCCUAUCAAC	CHLREINH
604	7 ORYSATIV	CGACGGAucgcAcggcCCU	ICCCUAUCAac	ORYSATIV
604	8 PORAERUG	UUVCGGAucgcaGCGC-assuUV-assuUV-	ICCCUAUCAAC	PORAERUG
604	9 ACACAST1	CUU-VCGGAucgeAUUCAugueeuecUU-gU	ICCCCUAUCAac	ACACAST1
604	10 PHRBALAM	AAGCUGAucgeuuucUA	IdAccuAUCAac	PHEBALAM
604	11 STYALSID	UUUCGGAucgcAuggc	ACCCUAUCAac	STYALSID
604	12 EMIHUXLE	GCUCGÀAucgcAcggcggc	aCccuAUCAgc	EMIHUXLE
604	13 OCHDANIC	UUCGGAucgaucuUuU	agCecuAUCAge	OCHDANIC
604	14 CAFROENB	GAGCGAAccucgAuAuAuAuAuAu	accouAUCAge	CAFROENB
604	15 LABMINUT	AAGCGAAucgcAG-uggcUUC	agCccuAUCAgc	LABMINUT
604	16 OXYGRANU	GAUCGAAucgcAu-ggacUUUuarter	aCcccAUCAge	OXYGRANU
604	17 BLEAMERI	UAGCGAAcucgA+guageaUUC-aaguUUc	acccuAUCAgc	BLEAMERI
604	18 HARVERMI	GA-+UCGGAucgu-++cggccCC++++++++++++++++++++++++++++++	IgCccuAUCAac	HARVERMI
604	19 THEANNUL	AUGCGAAucguacUacUacUacU-aaduUUc	JaAccuAUCAge	THEANNUL
604	20 SYMPILO1	CGAUGAAucguduggcUU	ICACCUALICAGE	SYMPTIO1
604	21 ZBBSR205	UA - GCGGAucgetua - concerta - conce		ZRESP205
604	22 ZBBSR206			ZERSE206
604	23 ZBBSR235	UAGCGGAucoc08-cGACUUC		75565735
604	24 ZBBSR218			
604	25 7BBCP217		ugueeuAucAge	ZBBSKZ18
	11200000 02	1.2.1.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.	IgCccuAUCAge	ZBBSR217
	TTTYYEAD7 07		ugCccuAUCAgc	ZBBSR211
	20 PUDDONA	00	1gCccuAUCAgc	Pchroma
400	Z8 EUGROTUN	GATTOCGAAucgedAttuggeCCUC-1111111111111111111111111111111111	agCccuAUCAgc	EUGROTUN
604	Z9 ENTOGING	UUU-ACA-AuuguaGaaaugAAUA	ugAucuAUCAac	ENTOGING
604	30 DICDISCO	UUGCAGAucgaggauUUgauUUgucu-agucu-agucu-a-CU-gucu-a-CU-gucu-aCU-gucu-a	JgCccuAUCAac	DICDISCO
604	31 ZTNUCI	UdduuacACUACCUACUddudacaenaenAGAguga-uaguu-UAguGAc	ugAcccAUCAgu	ZTnucl
604	32 W10279	UdguuacaCUACCUACUACUdguga-uaguucuaUU-UAguGAc	ugAcccAUCAgu	W10279
604	33 W10Z74	UdguuacaCUACcUACUACUAC	ugAcccAUCAgu	W10274
604	34 W10Z72	UdguuacaCUACcUACCUAC	ugAcccAUCAgu	W10Z72
604	35 WI0Z10	DGGuuacACUACUAGuuAc	ugAcccAUCAgu	01Z01M
604	36 ZBBSR7	UUGUAucgcAU-UUUAACauri	agAccuAUCAgu	ZBBSR7
604	37 ZBBSR173	ACGAuugcUUUACUUAC	IgAccuAUCAqu	ZBBSR173
604	38 Siphcyan	AdAuugcUGUACGUACAduUUc	adaccuAUCAgu	Siphevan
604	39 ZBBSR2	GGAGAAcgcUUUAAUUAA	aAccuAUCAgu	ZBBSR2
604	40 ZCR4	GGAGAAcgeUUCGAUCGAUCGAUCGAUUC-ULCACGCUC-CAGAUC-ULCACGCUUUC	JaAccuAUCAgu	ZCR4
604	41 ZCR16	AducacaUCACGGUAUAducucaCaUAGAducuCacacaUCAducUC	adAccuAUCAgu	ZCR16
604	42 ZCR6A	ACUAACAGAuugcUUVACUVAC	adaccuAUCAgu	ZCR6A
604	43 PHYPOLYC	GG+-UUA-Uccgcuu-CgaaaGCuucgGUGAGUACGGcggauuuucUgggugg-CUCUCGCugu-GugcUUc	IgAccuAUCAac	PHYPOLYC
604	44 NAEGRUBE	CCU-UCGGGGGGGGAAAGUGaauUaaCAAGGUUUUCAUaaggcCUUUCAGGUUUgcuuuUuCUAGUGG-ccaggcAGag-gaguUUc	IUAccuAUCAge	NAEGRUBE
604	45 euk heli	13 13 9	8 14 15	euk heli
604	46 rad	->> <>		rad

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TOT	י גטעבוורארא	Çara;	
705	1 1369mask		1369mas k
705	2 MNELEIDY	uUUCGaugguaagGUAUUOGcuu-accaugguGACAACgggU-AAcggagaauuAGgguucGAUu-ccggagAggGagccCGAGAAACggcuAccACAuc M	MNELEIDY
705	3 DIAGRAND	uUUCGaugguaagGUAGUGGcuu-accaugguUGCAACgggU-AAcggagaauuAGgguucGAUu-ccggagAgggggggcCUGAGAAAACggcuAccACAuc D:	DIAGRAND
705	4 ATHBOMBA	uUUCGaugguaggAUAGAGGccu-accaugguUUCAACgggU-AAcggggaauAAGGguucGAUu-ccggagAggggggccUGAGAAAACggcuAccACAuc A	ATHBOMBA
705	5 BLAEMERS	uUUCGacgguaggAUAGAGccu-accgugguGAUAACgggU-AAcggggaauaAGgguuuGAUu-ccggagAggGagccUGAGAAAACggcuAccACAuc BI	BLAEMERS
705	6 CHLREINH	uUUCGaugguaggAUAGAGGcu-accaugguGGUACgggU-GAcggaggauuAGgguucGAUu-ccggagAggGagccUGAGAGAUgguuAccACAuc CI	CHLREINH
705	7 ORYSATIV	uUUCGaugguaggAUAGGGGccu-accaugguGGUGACgggU-GAcggagaauuAGgguucGAUu-ccggagAggGagccUGAGAAAACggcuAccACAuc	ORYSATIV
705	8 PORAERUG	uUUCGacgguaggGUAGUGGccu-accgugguGUUUACgggU-AAcggagaauuAGgguucGAUu-ccggagAggGagccUGAGAAAUGgcuAccACAuc P	PORAERUG
705	9 ACACAST1	uUUCGaugguaggAUAGAGccu-accaugguCGUAACgggU-AAcggagaauuAGgguucGAUu-ccggagAggGagccUGAGAAAUggcuAccACUuc A	ACACAST1
705	10 PHRBALAM	uCGaugguaggAUAGUGGcu-accaugguUAUaACgggU-AACggggaAucAGggCucGAUu-ccggagAggGagccUGAGAAACggcuAccACUuc Pi	PHRBALAM
705	11 STYALSID	uUUCGaugguaggGUAGUGGccu-accaugguGUUCACgggU-GAcggggaauuAGgguucGAUu-ccggagAggGagccUGAGAAACggcuAccACAuc S	STYALSID
705	12 EMIHUXLE	uUUCGaugguaggAUAGAGGccu-accauggcGUUAACgggU-AAcggagaauuAGgguucGAUu-ccggagAggagcagccUGAGAAAUggcuAccACAuc 🖬	EMIHUXLE
705	13 OCHDANIC	uUUGGaugguaggGUAUUGGccu-accauggcAUUAACgggU-AAcggagaauuAGgguucGAUu-ccggagAggGagccUGAGAAAUggcuAccACAuc	OCHDANIC
705	14 CAFROENB	UUUCGaugguaggGUAUUGGccu-accauggcGUUAACgggU-AAcggagaauuAGgguucGAUu-ccggagAgGagccUGAGAAACggcuAccACAuc C	CAFROENB
705	15 LABMINUT	ue000augguaguaguaguaduA00daacu-accauggcG0UAACgggU-GAcggagaauuAGgguucGA0u-ccggagAggGagcc0GAQACggcuAccACAuc	LABMINUT
705	16 OXYGRANU	uUUCGaugguaguaguaGUAUUGGacu-accauggcUUUAACgggU-AAcggaggauuAGgguucGAUu-ccgggagAggGagccUGAGAAACggcuAccACAuc	OXYGRANU
705	17 BLEAMERI	uUUCGaugguaguaguaGUAUUGGacu-accauggcGAUGACgggU-GAcggagaauuAGgguucGAUu-ccgggagAggGagccUGAGAAAUUggcuAccACAuc	BLEAMERI
705	18 HARVERMI	uUUAGauggagagagagagucucauagucGUAACggggU-GAcgggggauuAGgguucGAUu-ccggagAggggggggcucGGAGAAACggcuAccACUuc H	HARVERMI
705	19 THEANNUL	uUUGGAcgguaggGUAUUGGccu-accgGggcAACGACgggU-AAcgggggaauuAGgguucGAUu-ccggagAggGagccUGAGAAACggcuAccACAuc	THEANNUL
705	20 SYMPILO1	uUCCGacgguagggUAUGGGccu-accguggcAAUGACgggU-AAcggagaauuAGgguuuGAUu-ccggagAggGagccUGAGAAAACggcuAccACAuc	SYMPIL01
705	21 ZBBSR205	uUUCGaugguaguaGuGUAUUGGacu-accauggcUUUGACgggU-AAcggagaauuAGgguucGAUu-ccggagAggGagccUGAGAAAACggcuAccACAuc Zi	ZBBSR205
705	22 ZBBSR206	uUUCGaugguaguaGUAUUGGacu-accauggcUUGGACgggU-AAcggagaaauuAGGGuucGAUU-ccggagAggGagccUGAGAAACggcuAccACAuc 21	ZBBSR206
705	23 ZBBSR235	uUUCGaugguRguGUAUUGGacu-accauggcUUUGACgggU-AAcggagaauuAGGGuucGAUU-ccggagAggGagccUGAGAAAACggcuAccACAuc 21	ZBBSR235
705	24 ZBBSR218	uUUCGaagguagugUAUUGGacu-accuuggcUUUGACgggU-AAcggagaauuAGGuucGAUU-ccggagAggGagccUGAGAAAACggcuAccACAuc 21	ZBBSR218
705	25 ZBBSR217	uUUCGaagguaguGUAUUGGacu-accuuggcUUUGACgggU-AAcggagaauuAGGGuucGAUU-ccggagAggGagccGGAGAAACggcuAccACAuc 2	ZBBSR217
705	26 ZBBSR211	uUUCGaagguaguaguaguaGUAUUGGacu-accuuggcAUUGACgggU-AAcggagaauuAGGGuucGAUU-ccggagAggGagccUGAGAAACggcuAccACAuc	ZBBSR211
705	27 Pchroma	uUUCGacgguaguGUAGAGGacu-accguggcGUUAACgggUGCAcggagaauuAGgguucGAUu-ccggagAggGagccUGAGAAACggcuAccACAuc	Pchroma
705	28 EUGROTUN	uUUCGaugguaguaguaguGUAAAGaacu-accauggcUAVAACgggU-AAcggggaauukGgguucGAUu-ccggagAggGagccUGAGAAAAUggcuAccACAuc	EUGROTUN
705	29 ENTOGING	uAGuugguaguAGAGGacu-accaagguDADAACggaU-AAcgaGaaauuAGgguuuGACA-ucggagAagGagcuUUCAAAAUggcuAcuACUuc 🗷	ENTOGING
705	30 DICDISCO	uUUCGaugguaCgGUAUUGGcCu-accaugguUGUAACgggU-AAcggggaauuAGgguucGAUu-ccggagAggGagccUGAGAAAUggcuAccACUuc D	DICDISCO
705	31 ZTnucl	uGUucUauUauGUAGUGAauU-auUgaggcUGAAACgggU-AGcggagaauuAGgguucCGUu-ccggagAaAGagccUGGAAACggcuACuAuc z	ZTnucl
705	32 W10279	uGUucUauUauGUAGUGAauU-auUgaggcUGAAAGgggU-AGcggagaauuAGgguucCGUu-ccggagAaAGagccUGCGAAACggcuACuACAuc	W10279
705	33 W10274	uGUucUauUauGUAGUGAauU-auUgaggcUGAAACgggU-AGcggagaauuAGgguucCGUu-ccggagAaAGagccUGCGAAACggcuACuACAuc	W10Z74
705	34 W10272	uGUucUauUauGUAGUGAauU-auUgaggcUGAAACgggU-AGcggagaauuAGgguucCGUu-ccggagAAAGagccUGCGAAACggcuACuAcAuc	W10Z72
705	35 W10Z10	uGUucUauUauGUAGUGAauU-auUgaggcUGAAACgggU-AGcggagaauuAGgguucCGUu-ccggagAaAGagccUGCGAAACggcuACuAuc W	W10210
705	36 ZBBSR7	uAGuACguaCuGUAUUGGaCu-acUGaggcGUUGACgggU-AAcAgagaauuAGgguucUGUu-cCggagAggGagcCUGAGAAAUAgcuAcuAuc 2	ZBBSR7
705	37 ZBBSR173	uA AuuagUagGGUCUUUAUcu - uuugaggcAUUUACgggU - AAcAgagaauuAGgguCcUAUu - cCggagAggGaguCUGGGAAAUAVAgcuAccACAuc	ZBBSR173
705	38 Siphcyan	uA AuuaguugCGUCUUGUAca - auugaggcAUUAACgggU - AAcAgagaauuAGgguucUGUu - cCgggggggggggggGggUCUGAGAAAUAgcuGccACAuc	Siphcyan
705	39 ZBBSR2	ua-euhaguaguaguaguaguaguaguaguaguaguaguaguagua	ZBBSR2
705	40 ZCR4	uA GucaguaguaGUACUGGacu - acugaagcGUUGACgggU - AAcAgagaauuAGgguucUGUu - cCggagAagAagGagcCUGAGAAACAgcuAcuAUAuc	ZCR4
705	41 ZCR16	uAGuGagUAgUAUAQGacu-UuuGaggcAUAUACaggU-AAcggagaauuAGgguucCAAu-ccggagAagGagcCUGCGAGACAgcuAcuACAuc 2	ZCR16
705	42 ZCR6A	uAAuuagUUGGUCUUGAUCU-UuugaggcAUUCACgggU-AAcAgagaauuAGgguCcUGUu-cCgggagAggGaguCUGCGAAAUAgcuAccACAuc	ZCR6A
705	43 PHYPOLYC	uAGauggcagCGUAACGGAcAugccaugguAACAACgggUAcagaggauAAGGguucGAUc-cuggagAgugggcCUGAGAGAUGACucacACUuc	PHYPOLYC
705	44 NAEGRUBE	uCGuŭguuuguŪŪAAGGaca-aacCAggcUŪŪGACgggUAcggggaauCAGŪguucGAŬccggagAggagGggagcGGAAAŪCgcuAccACAuc	NAEGRUBE
202	45 euk heli	16 15 14 17 17 18 18 19 e	euk hell
705	46 rad	X	rad

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906	1 12KOmerk		1.2 6 0
906	2 MNELEIDY	CoreCUterorSealing	MURLET DY
906	3 DIAGRAND	VagguuuuuguaAuugdAAugagUACAAUCUVUAACOAGUAACAauuggaggGGCAAAGUcuggUgCCAACGGGGGUAAUVccagcuccaaua	DIAGRAND
906	4 ATHBOMBA	CgggucuuauaAuugGAAugagUACAAUUUVAAUCCCUUAACGAGGAACAauuggagGGCAAGUcuggUgCCAGCAGCGGGGUAAUUccagcuccaaua	ATHBOMBA
906	5 BLAEMERS	UggccAucgcaAuuggAAuGagUACAAUUUAAAUCCCUUAACGAGGAACAauuggagGGCAAGUcuggUgCCAGCAGCGGGGUAAUUccagcuccaaua	BLAEMERS
906	6 CHLREINH	CgcgucugguaAuugGAAugagUACAAUCUDAAAUCCCUUAAGGAUCCauuggagGGCAAGUcuggUgCCAGCAGCGGGGUAAUUccagcuccaaua	CHLREINH
202	V UKYSATIV	Agrugu cuegu anung da Anger Di Kanung anger da Anger Di Kanung anger da Cada da Cada cada da Marau ana ana ana a	ORYSATIV
			PURAERUG
906	10 PHRBALAM	אינו אינוער א אינוער אינוער	ACACASTI NM
906	11 STVALSTD		TOLOGICAL
906	12 EMIHUXLE	נופא המרכיט המקריק ה המקריק המקריק המקריק המקריק המקריק	EMTHUX1.E
906	13 OCHDANIC		OCHDANIC
906	14 CAFROENB	AAUguegeee-AuugdAAugagGACAAUUUVAAAACCCUUACCGAGGAUCAauuggagGGCAAGUeuggUgCCAGCAGCGGGGUAAUUceageueeaaua	CAFROENB
906	15 LABMINUT	CgggucuuguaAuugGAAugagUACAAUCCUVAAUCCCUVAACGAGGAUCAauuggagGGCAAGUcuggUgCCAGCAGCGGGUAAUUccagcuccaaua	LABMINUT
906	16 OXYGRANU	UAUguuucggGAuugCAAugagUAGAAUUUAAACCCCUUUACGAGGAUCAauuggagGGCAAGUcuggUgCCAGCGGGUAAuUccagcuccaaua	OXYGRANU
906	17 BLEAMERI	UUUgueuugegAuugGAAugagUUAAGUGUAAAAGCCUUU-CGAGGACCCaeuggagGGCAAGUeu-gUgCCAGCAGCGGGGUAAUUECageuecagua	BLEAMERI
906	18 HARVERMI	AgaggcuuacgaUugGAAugagUACAAUUUAAAUCCCUUAACGAGUAACGauuggagGGCAAGUcuggUgCCAGCCGGGGUAAUUccagcuccaaua	HARVERMI
906	19 THEANNUL	AAagucuuguaAuugGAAugaUGGGAAUUUAAACCUCUUCCAGAGUAUCAauuggagGGGCAAGUcuggUgCCAGCAGCGGGGUAAuUccagcuccaaua	THEANNUL
906	20 SYMPILO1	CaugucuuguaAuugGAAugagVAGAAUUVAAACCCCUUUAVGAGUAUCAauugUagGGCAAGUcuggVgCCAGCGGGGUAAUUccagcuCcaaua	SYMPILO1
906	21 ZBBSR205	CaggugaguugAuugGAAugagUACAAUCUAAACACCUUAACGACUAUCCauuggagGGCAAGCcuggUgCCAGCGGGGUAAUUccagcuccaaua	ZBBSR205
906	22 ZBBSR206	CaggugaguugAuugGAAugagUACAAUCUAAACACCUUAACGACUAUCCauuggagGGCAAGCcuggUgCCAGCAGCGGGGUAAUUccagcuccaaua	ZBBSR206
906	23 ZBBSR235	CaggugaguugAuugGAAugagUACAAUCUAAACACCUUAACGACUAUCCauuggagGGCAAGCcuggUgCCAGCAGCGGGGUAAUUccagcuccaaua	ZBBSR235
906	24 ZBBSR218	CaagugaguugAuugGAAugagUACAAUCUAAACACCUUNAACGA-ACUCCauuggagGGCAAGUcuggUgCCAGCAGCGGGGUAAUUccaggcuccaaua	ZBBSR218
906	25 ZBBSR217	CaagugaguugAuugGAAugagUACAAUCUAAACACCUUVAACGA-ACUCCauuggagGGCAAGUcuggUgCCAGCAGCGGGUAAuUccagcuccaaua	ZBBSR217
906	26 ZBBSR211	UaagugaguugAuugGAAugagUACAAUCUAAACACCUUAACGA-AUUCCauuggagGGCAAGUcuggUgCCAGCAGCGGGGUAAUUccagcuccaaua	ZBBSR211
906	27 Pchroma	-UggucugguAauggGAAugagVGUAAVUVAAAVCCCUAVGCGAGGAVCCacuggagGGCAAGVcuggVgCCAGCAGCGGG-UAAuVccagcuccagua	Pchroma
906	28 EUGROTUN	UCggucugguaAucgGAAugagUACAAUUUAAAUCCCUUAACGAGGAUCCacugggagGGCAAGUcuggUgCCAGCAGCGGGUAAuUccagcuccagua	EUGROTUN
906	29 ENTOGING	AAaaagaawUgA-agGAAugaAGGGAAGGUACAUAGUUUUGUGA-AAGCAAuuggagGGCAAGUcuggUgCCAGCAGCGGGGUAAUUccagcuccaaUa	ENTOGING
906	30 DICDISCO	UUgg-agggCaAuugAAAugaACACAAAUUAAACUCUUAAUUA-ACACAauugragGGCAAGUcuggUgCCAGCRGCGGGGUAAUUccagcuccaaua	DICDISCO
906	31 ZTnucl	AggguuAaauUauuAUAUugaGGAUAGAUUAUUUAUUAUUAGACUauAggagGGCAAGUcuggugCCAGCAGCGGGGUAAuaccagcuccAauA	ZTnucl
906	32 W10Z79	AggguuAaauUauuAUAUugaGGAUAGAUUAUUUAUUAUUAACGAUUGACUauAggagGGCAAGUcuggugCCAGCGGGGUAAuaccagcuccAauA	W10279
906	33 W10Z74	AGgguuAaauUauuAUAUugaGGAUAGAUUAUUUUAUAUAUACGAUUGACUauAggagGGCAAGUcuggugCCAGCGGGGUAAuaccagcuccAauA	W10274
906	34 W10272	AggguuAaauUauuAUAUugaGGAUAGAUUAUUUAUUUAGACUAUGACUauAggagGGCAAGUcuggugCCAGCGGGGUAAuaccagcuccAauA	W10272
906	35 W10Z10	AGgguuAaauVaUAUaGGGAUAGAUUAUUAUUAUAUAGAUUGAUUGAUGaUAggagGGCAAGUcuggugCCAGCAGCAGCGGGUAAuaccagcuccAauA	W10Z10
906	36 ZBBSR7	AGggUUaaauAauugUAUugaGAACAGUGUACCAAUUUUACCGAUAAACUauuggagGGCAAGUcuggUgCCAGCAGCGGGUAAuUcccagcuccaauA	ZBBSR7
906	37 ZBBSR173	UUgguUaUgUAauugUAUUgaGAACAAUAUAAUAUAUCUAUAAGUUAGuggagGGCAAGUcuggUgCCAGCAGCGGGGUAAUUccagcuucaAAA	ZBBSR173
906	38 Siphcyan	AUGgcuaaauAauugUAUugaAAAMAUGUAGAAAUUUUAUCUAUAAGCUaGuggaggGCAAGUcuggUgCCAGCAGCGGGGUAuUccagcucuaAuA	Siphcyan
906	39 ZBBSR2	AGggUuaagUAauugUAUugaGAACAGAGUAGCCAUUUDAUCGAUAAACUauuggagGGCAAGUcuggUgCCAGCAGCGGGUAAuUccagcucuaauG	ZBBSR2
906	40 ZCR4	AGgguVaaguAauugAAVugaGAACACAGVAGCAAVUACCAAVAAACVauuggagGGCAAGVcuggVgCCAGCAGCAGCVGGGGUAAUVccagcuccaauG	ZCR4
906	41 2CR16	AAAguaaaUAUuugUACugaGAACAAAUUAGAUAUUUAUCGAUAAACAauuagagGGCAAGUcuggUgCCAGCAGCGGGGUAAuUccagcucuaauG	ZCR16
906	42 ZCR6A	UUGGUUAuguAauugUADUgaAAAAAAUAUDUUUAAUAUUCUAUAAGUUAGUggagGGCAAGUcuggUgCCAGCAGCGGGGGUAAUUccagcuucaAAA	ZCR6A
906	43 PHYPOLYC	AU-ggugggcaAuucAAAugggACUGUUUUAAACAUCCUAUCGAGUAACAauuagagGACAAGUcuggUgCCAGCACCCGGGGUAAuUccagcucuaaua	PHYPOLYC
906	44 NAEGRUBE	UCUUCUGAGGAUNUUCCANGAUUUGGGUGUAGAUAACCCUUAGAGUAGCCANUGGAGGAAAAGUcuggUgCCAGCACCCGGGGUAANUCccagGa	NAEGRUBE
906	45 euk nell	ZI 4 ZZ Z3 Z3 Z3 Z2	euk heli
906	46 rad	۲۰۰۰۰۰۰ ۲۰۰۰ ۲۰۰۰ ۲۰۰۰ ۲۰۰۰ ۲۰۰۰ ۲۰۰۰	rad

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	1369mask Witt TTOY		1369mask
	DTAGRAND	gcguauauurAaduroauudeaguraAageucoganordeanovitanovitanovitanovitanovitanovitanovitanovitanovitanovitanovitanovi Granismis a Safitikanovitano sa	MNELEIDY
	ATHBOMBA	ave successformed sources overways calculation of the operation of the ope	DIAGRAND
	BLAEMERS	geguauauuAAAGUVGuugeaeUVAAAAAgeuregUAGUVGAAUVVICAGGG	BLAEWERS
	CHLREINH	gcguauauuthadgtudguugcagtuceduagtucgdagtutucgggugcggugcguaauuthadgtubgagtutagguaggaggaggggggggggggg	CHLREINH
	ORYSATIV	gcguauauuUAAGUGeAgUUAAUAGAGCucGUAGUOGGACCUUGGGC	ORYSATIV
	PORAERUG	gcguauauaAAAGUUGuuGcagUUAAAAAgCucGUAGUCGGAGAUGGGGC	PORAERUG
	ACACAST1	gcguauauuAAAGUUGuuGcÄgUUAAAAAgCucGUAGUUCGAAGGA	ACACAST1
	PHRBALAM	guguàuacuaAAGCUGuuGcg-UUAAAACgCucGUAGUUGAAUUCCAACACCCGGUUUCAAGUUGAAUGGAAAGAAGGGUAUAUUUAGUAUUUAGAGGGAG	PHRBALAM
	STYALSID	gcguauauuAAAGUUGuuGcagUUAAAAAgCucGUAGUCGAACCUCGGGC	STYALSID
	EMIHUXLE	gcguauauuaAAGUUGuugcAgUUAAACgCucGUAGUCGGAUUUCGGGG	EMIHUXLE
	OCHDANIC	gcguauAcuAAAGUUGuuGcAgUUAAAAAgCucGUAGUUGAAAUUUCUGAU	OCHDANIC
	CAFROENB	gcguauauuAAAGUUGuuGcAgUUAAAAAgCucGUAGUUGAAUUUCUGRR	CAFROENB
	LABMINUT	gcguauauuAAAGUUGuuGcAgUUAAAAAgCucGUAGUUGGAUUUCUGGUguauauuAAAGUUGAguuGcAgUUGAAUUUCUGGU	LABMINUT
	OXYGRANU	gcguauauuAAAGUUGuuGcagUUAAAAAgCucGUAGUUGGAUUUCUGGGgcguauauuAAAGUUGuuGcagUUAAAAAgCucGUAGUUGGAUUUCUGGG	OXYGRANU
	BLEAMERI	gcguauauuAAAGUGuugcagUUAAAAAgCucGUAGUUGAAGCUCUGCggcgaaauuAAAGUGuugcagUUAAAAAgCucGUAGUGAGCUCUGCg	BLEAMERI
	HARVERMI	gcguauAuuAAdGUGuuGcagUUAAAAAgCucGUAGUUGGAUUUCG-GA	HARVERMI
	THEANNUL	gcguauauuAAAAUVGuuGcagtUbAAAAgCucGUAGUVGAAUVUCUGC	THEANNUL
	SYMPILO1	gcguauauuAAAGUUGuudeggUUAAAAAgCucGUAGUUGGAUUUCUGUUg	SYMPILO1
	ZBBSR205	gcguauacuAAUGUUGuugcAgUUAAAAAgCucGUAGUCGGAUUUCAGUgcguauacuAAUGUUGauacaaaaaguuAauaaaaguuaaaaguuaaaaguugaga	ZBBSR205
	ZBBSR206	gcguauacuAAUGUUGuuGcAgUUAAAAAgCucGUAGUCGGAUUUCAGU	ZBBSR206
	ZBBSR235	gcguauacuAAUGUGuuGcAgUUAAAAAgCucGUAGUCGGAUUUCAGU	ZBBSR235
	ZBBSR218	gcguauacuAAUGUUGuuGcAgUUAAAAAgCucGUAGUCGGAUUUCAGU	ZBBSR218
	ZBBSR217	gcguauacuAAUGUUGuugcAgUUAAAAAgCucGGAAUUUCAGUucucucucucucucucucucucucucucucucuc	ZBBSR217
	ZBBSR211	gcguauacuAAUGUUGuugcAgUUAAAAAgCucGGAGUUGGAUUUCAGU	ZBBSR211
	Pchroma	gcguauauuaaaauugcaguuaaaaakgcucguaguuggauuucugguuuuuaaaaaaaaaa	Pchroma
	EUGROTUN	gcguauAuuAAAGUUGuuGcAgUUAAAAAgCucGUAGUUGAQUUUCUGAU	EUGROTUN
	ENTOGING	guauauAUUAAAGUUGuuGugaUUAAAAGguuGUAGUUGAAUGAUACUA	ENTOGING
	DICDISCO	gcauauacuAAAGUUGuuGcAgUUAAAAAgCucGUAGUUGAAGUUUAAGU	DICDISCO
	ZTnucl	guguaugcuAACGUUguugcAgUUACAAAgCucGUAGUUCUAUUAUGA	ZTnucl
	W10Z79	guguaugcuAACGUUGuugcAgUUACUACGUAGUUGGUCUAUUAUGAguguaugcuAACGUUGuugcAgUUACGAAGCucGUAGUUGCAAAgCucGUAGUUGCAA	6/Z01M
	W1 0 Z 7 4	guguaugcuAACGUUGuuGcAgUUACAAAgCucGUAGUUGGUCUAUUAUGA	W10274
	W10272	guguaugcuAACGUUGuugcAgUUACUACGUCGUAGUUGGUCUAUUAUGAguarugcuAguuaugcuAACGUUGuugcAgUUACQUAGUUGGUUGUUGCAAAgCucGUAGUUGGUCUAUUAUGA	W10Z72
	01201M	guguaugcuAACGUUguugcAgUUACAAAgCucgUAGUUGGUCUAUUAUGA	01201M
	ZBBSR7	guguaugcuAACAUVGuugcAgUUAAAAAgCucGUAGUCGAAUVUVUAAGGguguaugcuAACAUVGuugcAgUUAAAAAgCucGUAGUCGAAUVUVAAGG	ZBBSR7
	ZBBSR173	guauaugcuAACAAUGcAAUUAAAAAgUucAUAGUCGAACUCCUUCAgg	ZBBSR173
	Siphcyan	gUUuaugcuAACAAUGuuGcAAUUAAAAgCucAUAGUCGAAUAUUUUCAGAguuaugcuAACAAUGuuGcAAUGuuGcAAUGuugcaAUAUUUAAAAgCucAUAG	Siphcvan
	ZBBSR2	guguaugeuAACMUGeuGeAefUDAAAAAecueGUAGUCGAAUUUUVAAGG	ZRRSR2
	ZCR4	guguaugcuAdUAUOoudcAgUUAAAAAgCucGUAGUCGAAUUUUUAAGA	ZCR4
	ZCR16	guguaugcuAACAUUguugcAgUUAAAAAgCuccUAgUCGAAUAUGUUAgg	2CR16
	ZCR6A	guauauguuAACAMUGauGcAAUUAAAAAgUucAUAGUCGAACUUUUCAGA	ZCR6A
	PHYPOLYC	gcauacguuAAAGUUGuuGeggUUAAAACgcucGUAGGCUCCAGACCUUCAQAGCCUUGAU	PHYPOLYC
	NAEGRUBE	gcguauauuAAUACUGcuGuagUUAAAACgCccGUAGUAAAACCUAAGAGUGGGUGUGUGUAGUAA	NAEGRUBE
	euk heli	3 24 25	euk heli
	rađ		
			7 4 4

Sept4a	ln* on 5-SE	P-96 15:33:41	
Posi- tion:	Sequence identity:	Data:	
1107	1 1369mask		1369mask
1107	2 MNELEIDY		MNELEIDY
1107	3 DIÀGRAND	AUGGAGG-G-GUGGAGG-G-GUGGAGG-G-GUGGAGG-G-GUGGAGG-G-GUGGAGG-G-GUGGACGGC	DIAGRAND
1107	4 ATHBOMBA		ATHBOMBA
1107	5 BLAEMERS	CuagcCaCurrentersessessessessessessessessessessessesse	BLAEMERS
1107	6 CHLREINH	0303010-0-0-000000	CHLREINH
1107	7 ORYSATIV		ORYSATIV
1107	8 PORAERUG	9dang-dys-y-nAgng-cy	PORAERUG
1107	9 ACACAST1	CGCGCAUU-UCAAGCGCCCGUGUCGUCGG	ACACAST1
1107	10 PHRBALAM	CAAUCCUTUUUAAGUAUUGAUGUAUCAGGUUCACCGUUUAACUCCGGGGAAGGCUAUCCACUCUAAUGCCUUAUUCCCGGCA	PHRBALAM
1107	11 STYALSID		STYALSID
1107	12 EMIHUXLE	C020-C02-V-C02-C02-C02-C02-C02-C02-C02-C02-C02-C02	EMIHUXLE
1107	13 OCHDANIC	++++++++++++++++++++++++++++++++++++++	OCHDANIC
1107	14 CAFROENB		CAFROENB
1107	15 LABMINUT	AGA-GUG-A-CGUUCCGAACUU	LUNIMENT
1107	16 OXYGRANU		OXYGRANU
1107	17 BLEAMERI		BLEAMERI
1107	18 HARVERMI	AGGUCCGC	HARVERMI
1107	19 THEANNUL		THEANNUL
1107	20 SYMPILO1	GGAUGACGGUCCGUCGUCGG	SYMPIL01
1107	21 ZBBSR205	AGCUCAGUV-UAGUCUUCAUAGGUCAGUV-UAGUCUCAU	ZBBSR205
1107	22 ZBBSR206	AGGUCAGUU-AAGUCU-CUUCU	ZBBSR206
1107	23 ZBBSR235	AGGCUCAGUU-DAGUCAUAGGCUCAGUU-DAGUCAUU	ZBBSR235
1107	24 ZBBSR218	AUUAGGUUUAUUAGGAUUAGGUCCACCUACUC	ZBBSR218
1107	25 ZBBSR217	AUUAGGUCCACCUACUA	ZBBSR217
1107	26 ZBBSR211	GAGAUGAGACCUCUUAUUGCAGAUGACCUCUU	ZBBSR211
1107	27 Pchroma	CGGG-CACCCGGG-CAC	Pchroma
1107	28 EUGROTUN	GAACCAAAUUGG-CCCGUUCC-C-UU	EUGROTUN
1107	29 ENTOGING		ENTOGING
1107	30 DICDISCO	CGGGCGUUCGGGCGGGCGGGCGGG	DICDISCO
1107	31 ZTnucl		ZTnucl
1107	32 W10Z79		W10279
1107	33 W10Z74		W10Z74
1107	34 W10Z72		W10Z72
1107	35 W10Z10		OIZOIM
1107	36 ZBBSR7		ZBBSR7
1107	37 ZBBSR173		ZBBSR173
1107	38 Siphcyan		Siphcyan
1107	39 ZBBSR2		ZBBSR2
1107	40 ZCR4		ZCR4
1107	41 ZCR16		ZCR16
1107	42 ZCR6A		ZCR6A
1107	43 PHYPOLYC		рнурогус
1107	44 NAEGRUBE		NAEGRUBE
1107	45 euk heli		euk heli
1107	46 rad		rad

Posi- Sequence tion: identity: Date

1010	TOGOT	íty: Data:		
		-		
1208	1 1369ma	1999 X 201		1369mask
1208	Z MNELEI	sidyuccUccUcug	GAUCGUG-UACUGAUC	MNELEIDY
1208	3 DIAGRAN	RAND ************************************	CGGCGAG-CACUGCUA	DIAGRAND
1208	4 ATHBOM	0MBAUAAUAAUAAUAAUAA		ATHROMBA
1208	5 BLAEME	AERSGAGCCUUURCGGCCAGUG		RI.AEMERS
1208	6 CHLREI	31NHucUCUC		CHLRETNH
1208	7 ORYSAT	ATIVUCAUCAUCAUCA		ORVSATTV
1208	8 PORAERI	ERUG GGCAACU		OTTO A ROOM
1208	9 ACACAS	AST1 GUCAAACCGGCGACUGCG-UUGGCGUUGCGGGCUCGGUCCGUCGGU		
1208	10 PHRBAL			TICADAU
1208	11 STYALS	USID GGCAAAGU		FHKBALAM
1208	12 EMTHIN			STYALSID
1208	13 OCHDAN			EMIHUXLE
1000				OCHDANIC
	TE LAPATION			CAFROENB
1 200	NTEGUNA CT			LABMINUT
		WINU THEFTER ARE ARE ARE ARE ARE ARE ARE ARE ARE A		OXYGRANU
2027	INTERNET	15K1 ***********************************		BLEAMERI
80ZT	18 HARVER		***************************************	HARVERMI
1208	19 THEANN		***************************************	THEANNUL
1208	20 SYMPIL	rloi guguguaucuggcu		10110700
1208	21 ZBBSR2(2205 UGUAAGAUCUA		TOUT TUTO
1208	22 ZBBSR2(3206 AUUGAGUUCUU		
1208	23 7.PRSR2	2235 TIGHAAGATICTIA		ODZYSHAZ
1 208	Casaa7 10			ZBBSR235
		2242 - 22200202000		ZBBSR218
0007T	.2728832 C2	1771/ UGUNGUAGUGU=============================		ZBBSR217
807T	Z6 ZBBSRZ	1211 CGAGGCAGC++++++++++++++++++++++++++++++	***************************************	ZBBSR211
1208	27 Pchrom	DMA GUCGOCGUCCU		Pchroma
1208	28 EUGROTI	DTUN	CGGGUAUGA	EUGROTIN
1208	29 ENTOGII			ENTOCING
1208	30 DICDIS(ESCO -UACCACUUCGU-GGUUAA		OTSTOTA DI
1208	31 ZTNucl	cl		
1208	32 W10279			TODULT
1208	33 W10274			6170TM
1208	34 W10Z72			8/20TM
1208	35 W10210		****************	ZIZOTM
1208			***************************************	W10Z10
		NUCUC		ZBBSR7
ROZT	J. ZBBSRI	<pre>X1/3 ************************************</pre>	***************************************	ZBBSR173
1208	38 Siphcy	2yanuccuuauucaauuuuguaugg-uccu	***************************************	Siphevan
1208	39 ZBBSR2	32 ************************************	***************************************	ZBBSR2
1208	40 ZCR4	uccuuccu		2.CR4
1208	41 ZCR16	5ucuvGAAUCAUUUUAUGUGA-UCUV		2.CR1.6
1208	42 ZCR6A	AUCAU-UCAUAUUUUUUUUUUUUUUUUAUGAGU-UCAU		2CB64
1208	43 PHYPOL	JLYC		PHYPOL YC
1208	44 NAEGRUJ	VUBE	;000AUCACUCUIIG-	NAEGRITEE
1208	45 euk he.	neli		euk heli
1208	46 rad			rađ

"Sept4	laln" on 5-Si	2P-96 15:33:41	
Posi-	- Sequence		
tion:	: identity:	Data:	
1311	1 1369mask		1369
1311	2 MNELEIDY		MNEL
1311	3 DIAGRAND	UCUCUGUGACAUCCUC	DIAG
1311	4 ATHBOMBA	ugacua-oucuucoucuu	ATHE
1311	5 BLAEMERS		BLAE
1311	6 CHLREINH	DUD2UD2CCACCUUCCUG2	CHLR
1311	7 ORYSATIV	CUGCCUGC-ACCCUUCUGC	ORYS
11211	8 PORAERUG		PORA
1311	10 PHERALAW	CC	ACAC
1311	11 STYALSID		
1311	12 EMIHUXLE		HIWE
1311	13 OCHDANIC		OCHD
1311	14 CAFROENB	CaAGUUCAUC	CAFR
1311	15 LABMINUT	GUCCGUCCGUCCCU	LABM
1311	16 OXYGRANU	GGCGCCUU-CCAUGGCGCCCUU-CCAU	оххо
1311	17 BLEAMERI	GACCUCGCAUCCAUC	BLEA
1311	18 HARVERMI		HARV
1311	19 THEANNUL	UGCAUVGUCCUCUGGG	THEA
1311	20 SYMPILO1	CAGCCUUGACAUCU	AMYS
1311	21 ZBBSR205	CNCGGCCCGGCNCGGCCCGGCCCGGCCGGCCG	ZBBS
1311	22 ZBBSR206	UUUUU	ZBBS
	23 ZBBSR235	CUUCU	ZBBS
	OTZYCHEZ 10		ZBBS
1121	25 ZBBSR217		ZBBS
1111	TTANCOON 02		5997
1311	2.8 FUGBOTIN		Pchr
1311	29 ENTOGING		CENE
1311	30 DICDISCO		
1311	31 ZTnucl	AUDGUA-CUAUUGACAAUGCCUAUDGUA-CUAUUGACAAUGCCU	ZTDU
1311	32 W10Z79	AUGUA-CUAUUAUGACAAUGCCUAUUGUA-CUAUUAUGACAAUGCCU	ZOIM
1311	33 WL0274	AUUGCA-CUAUUACUGACCA-CUAUUACUGACCA-CUAUUACUGACCA-UAUUCCU	ZOIM
1311	34 W10272	AUGUA-CUAUUAGUAAUGACUAAAUUGUA-CUAUUAGACAAUGCU	ZOIW
1311	35 WI0ZIO	AUUGUA-CUAUUGUA-CUAUUGUA-CUAUUGUA-CUAUUGUA-CUAUUGUCCU	Z0 [M
1151	JASBBSK/		ZBBS
1151	30 51-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2-2		ZBBS
1121	JG ZERCEZ		dqis oqqu
1311	40 ZCR4		
1311	41 ZCR16		2CR1
1311	42 ZCR6A	AUUUAUUUAUUAA-UU-GUAAAGAAGUUGAUUUAUUUAUUU	ZCR6
1311	43 PHYPOLYC		ахна
1311	44 NAEGRUBE	uuugguagacuggaucuuugguagacuggaugacuggaugacuggaugacuggaugacuggaugacuggaucuu	NAEG
1311	45 euk heli		euk
1311	46 rad		rad

1369mask Murility Diragrand Arneboynas CHLREINH CHLREINH CHLREINH PORXBRUG ACACAST1 PHRBALAM ACACAST1 PHRBALAM ACACAST1 PHRBALAM BLABMINUT CAFROENB EMTVALSID EMTVALSID EMTVALSID EMTVALSID EMTVALSID LABMINUT CAFROENB LABMINUT CAFROENB LEAMERLI HARVERWI THEANTUL SUBSR213 SUB

Posi- tion:	. Sequence identity:	Data:		
1411	1 1360mack			
1411	2 MNELEIDY	СССАРА – 2000 - 20000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000		ABBEROLL
1411	3 DIAGRAND		CENCINICA A AGC-	ULAUAND TO
1411	4 ATHBOMBA	CUUGGU-GAGCCO-GCGUOGCC-AUTUTAUU-UGG-GUCGGGGAAACCAGGACUUUUACCUUGAGAAAAUTUAG	GUGUUCAAAGC-	ATHBOMBA
1411	5 BLAEMERS	UGGGUG-CU-CC-UUUGGGOUGG-CUUUUGCUAGCUCGGGGGAUGUCUGCCCAGCACGUUUACUUUGAAAAAAUUAG	GUGUUCAAAGC-	BLAEMERS
1411	6 CHLREINH	CGGGGA-CGGGCUCCUGGG-CUUCACU-GUC-U-GG-GACUCGGAGUCGGCGAGGUUACUUUGAGUAAUUAG	GUGUUCAAAGC-	CHLREINH
1411	7 ORYSATIV	CGGCGA-UGCGCUCCUGGC-CUUAACU-GGC-C-GG-GUUCGUGCCUCCGGCGCCGUUACUUUGAAGAAAUUAG	GUGCUCAAAGC-	ORYSATIV
1411	8 PORAERUG	GOUGUGAGCGGUGC-UGG-CAUUAAG-UUG-U-UG-G-UAGCGUGAGCGCCGACUUUUACUGUGAAAAAAUUAGU	GUGUUCAAAGC-	PORAERUG
1411	9 ACACAST1	GGGCUCAUCG-VCGUC-AUG-CA-AAUGGCGGGGGGGGGGGCGCCCCUGGGGGCCCAGAUCGUUUACCGUGAAAAAUUAG	GUGUUCAAAGC-	ACACAST1
1411	10 PHRBALAM	CAUCCCAAAAACAACCUGGGUCGGGUGGCACCGGGGUUGGAGGGUUUGAUAUGAGGAGAUAAUGAGGUGGUG	IGCAAUCAAAAGU	PHRBALAM
1411	11 STYALSID		GUGUUCAAAGC-	STYALSID
1411	13 OCHDANTC		GUGUTUCAAGC-	EMIHUXLE
1411	14 CAFROENB		CENCENTIA AGC-	CAUANAC
1411	15 LABMINUT	guggaga Acuuut cuugc - Auvaauvugu - A - 06 - 64 Uggga Aucuuvu Acugu Aucuuvu Aucuuvu Aucuuvu Aucuvu Aucuvu Aucuvu Aucuvu Aucuvu	GUGUUUAAAGC-	LABMINUT
1411	16 OXYGRANU	UGUVAACGUVUCUVGGU-AUVCAUVUACU-GG-UVUCGGGCUCAGAUACUVUACCUVGAGAAAAUVAG	GUGUUCCAGGC-	OXYGRANU
1411	17 BLEAMERI	UGAGCAACGGCUCCGGC-AUVAACUVGUC-GC-UGUCGUGAUCAGGUACUVUACCUVGAGCAAAUGAG	-cuguuccagec-	BLEAMERI
1411	18 HARVERMI	CUAACGGUCCUCAUCC-GC-GAGG-GUG-G-GG-AAUCAACCGCUAGGAUCGUUUACUUUGAGGAAAUUAG	GUGUUCAAAGC-	HARVERMI
1411	19 THEANNUL	gucugugcauguggcuuru-rurcggAcggagguucuurgu-cugaauguuacuuugaggaaaauuag	GUGCUCAAAGC-	THEANNUL
1411	20 SYMPILO1	UCCUAAGAACGUAUCU-GC-ACUUCAUUGU	GUGUUUCAAGC-	SYMPILO1
1411	21 ZBBSR205	UUGAC-AGAAACUUCUAUGU-UAUUCAUUUVAGCGC-GGUAGGGACUGU-CUCUUUVACUUUGAGAAAAUUAG	GUGUUCAAAGC-	ZBBSR205
1411	22 ZBBSR206	UIGAC-AGAAACUUCUAUGU-UAUUCAUUUAGCGUGGGUAGCGACUGU-CUCUUUUACUUUDAGUAGAAAAUUAG	GUGUUCAAAGC-	ZBBSR206
1413	23 ZBBSR235	UTGAC-AGAAACUUCUAUGU-UAUUCAUUUAGCGCGUGGGCAGCUGU-CUCUUUACUUUGAGAAAAUUAG	GUGUUCAAAGC-	ZBBSR235
1411	24 ZBBSR218	UNASC-AGAMOUUUCAUCG-CAUUAAUUUAGGGUGUUUGGGGGCCUGU-UUCUUUUACUUUGAGAAAAUUAG	GUGUUCAAAGC-	ZBBSR218
1411	72 ZBBSR217	UNAC-AGAANCUUUCAUCG-CAUUAAUUUACGCG-CUCGGGCCUGU-UUCUUUACUUUGAGAAAAUUAG	GUGUUCAAAGC-	ZBBSR217
1411	26 ZBBSR211	UCAC-AGAMACAUUCAUCG-CCUUCAUUGGUGUG-UCUUUUGGGACUGU-CUCUUUUACUUUGAGAAAAUUAG	GUGUUCAAAGC-	ZBBSR211
1141	20 STICECHE	UUCCA - GARANGUGU GCCUA-CCCUGUC - C - GG-CAG	GUGUUCCAAGC-	Pchroma
1411	29 FUTORIUS		GUGUUUAAAGC-	EUGROTUN
1411	30 DICDISCO	UGG-UU- ACCOUNTING AND	NGUGUUUAAAGC-	ENTOGING
1411	31 ZTnucl		SUGGOOORAAGC -	27nuc1
1411	32 WL0279	UDACUUDAGAACAUGUUUAUAUUGAAAUUUGCAUUUUCCUUAUGUUAUUAUUAUUAUUAUUAUUAU	SUUGAUTUAAG	6/201M
1411	33 W10Z74	URCUUAGAACAUGUAUUAUUAUUAUUAUUUC	suugauuuaag	W10274
1411	34 W10Z72	UVACUUAGAACAUGUCUUAUUUGAAAUUUACUUUUC	suugauruaag	W10Z72
1411	35 W10210	UVACUUAGAACAUGUCUUAUAUNUGAAAUUUAC	sungauruaag	W10Z10
1411	36 ZBBSR7	UUACUCCAUUUUUUCACCAAUGGAAUUCAUUUUCUGAUAGUGAAGUAAGUUUGAAUUUACUUUGAGAAAUUAG	GUGUUCAAAAC-	ZBBSR7
1411	37 ZBBSR173	AAUAUAAAUAUUUACUCUGUUAGCAUUAAUUUUCUGACAGUAA-UUAAAGUAAUUUUUAGUAAAAAAAUUAG	GUGUUCAAAGC-	ZBBSR173
	38 Siphcyan	AGUUAUAUUUAUUAUUUAUACUGUUGACAUUAAUUUUUGUUAUAUUUAAA-UUUGUUAUUUAAA-UUUGAUAAAAAUGAG	reveruuuaage-	Siphcyan
1181 1781	19 TOBSKZ		AGUGUUCAAAGC-	ZBBSR2
	41 70915		GUGUUCAAAAC-	ZCR4
1411	42 2CR6A	ער איז	NGUGUUUUAGAC-	SCRI6
1411	43 PHYPOLYC	UCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	AUGATTIAACC-	DHVPOLVC
1411	44 NAEGRUBE	GUCUGACAGUUGCUAC GUACUUA-CUAA-CCACGGUUCAUCCGU GAGGCCC-UU GG-CUUGCAACUGUAAAUAAAUCGU	JGUGCUUAAAGC-	NAEGRUBE
1411	45 euk heli			euk heli
1411	46 rađ			rad

Posi- Sequence

		A -+		
UOTA	таепсису:	UACA:		
1511	1 1369mask		1111111111111111111111111111111111	1369mask
1511	2 MNELEIDY	AGGCAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU	CGCUYGAAUAUCUCAGCAUGGAAUAAUAGAAUAGGACUUUGG-U	MNELEIDY
1511	3 DIAGRAND	AGGCUAUUUAUU	UGCUUGAAUAUAUUAGCAUGGAAUAAUGGAAUAGGACUUUGG-U	DIAGRAND
1511	4 ATHBOMBA	AGGCUUA	CGCCUGAAUACAUUAGCAUGGAAUAAUAAAAUAGGACG-UGCGG-U	ATHBOMBA
1511	5 BLAEMERS	AGGCUUUUUUA	AGCUUGAAUAUCUUAGCAUGGAAUAAUAGAAUAG	BLAEMERS
1511	6 CHLREINH	AGGCCUA	CGCUCUGAAUACAUUAGCAUGGAAUAACACGAUAGGACUCUGG	CHLREINH
1511	7 ORYSATIV	AAGCCAU	CgcuCUGGAUACAUUAGCAUGGGAUAACAUCAUAGGAUUCCGG-U	ORYSATIV
1511	8 PORAERUG	AGGCGUU	UGCUGUGAAUACAUUAGCAUGGGAUAUUGGAA-GAAGCUUUUG	PORAERUG
1511	9 ACACASTI	AGGC AGAUCCAAUUUUCAGAUCCAAUUUUC	UGCCACCGAAUACAUUAGCAUGGGAUAAUGGAAUAGGACCCUGUCC	ACACAST1
1511	10 PHRBALAM	UAUAGUAGCCUCAAUGGUUCCGUUUGGUUUUCCUGAGGGGGGUUCGG	ACUUGGUCA-UCUGUAG-GUAUUUCA-GGGGUGAUGGGCUCCGGUCUGUUAU-U	PHRBALAM
1511	11 STYALSID	AGGCCUUCCUUC	AGCUAUGAAUACACUAGCAUGGAAUAAUAGAAUAG	STYALSID
1511	12 EMIHUXLE	AGGCAGUAGUAGUAGUAGUAGU	CGCUCUUGCAUGGAUUAGCAUGGGAUAAUGAAAUAGGACUCUGG-U	EMIHUXLE
1511	13 OCHDANIC	AGACAUCAAUCAAUCAAUCAAUCAAUCAAUCAAUCA	UGUCAUUGAAUACGUUAGCAUGGAAUAAUAAGAUAGGACCUUGG-U	OCHDANIC
1511	14 CAFROENB	AGGCUUUA	GGCUUGAAUACAUUAGCAUGGAAUAAUGAGAUAGGACCA-RG-U	CAFROENB
1511	15 LABMINUT	AGGCAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAUAAU	CGCUUGAAUACAUUAGCAUGGAAUAAUAAGAUAGGACUUUGG-U	LABMINUT
1511	16 OXYGRANU	AGGCDUG	CGCCGGAAUACAUUAGCAUGGAAUAAUAGAAUAG	OXYGRANU
1511	17 BLEAMERI	AGGCUUG	GGCCUGAAUCGUCCAGCAUGGAAUAAUAGAAGAGGAC+-UGGGC-U	BLEAMERI
1511	18 HARVERMI	AGGC GUAA	CUCGCCUCCGAAUACGUUAGCAUGGAUAAUGGAAUACGACUUCGG-U	HARVERMI
1511	19 THEANNUL	AGGC+UUV	CGCCUUGAAUAGUUUAGCAUGGAAUAAUAAGAAGUAGGACUUUGG-U	THEANNUL
1511	20 SYMPILO1	AAGCGAU	UGCCUUGAAUACAUUAGCAUGGAAUAAUAAUAAGAUAGGACCUCAG-U	SYMPIL01
1511	21 ZBBSR205	AGGUAGA	UGCCUGAAUAUUACUCUUGGAAUAAUGCUAUAAGACUUUGG-U	ZBBSR205
1511	22 ZBBSR206	AGGUAUU	CGCCUGAAUAUUACUCUUGGAAUAAUGCUAUAAGACUUUGG-U	ZBBSR206
1511	23 ZBBSR235	AGgUAGA	UGCCUGAAUAUUACUCUUGGAAUAAUGCUAUAAGAC-~UUUGG-U	ZBBSR235
1511	24 ZBBSR218	GGGUUUU	CGCCUGGAUAUUACUCUUGGAAUAAUAAUAUAGGACUUUGG-U	ZBBSR218
1511	25 ZBBSR217	GGguUUU	CGCCUGGAUAUUACUCUUGGAAUAAUAUAUAGGACUUUUGG-U	ZBBSR217
1511	26 ZBBSR211		CGCCAGAAUAUUACUCUUGGAAUAAUACUAUAGGACUCCGG-U	ZBBSR211
1511	27 Pchroma	AAGCUUA	CGCUUUGAAUACAUUAGCAUGGAAUAAUAACAUAGGACUUCUG-U	Pchroma
1511	28 EUGROTUN	AGGCUUA	UGCUGUGAAUACAUUAGCAUGGAAUAAUAAUUUAGGACUUUUGG-U	EUGROTUN
1511	29 ENTOGING	AAAACA-A	UGUUAAUGAAUAAUGAAGCAUGGGACAAUAAGAAGGAGAUUUGA	ENTOGING
1511	30 DICDISCO	AGGC GUC	-UCGCCUGAUCUUU-UGCAGCAUGGUAUGAUGAAGCAUGACAU	DICDISCO
1511	31 ZTnucl	AGAAGAAA	UGAUAUVGUACUAVAGUACAGAAUAAVACUVGAAGAUCUCAG-V	ZTnucl
1511	32 W10Z79	AGAAGAAA	UGAUAUVGUACUAUAGUACAGAAUAAUAUVGAAGAU~-CUCAG-U	W10Z79
1511	33 W10Z74	AGAAGAAA	UGAUAUUGUACUAUAGUACAGAACAAUACUUGAAGAUCUCAG-U	W10274
1511	34 W10Z72	AGAAGAAA	UGAUAUUGUACUAUAGUACAGAAUAAUACUUGAAGAUCUCAG-U	W10272
1511	35 W10Z10	AGAAGAAA	CGAUAUUGUACUAUAGUACAGAAUAAUACUUGAAGAUCUCAG-U	OIZOIM
1511	36 ZBBSR7	AGUCCGUCU	CACGGCUGAUUAG-+GAAAGCAUGGAAUGAUGAGUAACGACAGUGGUU	ZBBSR7
1511	37 ZBBSR173	AGUCGUU-+	CGAAAUDAUUCUAAAGCACGGGAAUGAUAAGUAAUGAUGCUAG-U	ZBBSR173
1511	38 Siphcyan	AGUCGUU	CGUUAUVAUUCUAAAGUAUGGAAUGAUAAGUAAUGAUGUUGG-C	Siphcyan
1511	39 ZBBSR2	AGUCDUA	CGGCUUAAUAU-+UAAAGCAUGGAAUGAUAAAUAAUGACAUCGG-U	ZBBSR2
1511	40 ZCR4	AGCCUUUG	CGGAUUUAUAUUAAAGCAUGGAAUGAUAAAUAAUGACAUCGG-C	ZCR4
1511	41 ZCR16	AAUCUUA	UGGAUGUAUAUUAAAGCAUAGAAUGGUAGAUAAUGACAUCAG-U	ZCR16
1511	42 ZCR6A	GGUCGUA	CGAUAUUGUUCCAAAGCAAGGAAUAAUAAGUAAUGAU-~GUUAG-U	ZCR6A
1511	43 PHYPOLYC	-GUAGU-GACCAAAGCACC	GUCUUUNAGA-CGGGCACGGCAUGGGACGAAACGCACCGGGCUCGC-C	ритрогус
1511	44 NAEGRUBE	GGGCUAUGAUAUGAUACI	UCUGCCAGAGCGAUUUAGCAUGGGACUGCAGAGUAGCUG-UAUUUG-A	NAEGRUBE
1511	45 euk heli			euk heli
1511	46 rad			rad

Posi- Sequence tion: identity: Data:

	1369mask MNELEIDY DIAGRAND	ATHBOMBA BLAEMERS CHLREINH	ORYSATIV	PORAERUG	ACACAST1	UGUAUGA PHRBALAM	STYALSID	THE BATHOXIE	CAFROENB	TUNIWER TABMINUL	OXYGRANU	BLEAMERI	HARVERMI	THEANNUL THEANNUL	SYMPILO1	ZBBSR205	ZBBSR206	ZBBSR235	ZBBSR218	ZBBSR217	ZBBSR211	Pchroma	EUGROTUN		DICDISCO	M10279		W10274	W10274 W10272	W10274 W10272 W10210	W10274 W10272 W10210 ZBBSR7	W10274 W10272 W10210 ZBBSR7 ZBBSR173	W10274 W10272 W10210 ZBBSR173 ZBBSR173	M10274 M10272 M10210 2BBSR713 Siphcyan Siphcyan	M10274 M10272 2BBSR7 2BBSR73 51phcyan 51phcyan 2CR4	M10274 M10272 M10772 M10772 M10772 M10772 M10772 M10772 M10772 M10772 M10772 M1	M10274 M10272 M10210 ZBBSR773 Siphcyan Siphcyan ZBBSR2 ZCR16 ZCR16	M10274 M10272 M10210 ZBBSR773 ZBBSR2173 ZBBSR2 ZCR16 ZCR16 ZCR6A	M10274 M10272 M10210 2BBSR73 22BSR23 22BSR2 22B5 22R54 	M10274 M10274 M10272 ZBBSR7 ZBBSR7 ZBBSR7 ZBBSR7 ZBBSR7 ZBBSR2 ZBBSR2 ZCR4 ZCR4 ZCR4 ZCR4 NARGRUBE
	.111111111	iggauaGuu	IgggacaGuc	vggaacgGuc	เชิญชัลนลดินนเมือนระระระ	igguCuAAccAGCAAUGGUUAUAUUAUGAGUU	lgggauaGuu		ggggcaGuu	iggaacaGuuti	igggauaGuc	igggauaGuu	/gggacaGuu	vggaacaGuu	/gggauaGuu	1gggacgduu	vgggacgGuu	raggacgGuuu	\gggacaGuu	\gggacaGuu	\gggacaGuu	lgggauaGuu	lgggauaGuu	\ggaauaauu	19999809680			igaguuagcuigaguuagcuigaguuagcu	isaguagcuisaguagcuisaguagcuigaguuagcuigaguuagcu	isayuuagou gaguuagouisayuuagoui gaguuagouisayuu	ເອລອບແລອບດີ ເອລອບແລອດປະ	ເອຊຊູນແຊຊູດ. ເຊສູຊູແນຂູດູດ. ເຊສູຊູແນຂູດດ. ເຂສູຊູແປຂູດູດ.	ທ່ອງຊຸມແລຍດ. ເຊື່ອຊານແລຍດ. ເຊື່ອຊານແລດດ. ເລື່ອຊານຈິຊາດ. ເລື່ອຊານປັນດ.	ຜ່ອງຜ່ານຂອບ ເຊື່ອວູບາຂຽບແ ເຊື່ອວູບາຂຽບແ ເຂື່ອວູບາຂຽບ ເຂື່ອວູບາຂຽບ ເດືອດປັຊແນດ	ຜ່ອງພາສຽບແ ເງສີສງເມເສຽບແ ເງສີສງເປນສຽບແ ເຊສີລູບເນສຽບແ ເຊສີວູບເປັນເບ ເວສີວູບເປັງສາເພດ ເງສີສູນເປັງສູບແດ	ຜ່ອງພາສຽບປ ເງສ່ອງເນສຽບປ ເງສອງເປນສຽບປ ເງສອງປາສຽບປ ເງສອງປານີ້ປຸດ ເງສອງປາກີ່ອຸດມານ ເງສອງປາກີ່ປານ	ຜ່ອງຜູນແລງເປ ຜູສູດແນຂຽເບ ເຊສດູນປະສູດບ ເຊສດູປັນດູດບ ເຊສດູປັນປາດ ເຊສດູປັນດູດເບ ເຊສດູປັນບັນແດ ເຊສດີປັນບັນແດ	ບຮອງເປນຂອງດູດ. ຜູ້ຂອງເປນຂອງດູດ. ເຂື້ອອງເປນຂອງດູດ. ເຂື້ອອງເປນອງແດ ເດືອງຜູ້ປັນອານາດ. ເດືອງຜູ້ປັນດີເດດ. ເລື້ອອງເປລີດເດດ. ເລື້ອອີງເປັນປູນແດດ. ເລື້ອອີງເປັນປູນແດດ. ເລື້ອງແດດ.	ບຮອງເປນຂອງດີແ ຜູ້ຂອງເປນຂອງດີແ ເຮືອງເປັນຂອງປະ ເຮືອງເປັນຕົນແດ ເດືອງເປັນອາເນດ ເດືອງເປັນຜູ້ແດ ເຮືອງເປັນເປັນແດ ເຮືອງເປັນເປັນແດ ເຊື້ອງເປັນເປັນແດ ເຊື້ອງເປັນເປັນແດ ເຊື້ອງເປັນເປັນແດ ເຊື້ອງເປັນເປັນແດ ເຊື້ອງເຊື້ອງ ເຊື້ອງເຊື້ອງ ເຊື້ອງເຊື້ອງ ເຊີອງ ເຊີອງ ເຊີອງ ເຊື້ອງ ເຊີອງ ເຊື້ອງ ເຊີອງ ເຊີອງ ເຊີອງ ເຊື້ອງ ເຊີອີງ ເຊີອີ ເຊີອງ ເລີອ ເຊີອ ເຊີອ ເຊີອງ ເຊີອງ ເຊີອ ເຊີອີ ເອີອ ເອີອ ເອງ ເລີອ ເຊີ	ທ່ອງຜູ້ແຜ່ລອບ ຜູ້ສອງເປນຂອງດີດ ເຮັດອຸດປິນຂອງດີດ ເຮັດອຸດປິນຊານດີ ເຮັດອຸດປິນຊານດີ ເຮັດອຸດປິນຊານດີ ເຮັດອຸດປິນຊານດີ ເຮັດອຸດປິນຊານດີ ເຮັດອຸດປິນເປັນແດ້ ເຮັດອຸດປານເປັນແດ້ ເຮັດອຸດານອານອານອານອານອານອານອານອານອານອານອານອານອາ
	COAGACC-GAAGUA-ugauuaaUA COAGACC-GAAGUA-ugauuaaUa UAGOACU-GAAGUAA-ugauuaaua	UAGAGUC-GCCGUAA-ugauuaauA UGGGACU-GGAGUAAAugauuaauA UGGGACC-GGAGUAA-ugauuaaGA	CGGGAUC-GGAGUAA-ugauuaaua	AUAGGCY-GGAAGCA-uggucaaGA	GCGCGAGGACUAGGGUAA-ugauuaaua	UAUUCGGA-ugauugagg	CORRECC-GAAGUAA-UGBUUAAUA	ucastatte - seasona - ucasuuaatua ucastatte - AAGGUAA - ucasiiiaatua	GCGCGAU-UCGGUAA-ugauuaauā	GCAUACC-AAAUUAA-ugauCaaCA	GAGGGACU-GAAGUAA-ugauuaauA	UAUGGCGC-UUAGUAA-ugauuaaua	CUUGGCU-GAAGUAA-ugauugaUA	UAGGUACC-AAAGUAA-ugguuaauA	CUAGAGCU-GAGGUAA-uggucgauA	UGGGACC-AGAGUAA-ugauugauA	UGGGACC-AGAGUAA-ugauugauA	UGGGACC-AGAGUAA-ugauugauA	UAGAACC-GAAGUAA-ugauugauA	UAGAACC-GAAGUAA-ugauugauA	UAGGACC-GGGGUAA-ugauugauA	AGAGCC-GAAGUAA-ugauugaUA	UAGGACU-GAAGUAA-ugauugaUA			GGAUAC-UGGUGUAA+ugCucUUA		GGAUAC-UGGUGUAA-ugCucUUUA	GGAUAC-UGGUGUAA-ugCucUUUA	GGAVAC-UGGUGUAA-ugCucUUVA GGAVAC-UGGUGVAA-ugCucUUVA GGAVAC-UGGUGVAA-ugCucUUVA	GGAUAC-UGGUGUAA-ugCucUUUA GGAUAC-UGGUGUAA-ugCucUUUA GGAUAC-UGGUGUAA-ugCucUUUA CAGUGGC-CAGUGUAA-ugauGaCUa	GGAUAC-UGGUGUAA-ugCucUUUA GGAUAC-UGGUGUAA-ugCucUUUA GGAUAC-UGGUGUAA-ugCucUUUA GGAUAC-UGGUGUAA-ugGaUGAUUA GAGAGGU-UGAUGUAA-uUauUUCUa	GGAUAC-UGGUGUAA-ugCucUUUA GGAUAC-UGGUGUAA-ugCucUUUA 						GGAUAC- UGGUGUAA - ugCucUUUA GGAUAC- UGGUGUAA - ugCucUUUA 	
שבמי	เป็นปีลบับบับธุรณีนอยู่บันปีร	UCUAUUUUGUUGUUUUC	ccuAUUGUGUUGGCCUU	CUUAUUCGUUGGUU-G	UCCUAUUUUCAGUUGGUUUUGGCA			CUAUUUUGUUGGUU	CGUAUUUUGUUGGUU	ACUAUUUGUUGGUUU		C-C-C-AUUUAUUGGUGU	CUUGUUUCGUUGGUUUCG	UCUAUUUUGUUGGUUU	UCUAUUUUGUUGGUUU	UCUAAUGUAUUGGUGAUUCUA	UCUAAUGUAUUGGUGAU	UCUAAUGUAUUGGUGAU	ucuuuuuguuggugacu	ucuuuuuuguuggugAcu	UCUUUUUUGUUGGUGACU		**************************************			AAGACUU-AAACUUUU			AGACUU-AAACUUUU	AAGACUU-AAACUUUU	AAGA CUU-AAACUUUU	AAAA - CUU - AAACUUUU	AAAA - CUU - AAACUUUU	AAAA - CUU - AAACUUUU	AAAA - CUU - AAACUUUU	AAAA - CUU - AAACUUUU	AAAA - CUU - AAACUUUU	AAAA - CUU - AAACUUUU	AAAA - CUU-AAACUUUU	AAAA - CUU - AAACUUUU
	1 1369mask 2 MNELEIDY 3 DIAGRAND	4 ATHBOMBA 5 BLAEMERS 6 CHLREINH	7 ORYSATIV	8 PORAERUG	9 ACACAST1	10 PHRBALAM	12 FMTHTNLE	13 OCHDANIC	14 CAFROENB	15 LABMINUT	16 OXYGRANU	17 BLEAMERI	18 HARVERMI	19 THEANNUL	20 SYMPILO1	21 ZBBSR205	22 ZBBSR206	23 ZBBSR235	24 ZBBSR218	25 ZBBSR217	Z6 ZBBSKZII	27 PCDTOMA	26 EUGROTUR	AD DTCDTCDC	31 2Thurl	32 WL0279	33 W10Z74		34 W10Z72	34 W10272 35 W10210	34 W10272 35 W10210 36 ZBBSR7	34 W10272 35 W10210 36 ZBBSR7 37 ZBBSR173	34 W10272 35 W10210 36 ZBBSR7 37 ZBBSR173 38 Siphcyan	34 W10272 35 W10210 36 ZBBSR7 37 ZBBSR173 38 Siphcyan 39 ZBBSR2 40 77784	34 W10272 35 W10210 36 ZBBSR7 37 ZBBSR173 38 Siphcyan 39 ZBBSR2 41 7CR16	34 W10272 35 W10210 36 ZBBSR7 37 ZBBSR173 38 Siphcyan 39 ZBBSR2 41 ZCR16 42 ZCR64	34 W10272 35 W10210 35 W10210 37 ZBBSR17 38 S15h5Y17 38 S15h5Y3 38 S15h5Y3 40 ZCR4 41 ZCR16 41 ZCR16 43 ZCR6 43 PTY501YY	34 W10272 35 W10210 35 W10210 37 ZBBSR173 38 Sipheyan 38 Sipheyan 39 ZBBSR2 41 ZCR4 41 ZCR16 43 PHYPOLYC 44 NAEGRUBE 44 NAEGRUBE	34 W10272 35 W10270 35 W10210 37 ZBBSR173 38 Sipheyan 38 Sipheyan 39 ZEBSR2 41 ZCR16 41 ZCR16 42 ZCR6A 44 NAEGRUBE 45 euk heli	34 W10272 35 W10270 35 W10210 37 ZBBSR7 37 ZBBSR73 38 Siphcyan 39 ZBBSR2 41 ZCR4 42 ZCR6A 42 PHYPOLYC 44 NAEGWUBE 44 NAEGWUBE 45 euk heli
	1611 1611 1611	1611 1611 1611	1611	1611	1611	1611	1611	1611	1611	1611	1611	1611	1611	1611	1611	1611	1611	1611	1611	1101		1101	1191	1611	1611	1611	1611		1011	1611	1611	1611 1611 1611	1611 1611 1611 1611	1611 1611 1611 1611 1611 1611	1611 1611 1611 1611 1611 1611 1611 161	1611 1611 1611 1611 1611 1611 1611 161	1611 1611 1611 1611 1611 1611 1611 161	1611 1611 1611 1611 1611 1611 1611 161	1611 1611 1611 1611 1611 1611 1611 161	1611 1611 1611 1611 1611 1611 1611 161
Sept4	aln" on 5-Si	2P-96 15:33:41																																						
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-1801-	· sequence identity:	Data:																																						
1712	1 1369mask		1369mask																																					
1712	2 MNELEIDY 3 DIAGRAND		MNELEIDY DIAGRAND																																					
1712	4 ATHBOMBA	Χ	ATHBOMBA																																					
1712	5 BLAEMERS		BLAEMERS																																					
1712	6 CHLREINH	D	CHLREINH																																					
1712	7 ORYSATIV	0	ORYSATIV																																					
1712	8 PORAERUG		PORAERUG																																					
717	ALACASTI		ACACASTI																																					
1712	11 STYALSID		PHRBALAM STYALSTD																																					
1712	12 EMIHUXLE		EMIHUXLE																																					
1712	13 OCHDANIC	O	OCHDANIC																																					
1712	14 CAFROENB	Ο	CAFROENB																																					
1712	15 LABMINUT	1	LABMINUT																																					
1712	16 OXYGRANU	0	OXYGRANU																																					
1712	17 BLEAMERI	22	BLEAMERI																																					
1712	18 HARVERMI	╫╴ ╻╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸╸	HARVERMI																																					
1712	19 THEANNUL	2	THEANNUL																																					
1712	20 SYMPILO1	5	SYMPIL01																																					
1712	21 ZBBSR205	2	ZBBSR205																																					
1712	22 ZBBSR206	8	ZBBSR206																																					
71/1	252X2BBSK235		ZEBSRZJS																																					
71/12	24 ZBBSK218		ZBBSR218																																					
1712	112ASAAZ CZ		ZBBSKZI/																																					
1712	27 Pchroma		Pchroma																																					
1712	28 EUGROTUN		EUGROTUN																																					
1712	29 ENTOGING		ENTOGING																																					
1712	30 DICDISCO		DICDISCO																																					
1712	31 ZTnucl	Σ	ZTnucl																																					
1712	32 W10279	Μ	W10Z79																																					
1712	33 W10Z74	M	W10274																																					
1712	34 W10Z72	Μ	W10Z72																																					
21/12	OIZOIM SE		OIZOIM																																					
1712	17 78868173		175907																																					
4																																								
1712	39 ZRRSR2		sipncyan 75557																																					
1712	40 ZCR4		2084																																					
1712	41 ZCR16		ZCR16																																					
1712	42 ZCR6A	8	ZCR6A																																					
1712	43 РНУРОГУС	Ä	PHYPOLYC																																					
1712	44 NAEGRUBE	Ν	NAEGRUBE																																					
1712	45 euk heli	α.	euk heli																																					
1712	46 rad	Li di	rad																																					

Pos1-	Sequence		
tion:	identity:	Data:	
1812	1 1369mask	111111111111111111111111111111111111111	1369mask
1812	2 MNELEIDY		MELEIDY
1812	3 DIAGRAND		DIAGRAND
1812	4 ATHBOMBA		ATHBOMBA
1812	5 BLAEMERS		BLAEMERS
1812	6 CHLREINH		CHLREINH
1812	7 ORYSATIV		DRYSATIV
1812	8 PORAERUG		PORAERUG
1812	9 ACACAST1		ACACASTI
1812	10 PHRBALAM	AAUCGAAAUCGUDAACGADAAUAAUAGGACAGCGGGGgggggUDAUACAcuccgug-CUAggggGUGAAAuccUAUGAUuacggaaaAgAUUAACUAGUgcgAAA	PHRBALAM
1812	11 STYALSID		STYALSID
1812	12 EMIHUXLE	Automoto and a second a s	EMIHUXLE
2121	13 OCHDANIC		DCHDANIC
7101	15 LAFROENB		CAFROENB
7191	TUNIMENT CI	GAGgauaUUCGUAugaACAUg-UCGUAugaACAUg-UCAgagGUGAAAuucUUGGAUuGAUuUUGAucaGACGAACUACUgcGAAA	LABMINUT
2191	16 OXYGRANU		OXYGRANU
1812	17 BLEAMERI		BLEAMERI
1812	18 HARVERMI		HARVERMI
1812	19 THEANNUL		THEANNUL
1812	20 SYMPILO1		SYMPILO1
1812	21 ZBBSR205		ZBBSR205
1812	22 ZBBSR206		ZBBSR206
1812	23 ZBBSR235		ZBBSR235
1812	24 ZBBSR218		ZBBSR218
1812	25 ZBBSR217		ZBBSR217
1812	26 ZBBSR211		ZBBSR211
1812	27 Pchroma		Pchroma
1812	28 EUGROTUN		EUGROTUN
1812	29 ENTOGING		DNIDOLNE
1812	30 DICDISCO		DICDISCO
1812	31 ZTnucl	GAAGauaUVAACAAGUGCCAAA	ZTnucl
1812	32 WI0Z79		W10Z79
1812	33 WI0Z74		W10Z74
1812	34 WL0Z72		W10Z72
7181	DIZOIM SF	GAAGauaUUAACAAGuaUUAACAAUAUUuagCg-UUAgagGUGAAAucAuuaUuagCg-UUAgagGUGAAAucAuagagGUGAAA	W10Z10
7121	JO ZBESR/		ZBBSR7
1812	37 ZBBSR173		ZBBSR173
1812	38 Siphcyan	GAAGaaGagaAAVCG0AuuuuGucg-UVAgaaGUGAAAugaGGGAAUgaGaGagaaGGCAAACAAVAgcAAAA	Siphcyan
1812	39 ZBBSR2		ZBBSR2
1812	40 ZCR4		ZCR4
2101	41 ZCKI6	GAAgAudUAGGAAUAUAGAGAAUAUUAGucg-UUAgagGUGAAAuucUGGGAUCgacaaagAUUACCAAGAgcGGAA	2CR16
1812	43 PHVPOLYC		ZCR6A
1812	44 NAEGRUBE	Akubaryo karina kana karina mana kana kana kana kana kana kana ka	
1812	45 euk heli	27 29 29 29 29 29 29 29 29 29 29 29 20 28 2	ank heli
1812	46 rad		rad
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Siphcyan ZBBSR2 PHRBALAM STYALSID EMIHUXLE ENTOGING DICDISCO SYMPILO1 ZBBSR205 ZBBSR173 NAEGRUBE EUGROTUN PHYPOLYC L369maask MNELEIDY DIAGRAND ATHBOMBA BLAEMERS CHLREINH ORYSATIV PORAERUG OCHDANIC CAFROENB LABMINUT OXYGRANU BLEAMERI HARVERMI THEANNUL ZBBSR206 ZBBSR235 ZBBSR218 ZBBSR217 ZBBSR211 euk heli ACACASTJ Pchroma W10272 W10210 W10279 ZTnucl W10274 ZBBSR7 **ZCR6A** ZCR16 ZCR4 rad gcAUUug----ccAAggAuguuuuCauuaaucaAgaAcGAAAguuaaggGAUCAAAgacgAUCAGAUAGucuuaaacCAUAAAACUAUgccgacU gchUUug---acUAggAuguuccCguugaucaAgaAcGAAAguuggggGAUCGAAgacgAUCAGAUACcgucGUAGucucaacCAUAAACUAUgccAgcU gcAAUua - - - ucUAagAuuaauucAUUgaVcaAgaAcGUAAguugaAgGAUUGAAgacgAUCAGAUACcgucGUAAuCucaauUGUAAACUAUaucaacU gcÅÅUua---ucUAagÅuuaauucAWgaVcaAgaÅcGUÀguugaÅgGAWGÅÅgacgÅVCAGÅVÄCcgucGUÅAuCucaauVGVÅÅÄCUÅVaucaacV gcAAUua---ucUAagAuuaauucAUUgaUcaAgaAcGUAAguugaAgGAUUGAAgacgAUCAGAUACcgucGUAAuCucaauUGUAAACUAUaucaacU gcAAUua---ucUAagAuuaauucAUUgaUcaAgaAcGUAAguugaAgGAUUGAAgacgAUCAGAUACcgucGUAAuCucaauUGUAAACUAUaucaacU gcAAUua---ucUAagAuuaauucAUUgaUcaAgaAcGUAAguugaAgGAUUGAAgacgAUCAGAUACcgucGUAAuCucaauUGUAAACUAVaucaacU gcAGAGg----ccVAgaAuuVacuuvUuGaucaAgaAcGVAAguuggggGAVCGAAgacgAVCAGAVACcgucGUAGucucaacUVVAAACUAVaccGVcV gcAUUCA---ucUAggCUaUAuuuUUUVauCaAgaAcGUAAguugggGAUCGAAgacgAUCAGAUACcgucGUAGucucaacUAUAAACUAUaucAacU gcAUVCa---ucUAgaaucUAcUCCuUggucaAgaAcGUAAguugUggGAUCGAAgacgAUCAGAUACcgucGUAGucUcaacUAUAAACAAUauuAauU gcAVVug---CcVAgaAVVUcCuCVuVgaucaAgaAcGVAAguugaGgGAVCGAAgacgAVCAGAVACcgucGVAGuGucaacVGVAAACUAVauuAgcV gcAUUug---ccAAggAuguuuuCRuuaaucaAgaAcGAAAguuagggGAUCGAAgacgAUCAGAUACcgucGUAGucuuaacCAUAAACUAUgccgacU gcAUUug---ccAAggAuguuuuCauuaaucaAgaAcGAAGguuagggGAUCGAAaacgAUCAGAUACcguuGUAGucuuaacAGUAAACUAUgccgacU gchUUug---ccAAggAuguuuuCauuaaucaAgaAcGAAAguuaaggGAUCGAAgaugAUUACcaucGUAGucuuaacCAUAAACGAUgccgacC gchWuug---ccAAggAuacuuuCAuugaucaAgaAcGAAAguuggggGCUCGAAgacgAWAGCgUcGAUGGUGGAGGucGAAGAUgccgacU gchUUug - - - ccAGggAuguuuuCACugaucaAgaAcGAAAguuagggGAUCGAAgacgAUCAGAUACcgUcGUAGucuuaacCAUAAACCAUgccgacU gchUUua---ccAAggAuguuuUCAuuaaucaAgaAcGAAAgucagggGAUCGAAgaggAUUACccucGUAGucuugacCAUAAACUAUgccgacU gcAUUua----ucAAgAuguuuuCAuuAaucaAgaAcGAAAguuagggGAUCGAAgaugAUAAGAUACcaucGUAGucuuaaacCAUAAACUAUgccgacU gcåVVug+++ccAåggåuguuuuCauuaaucaågaåcGåÅåguuagggGåVCÅÅågacgåVCÄGÄUCÄGGucCVåGuccuuaacCåVÅÅÅCVåVgccgacV gcAUUug----ccAAggAuguuuuCAuuaaucaAgaAcGAAAguagggGAUCGAAgacgAUCAGAUACcgucGUAGucucuaaCGUAAACUAVgccGacC gcAUVug---ccAAggAuguuuuCauuaaucAAgaAcGAAAguuagggGAUCGAAgacgAUCAGAUACcgucGUAGuccuaacCAUAAACUAUgccgacU g-AUVug---ccAAggAuguuuuCauugaucaAgaAcGAAAguuagggGAUCGAAgacgAUCAGAUACcgucCUAGucuuaacCAUAAACUAUgccAacU gcλUUgg---acUAggAcguuccCguugaucaAgaAcGAAAguuggggGAUCGAAgacgAUCAGAUACcgucGUAGucucaacCAUAAACUAUgccAgcU gchUUgg----acVAggAcguuccCguugaucaAgaAcGAAAguuggggGAUCGAAgacgAUCAGAUACcgucGUAGucucaacCAUAAACUAUgccAgcC gcAUVgg----acVAggAcguuccCguugaucaAgaAcGAAAguuggggGAUCGAAgacgAUCAGAUACcgucGUAGucucaacCAUAAACUAUgccAgcU gchUUug---acUAggAuguuccCguugaucaAgaAcGAAAguuggggGAUCGAAgacgAUCAGAUACcgucGUAGucucaacCAUAAACUAUgccAgcU gcAUUug~~~acUAggAuguuccCguugaucaAgaAcGAAAguuggggGAUCGAAgacgAUCAGAUACcgucGUAGucucaacCAUAAACUAUgccAgcU gcAUUca---ccAAggAugucuuCUuuaaucaAgaAcGAAAguuggggGAUCGAAgacgAUCAGAUACcgucGUAGucucaacCAUAAACUAUaccgacU gcAUVca---ccAAggAugucuuCUuuaaucaAgaAcGAAAguuggggGAUCGAAgacgAUCAGAUACcgucGUAGucucaacCAUAAACUAUaccgacu gcAUUuu---acUCaauuauAuucAuuaaucAAgaAcGAAAguuagggGAACAAAgacgAUCAGAUCGGUcGUAGUccuaacUAUAAACGAUguuAacC gcAUTca---ccAAauAcUucccCauuaaucaAgaAcGAAAguuugggGAUCGAAgacgAUCAGAUACcgucGUAGuccaaaacUAUAAACUAUgucGacC yuhUUug - - - - cCVAgaAuCUgcucCUugaucaAgaAcGUAAguuggggGAUCGAAgacgAUCAGAUACcgucGUAGucucaa.cUUUAAACUAUaucAgcU gcAUUua - - - ccUAgaAuauucuCCuUgaucaAgaAcGUAAguugaggGAUCGAAgacgAUCAGAUACcgucGUAGucucaacUGUAAACUAUaccGgcU gcAUUCA---ucUAggaUaUAuuuCuUUAuCaAggAcGUAAguugggUGAUCGAAgacgAUCAGAUACcgucGUAGUcucaacUAUAAAAAUAAUAAUAAU gcAGUca---ucAAgggcauuccCGuuQAUCAAgagcGAAAguuaaggGUUCGAAgacgAUCAGAUACcgucGUAGucuuaacUAUAAAUGAUgcAgacC gcVGUGGUgggccACCACAaGcuCguCUAucaGggAcAAAAguuggggGAUCGAAgacgAUUAACGUUGGUAGucccaaacUAUAAACGAUaccAacC gchUUug - - - ccAAggAuguuuuCAuuaaucaAgaAcGAAAguuggagGCUCGAAgacgAUCAGAUACcgucCUAGuuccaacCAUAAACGAUgccgucU ---ccAAggAuguuuuCauuaaucaAgaAcGAAguuggggGCUCGAAgacgAUCAGAUACcgucCUAGucucaacCAUAAACGAUgccgacC gcdWug----ccAAggAcguuuuCAuugaucaAgaAcGAAAguuagggGAVCGAAgacgAUCAGAVACcgucGUAGucuuaacCAVAAACUAVgccGacU gcAUCug---ccAAggAuguuuucauuaaucaAgaAcGAAAguuagggGAUCGAAgacgAUCAGAUAcgucGUAGucuuaacCAUAAACGAUgccgacC gchUUcc---acAAggaUguuuuCAuuaaucaAgaAcGAAAguuggggGAUCGAAgacgAUCAGAUACcgucGUAGucucaacCAUAAACUAUgccGaCC gchUCug----ccAAggAugucuuCAuugaucaAgaAcGAAAguuagggGAUCGAAgacgAUCAGAUACcgucGUAGucuuaacCAUAAACUAUgccGacU gcAUUua---ccAAggAuguuuuCauuaaucaAgaAcGAAAguuagggGAUCGAAgaugAUDAGAUACcaucGUAGucuuaacCAUAAACUAUgccgacU A ñ ----H ä î 32 37 1 25 ł 36 ł ł ----> Sept4aln* on 5-SEP-96 15:33:41 gcAUUug-Data: õ J Pchroma EUGROTUN **1369mask** identity: STYALSID EMIHUXLE ENTOGING DICDISCO ZBBSR173 Siphcyan DIAGRAND BLAEMERS PORAERUG PHRBALAM CAFROENB BLEAMERI THEANNUL ZBBSR205 ZBBSR206 ZBBSR211 PHYPOLYC NAEGRUBE ATHBOMBA CHLREINH ORYSATIV OCHDANIC LABMINUT OXYGRANU HARVERMI SYMPILO1 ZBBSR235 ZBBSR218 ZBBSR217 euk heli MULELEIDY ACACASTJ Sequence W10274 W10272 W10Z10 ZBBSR7 ZTnuc1 W10279 ZBBSR2 ZCR16 ZCR6A ZCR4 rad ្ឋ H 40 41 42 43 44 45 46 Position: 1912 1912 1912 1912 1912 1912 1912 1912 912 1912 1912 1912

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MUNELEID	Y gcgdAucggaggUCGCUCAAUU	XUIALANM
DIAGRAN	D cggdAucggugug-GUGAAA	DIAGRAND
1 ATHBOMB	A aggAucggacaacCUCAAUUUU	ATHBOMBA
5 BLAEMER	s aggavegggegucauguaguuauucacaua	PLAEMERS
6 CHLREIN	H aggAuuggeagaUgUUCUUU	CHLERINH
7 ORYSATI	V aggAucggcggaUgUUGCUJA	ORVSATTV
8 PORAERU	g gggdAuugguggaCguuCCAA-U	PORAERUG
9 ACACAST	1 agcGAuuaggAgaCGUUGAAUACAAAACAccaccAUCggcGCgggucguccuucggcgucguccugucccuUUCAACggggggggggggggggggggggggggggggg	ACACAST1
0 PHRBALA	M agAGAucggaAgacGCUGUCCUAGAAGGAC	PHRBALAM
1 STÝALSI	D gggdAucgguagcuVCUVUVCA	STYALSID
2 EMIHUXL	s aggàuggaggauguccatu	EMIHUXLE
3 OCHDANI	c aggdyuugguuggvoguuduh	OCHDANIC
4 CAFROEN	B cagdAuuggcaccc-W-WW	CAFROENB
S LABMINU	T aggdAuuggcggAcdUUGUCUA	LABMINUT
.6 OXYGRAN	d aggAucgaagg-cgCdCUUU	OXYGRANU
7 BLEAMER	I agadAuuggagg-UgCCAUUAA	BLEAMERI
18 HARVERM	I aggdauccggàga-guuugcalugga	HARVERMI
9 THEANNU	L agAdAuuggaggucguCagU	THEANNUL
O SYMPILO	1 agAGAuuggaggucguUAC	SYMPILO1
1 ZBBSR20	5 aggAucggaggaAguuAUU	ZBBSR205
2 ZBBSR20	6 aggAucggaggaCguuACA	ZBBSR206
3 ZBBSR23	5 aggAucggaggaAguuAUU	ZBBSR235
4 ZBBSR21	8 aggAuuggaagaAgau-cA	ZBBSR218
5 ZBBSR21	7 aggAuuggaagaAgau-CA	ZBBSR217
6 ZBBSR21	1 aggdAuuggugggUguuACU	ZBBSR211
7 Pchroma	gaggauccguggaCgUCUAAU	Pchroma
8 EUGROTU	N cagdAucagugaaCdUUGCAUU	EUGROTUN
NIDOLNE 6	G aagdauuggauaaaUaCAUUAAUACAUUUGUAUUG	ENTOGING
0 DICDISC	0 aggAucgguuaaaaUUUUU	DICDISCO
1 ZTnucl	aggdAuuaacaaCUGUUUUU	ZTrucl
2 W10279	aggAuuaacaaCugururuu	6LZ0TW
3 W10274	aggAnuaacaacUgUUUCUU	W10274
4 W10Z72	aggAuuaacaacUgUUUU	W10272
5 W10Z10	aggAuuaacaacUgUUUUU	W10Z10
6 ZBBSR7	aggduuggcacAcdUUUU	ZBBSR7
7 ZBBSR17	3 aggAnuagcgAUUAUUUU	ZBBSR173
8 Siphcya	n aggAnuagcgAAUGUUAU	Siphevan
9 ZBBSR2	aggdduuggcaaAudtruuAu	ZBESR2
0 ZCR4	aggdduagcaAAUGUUAU	ZCR4
1 ZCR16	aGguduggcaAAUGUUAA	2CR16
2 ZCR6A	aggdauuagcgAaUdUdua	2CR6A
З РНУРОЦУ	c aggdAuAggacAdUoUccA	рнурогус
4 NAEGRUB	E gagtAuuugggaagaCACUAUC	NAFGRURE
5 euk hel	1 34	euk heli
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		557

SYMPILO1 ZBBSR205 siphcyan STYALSID ZBBSR235 ZBBSR218 EUGROTUN ENTOGING DICDISCO ZBBSR173 NAEGRUBE VIELEIDY DIAGRAND ATHBOMBA BLAEMERS THLREINH DRYSATIV PORAERUG PHRBALAM EMIHUXLE OCHDANIC CAFROENB TUNIMER OXYGRANU BLEAMERI HARVERMI THEANNUL ZBBSR206 ZBBSR217 ZBBSR211 DALOUYC euk heli ACACAST1 Pchroma W10Z72 W10Z10 W10Z79 W10Z74 ZBBSR7 ZBBSR2 Thucl ZCR16 **ZCR6A** 2CR4 rad ------UCAUacgaCUccuucagCACc-uUAUgaQAAAucA--AAguCUUUGgguUccgGggGggaguAuggucGCAAggcugAAacuuAAaggaAUU AAAUGAAAAAC-AAUACuuuauucagAAcu-uGAAgaGAAAucU-UGAguGUAUGaacUucaGggGggggggguAuggucACAAggcugAAacuuAAAGGAAUU -----AUGACAuuguuggCAcc-uUGUgaGAAAuuA--GAguuCUCAgauUcCgGggGgaguAuggUuGCAAgUcugAAacuuAAaggaAUU ----------AAAACAVuguuagAAcc-uAAAgaGAAAucA--AAguAUVGgauVoCGGggGggguAugguuGCAAggcugAAacuuAAaggaAVV --------ANUGUguuguucggCAcc-uUACgaGAAAucA--AAgucUUGgguUcugGggggggaguAuggucGCAAggcugAAacuuAAaggaAUU -----AAAGACgcgcccggCAcc-uUUVgaGAAAucA--AAguuUUVGgguUcugGggGgaguAuggucGCAAggcugAAacuuAAaggaAuV ------Adu-AaguaucggCAcc-cUAAgaGAAAucA--AAguCUUUGgguUcugGggGgggGgagCAuggucGCAAggcugAAAcuuAAaggaAUU ---------AUVgACuccaucagCAcc-uUAVgaGAAAucA--AAgucVUVGgguUcCgGgggggggguAuggucGCAAggcugAAacuuAAagaaAVU -----ACAggugugucagCAcu-gUAUgaÀÀÀAucÀ--ÀAgucUUGgguUcCgGgggggaguAuggucGCÀÀggcugAAacuuÀAggaAAU ------UAUgACUccgccagCAcc-uCAUgaGAAAucA--AAgucUUUGgguUcCgGgggggaguAuggucGCAAggcugAAacuuAAaggaAUU -----AUCcgccuucggCAcc-uVAUgaGAAAucA--AAgucUVUGgguUcugGggGgaguAuggucGCAAggcugAAacuuAAaggaAAU -----AAGUAcUccuucagCAuc-uUCCgaGAAAucA--AAgucUUUGgguUcugGggGgaguAuggucGCAAgacugAAacuuAAaggaAuU ------UGACucCccgggCAcc-uUGUgaGAAAucA-UAAguGUUUGgguUuugGggGgaguAuggucGCAAggcugAAacuuAAaggaAUU ------buvVacgacucCuucagCACc-uVGAgaGAAAucA--AAgucVVVGgguVcugGgggggggugudgucGCAAggcugAAacuuAAaggaAVV ------GUUCgacuccuucggCAcc-uUAUgaGAAAucA--AAgcAUUUGgguUccgGgggggguAuggucGCAAggcugAaacuuAaggaAUU -----VGUUC9acuccuuc99CAcc-uVAU9aGAAAucA--AAgcAVUUG9guUcC9G9gGgaguAuggucGCAAggcugAaauvAaggaAUU ------CAUACgucucuuucagCAcc-uUAUgaGAAAucA--AAgcAUUUGgguUcCGGGggGggguAuggucGCAAggcugAAacuuAAaggaAUU -----CAUACgucucuuucagCAcc-uUAUgaGAAAucA--AAgcAUUUGgguUcCgGggggggguguAuggucGCAAggcugAAacuuAAaggaAUU -----CUUGACuccaugggCAcu-cUAUgaGAAAucA--AAgucVUUGgguUcCgGggggggguduggucGCAAggcugAAacuuAAaggaAUU ---------CaAAAuuuaaucggCAcc-uUGUgaGAAAucA-UGAguGUUUAgauUccgGggggggguduggUcGCAAgUcugAAacuuAAaggaAUU -------AUGACAuuguuggCAcc-uUGUgaGAAAuuA--GAguuCUCAgauUcCgGgggggggguAuggUuGCAAgUcugAAacuuAAaggaAUU ------VGACAuuguuggCAcc-uUGUgaGAAAuuA--GAguuCUCAgauUcCg6ggGgaguAuggUuGCAAgUcugAAacuuAAaggaAUU -----AUGACAuuguuggCAcc-uUGUgaGAAAuuA--GAguuCUCAgauUcCgGgggggggguguuggUuGCAAgUcugAAacuuAAaggaAUU ---------UGACUUugucagAAcc-uUAUgaGAAAucA--AAgCGUUUGgguUccgGggggggguAuggucGCAAggcugAAacuuAAaggaAUU ----AUGACUUuguuagAAcc-uUAUgaGAAAucA--AAgcGUUUGgguUcCgGgggggguauggucGCAAggcugAAacuuAAaggaAUU ---------AUGCCAVuguuagAAcc-uUV0gaGAAAucA--CAgcGUUV0gguUcCgGggggaaguAugguuGCAAggcuaAAacuuAAAggaAUV -----AUGUCUUNGUCAGAAcA-UUGAGAGAAAuuA--AAgcAUUUGgauUcCGGGGGGGGgGgaguAugguuGCAAggcugAAacuuAAaggaAUU ---------UAUACU-uguuagAAcc-uCAAgaQAAucA-AGAguAVCUGgauUcCGGggGgaguAuUgucGCAAggcUgAAacuuAAaggaAUU -------CCAGCCAucuucucagaAcu-cAA-ggGAAAcc-UVAAguCUVVGggUUcugGggGgaguAuAgucGCAAgacCgAAacuuAAaggaAVV -----AddrocoucoucogCAcg-cUAUgaGAAAucA--AAgacUUC6gguUcCg6gggggggguucGCAAgaaugAAacuuAAaggaAUU ------UVAGCcgcaucggCAcc-gUAUgaGAAAucA--AAguuUUUGgguUcugGggGgaguAuggucGCAAggcugAAacuuAaggaAUU ------GAUGAcucugccagCAcc-uUAUgaGAAAucA--AAguuUUGgguUcCgGgggggggguaugucGCAAggcugAAacuuAAaggaAUU ----------DÅGAcuccgcCAcc-uUAUgaGAAAucA--AAgucUUUGguUcCgGggGgaguAuggucGCAAggcugAAacuuAAaggaA ----------CU9acuccaucagCAcc-cUAUgaGAAAucA--AaguGUUUGgguUcugGggGgaguAuggucGCAAggcugAacuuAAaggaAUU guggcAcCGGGGAANGACucCccuagCAgc-uUGUgaGAAAucA-UAAgucUUUGgguUcCGGggggggguAuggucGCAAgggcugAAacuuAAaggaAUU ------GCGUGGcucCuccggCACcuUUGAgaGAAAucAUUGAGUGUCuGggcUUcgGggggggguAuggucGCAAgggcugAaacuuAAaggaAUU --------UGUGACuccuucagCAcc-uUUCggGAAAcuA--AAgucUUUGgguUccGGgggGggguaucGCAAggcugAAacuuAAaggaAUU 36 ----^----36 24 ---u u ŝ î -----34 -----Sept4aln" on 5-SEP-96 15:33:41 Data: 1369mask identity: MNELEIDY DIAGRAND ATHBOMBA BLAEMERS CHLREINH PORAERUG STYALSID EUGROTUN ENTOGING DICDISCO ZBBSR173 Siphcyan PHYPOLYC ORÝSATIV ACACAST1 PHRBALAM EMIHUXLE OCHDANIC CAFROENB LABMINUT OXYGRANU BLEAMERI HARVERMI THEANNUL **SYMPILO1** ZBBSR205 ZBBSR206 ZBBSR235 ZBBSR218 ZBBSR217 ZBBSR211 NAEGRUBE euk heli Sequence Pchroma W10279 **ZTnucl** W10274 W10272 W10210 ZBBSR7 ZBBSR2 ZCR16 **ZCR6A** ZCR4 rad ч œ 2 ទា ഹ თ 5 ñ 2 41 16 5 13 8 5 22 2 24 25 26 5 28 59 õ 31 32 33 34 36 37 38 66 40 41 2 ÷ 5 46 Position: 2112 2112 2112 2112 2112 2112 2112 2112 2112 2112 2112 2112 2112

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 ZBBSR2106 GacGggagggeacCACAa - ggaguGGagccuguggeUUXAuuugACUCAACagggAAAACUUAccaggUCCGGAcauagUAAGAUUgacGgauuGAAa ZBBSR2118 GacGggagggeacCACACa - ggaguGGagccuguggeUUXAuuugAUUCAACaGggFAAAACUUAccaggUCCGGAcauagUAGGAUUGAAA ZBBSR2118 GacGggagggeacCACACCa - ggaguGGagccugggeGUUXAuuugAUUCAACAGggFAAAACUUAccaggUCCGGAcauagUAGGAUUGAAC ZBBSR2118 GacGggagggeacCAACCA - ggaguGGagccuggeGUUXAuuugAUUCAACAGggFAAAACUUAccaggUCCGGAcauagUAGGAUUGAAC ZBBSR211 GacGggagggeaCCAACCA - ggaguGGagccuggeGUUXAuuugAUUCAACAGggFAAACUUAccaggUCCGGAcauagUAGGAUUGAAC ZBBSR211 GacGggagggeaCCAACA - ggaguGGagccuggeGUUXAuuugAUUCAACAGggGAAACUUAccaggUCCGGAcauagUAGGAUUGAAC ZBBSR211 GacGggagggeaCCAACA - ggaguGGagCUUAAuuugACUCAACAGggAAAACUUAccaggUCCGGAcauagUAAGGAUUgaCagauuGAAg EURROTW GacGgaagggcaCCACAC - ggaguGGagCUUAAuuugACUCAACAGgggAAAACUUAccaggUCCGAAcauagUAAGGAUUgaCagauuGAAg EURROTW GacGgaagggcaCCACAC - gfuguGGauAcuguggCUUAAuuugACUCAACCGgggAAAACUUAccaagUCAGAacauaUUAAGAUUgaCagauuGAAg ENTOGTIG GacGgaagggcaCCACAA - gfuguGGauAcuguggGUUAAuuUgAACUCAACCGgggAAAACUUAccaagUCAGAAcauaUUAAGAUUgaCagauuGAAG ETTNUCI GacGgaagggcaCCACAA - gfuguGGauAcuguggGUUAAuuUgAACUCAACCGgggAAAACUUAccaagCUCAGAcauaUUAAGAUUgaCagauuGAAG M10271 GacGgaagggcaCCACAA - gfuguGGauAcuuguggCUUAAuuUgAACUCAACCGGGGACauaggGUCCAAAcauaUUAAGAUUGAACAGACUGAUA M10272 GacGgaagggcaCCACAA - gfuguGGGauAcuuguggCUUAAuuUgAACUCAACCGGGGACACAAcauaUUAAGAUUgaCagaUUAAUA M10271 GacGgaagggcaCCACAA - gfuguGGGauAcuuguggCUUAAuuugAACUCAACCGGGGAACauagGUCCAAAcauagUUAAUA M10272 GacGgaagggcaCCACAA - gfuguGGGauAcuugaggCUUAAuuugACUCAACCGGGGGAACauaggUCAGAACagAUUAAUA M10273 GacGgaagggcaCCACAA - gfuguGGGUUCAAuuugAQCUCAACCGGGGGGGGAACAACAACGGGAUGAUA GacGgaagggcaCCACAA - gfuguGGGUUAAuuugGGUUAAuuugACUCAACCGGAAcauag	 ZIBSRZ206 Gac6ggagggcaCCACCa-ggaguGGagccuguggcUUAAuuugAUCAACAcgggAAAACUUAccaggUCCGGAcauagUAAGGAUUgaC ZIBSRZ218 Gac6ggagggcaCCACCa-ggaguGGagccuguggcUUAAuuugAUUCAACAcgggAAAACUUAccaggUCCGGAcauggGAAGGAUUgaC ZIBSRZ11 Gac6ggagggcaCCACCa-ggaguGGagccugcggcUUAAuuugAUUCAACAcgggAAAACUUAccaggUCCGGAcauggGAAGGAUUgaC ZIBSRZ11 Gac6ggagggcaCCACCa-ggaguGGagccugcggcUUAAuuugAUUCAACAcgggAAAACUUAccaggUCCGGAcauggGAAGGAUUgaC ZIBSRZ11 Gac6ggagggcaCCACCa-ggaguGGagccugcgggUUAAuuugAUUCAACAcgggAAAACUUAccaggUCCGGAcauggGAAGGAUUgaC ZIBSRZ11 Gac6ggagggcaCCACCa-ggaguGGagccugcgggUUAAuuugAUUCAACAcgggAAAACUUAccaggUCCGGAcauggGAAGGAUUgaC ZIBSRZ11 Gac6ggaagggcaCCACCa-ggaguGGagcCugcgggUUAAuuugACUCAACAcgggAAAACUUAccaggUCCGGAcauagUAAGGAUUgaC ZIPCDISC0 Gac6gaagggcaCCACCa-ggaguGGagCUUAAuuugACUCAACAcgggAAAACUUAccaggUCCGAAcauaAgaAGGAAUgaC ZINOC1 Gac6gaagggcaCCACCa-ggaguGGagCUUAAuuugACUCAACACGgggAAAACUUAccaggUCAGAcauaAgaAGGAAUgaC ZITNeL Gac6gaagggcaCCACCA-gUuguGGauAcuguggCUUAAuuUgACUCAACACGgggAAAACUUAccaggUCAGAcauaAgaAGGAUUgaC ZITNeL Gac6gaagggcaCCACAa-gUuguGGauAcuguggCUUAAuuUgACUCAACACUggAAAACUUAccaggUCAGAcauaAgaAGGAUUgaC M10274 Gac6gaagggcaCCACAa-gUuguGGauAcuguggCUUAAuuUgACUCAACACUggAAAACUUAccaggUCAGAAcauagGUAGGAUUgaC M10274 Gac6gaagggcaCCACAa-gUuguGGauAcuguggCUUAAuuUgACUCAACACUggAAAACUUAccaggUAAGAAuuagGUAGGAUUgaC M10274 Gac6gaagggcaCCACAA-gUuguGGauAcuguggCUUAAuuUgACUCAACACUggAAAACUUAccaggUAAAAcauaagCUAGGAUUgaC M10274 Gac6gaagggcaCCACAA-gUuguGGaUAcuguggCUUAAUAACACUggAAAACUUAccaggUAAAGAAuuagGUAAGAAUUgaC M10274 Gac6gaagggcaCACAA-gUuguGGaUAcuguggCUUAAUAACACUggAAAACUUAccaggUAAACUAAcaauagCUAGAAuuaggUAAGAAUUgaC M10274 Gac6gaagggcaCACAA-gUuguGGaUAcuguggCUUAAUAACACCUggAAAACUUAccaggUAAAACUAAcaAGAAUAAAAUAA Gac6gaagggcaCCACAA-gUuguGGaUAcuuuUgACUCAAACACUggAAAACUUAccaggUAAAAAAuuagGAAUgaC 	1 ZBBSR205	GacGgggggggcaCCACCa-ggaguGGagccuguggcUVAAuuugACUCAACAcgggAAAACUUAccaggUCCGGAcauagUAAGGAUUgaCagauuGAAa	ZBBSR205
 ZBSR715 GacGgsaggcaccAACa -ggsguGGagccugrageUUAAuuugAUUCAACAcgggAAAACUUA.ccasgUCCGGAcauggGAAGGAUUGAAG ZBSR715 GacGgsagggcacCAACCa -ggsguGGagccugrageUUAAuuugAUUCAACAcgggAAAACUUA.ccasgUCCGGAcauggGAAGGAUUGAAG ZBSR711 GacGgsagggraggcacCAACCa -ggsguGGagccugrageUUAAuuugAUUCAACAcgggAAAACUUA.ccasgUCCGGAcauggGAAGGAUUGAAG ZBSR711 GacGgsagggraggcaCCAACCa -ggsguGGagccugrageUUAAuuugAUUCAACAcgggAAAACUUA.ccasgUCCGGAcauagGGAAGGAUUGAAG ZBSR711 GacGgsagggraggcaCCACCA -ggsguGGagCUUAAuuugACUCAACAcgggAAAACUUA.ccasgUCCGGAcauagGGAAGGAUUGAAG ZBSR711 GacGgsagggragCCACCA-ggsguGGagCUUAAuuUgACUCAACAcgggAAAACUUA.ccasgUCCGAAcauagGGAAGGAUUGAAG ZBNOGTNG GacGgaagggragCCACCA-ggsguGGagCUUAAuuUgACUCAACACGgggAAAACUUA.ccasgUCCGAAcauaagGUAGGAUUGAGGAUUGAAG ZTMUCI GacGgaagggragCCACCA-gUUGGGaUACUUGGAUACUUGACCGGGAACAUAAUAAGGAUUGAGGAUUGAAG ZTMUCI GacGgaagggragCCACAA-gUUUGGAUACUUGACCUGGGGCUUAAUUUGACUUA.ccasgUCCGAAcauaagGUAGGAUUGAGGAUUAAUA M10774 GacGgaagggragCCCACA-gUUUGGAUACUUGGAUACUUA.cCUGGAAcauaagGUAGGAUUGGAGUUAAUUA M10774 GacGgaagggragCCCACA-gUUUGGAUACUUGACCACCUGGGAAAUAUUUAACGACUUAACAGGAUUGACGAGAUUAUA M10774 GacGgaagggragCCCACA-gUUUGGAUACUUGACCAACACUGGGAAACAUAAUUUGACGACUUAUA M10774 GacGgaagggragCCCACA-gUUUGGAUACUUGACCAACACUGGGAAAAUAUUGACGAACAUAAUAUUAGAUUGACUCAACAA-GUUUGGAUUCUGAACUUAACAGGACGAACAUAAUUAU M10774 GacGgaagggragCCCACA-gUUUGGAUACUUGGAUACUUAACACCUGGGAACAUAAGCAUAGGAUUGGAUUAUUA M10773 GacGgaaggggragCCACAA-gUUUGGAUUCUUGACACACUGGAAACAUAAGCUUAACAACAUAAGAUUGGAUUAUUA M10779 GacGgaaggggragCCACAA-gUUUGGAUUCUUAUCACACUGGGAAACUUA.ccagGUCCAACAAUAAGUUAGGAUUGAUUAUUA ZZBSR77 GacGgaaggggragCCACAA-gUUUGGAUUCUUAACAACUUAACAGGAACAAUAAGCUUAACAAUAUUACUAUUA ZZBSR77 GacGgaaggggragGCCACAA-gUUUGGAUUCUUAUUUGACUCAACACUGGGAAGGGAUAGGAUUAUUA ZZBSR77 GacGgaaggggaCCACAA-gUUUGGAUUCUUAUUGACUUAACACUUAACAAUAAUUUA	 ZEBSTR15 Gac099499745CACCA-998406495 cu99495 cU7AAuuu9AUUCAACA c9995AAACUUA cc399705060 cau39704054 ZEBSTR218 Gac099499745 CACCA-998406495 cu9595 cU7AAuuu9AUUCAACA c9995AAACUUA cc399705 co50 cu39595A66AUU954 ZEBSTR211 Gac09949995 CACCACA-998406495 cu9595 cU7AAuuu9AUUCAACA c9995AAACUUA cc399705 co50 cu39595A66AUU954 ZEBSTR211 Gac09949995 CACCACA-998406495 cu9595 cU7AAuuu9AUUCAACA c9995AAACUUA cc399705 co50 cu397636AUU954 ZEBSTR211 Gac09949995 CACCACA-998406495 cu9595 cU7AAuuu9AUUCAACA c9995AAACUUA cc399705 co50 cu397636AUU954 Perbroma Gac09849995 caCACACA-998406495 cu9595 cU7AAAUU95 co5995AAACUUA cc399705 co50 cu397636AUU954 ZED07110 Gac09849995 caCACACA-997401668 cu3 cu9595 cU7AAAUU95 co5995AAACUUA cc399705 co50 cau39703 co59849995 caCACAA-99704068 cu39595 cu50 cu30595 cu50 cu39595 cu50 cu39505 cu50 cu3950 cu50 cu39505 cu50 cu39595 cu50 cu39595 cu50 cu39595 cu50 cu39595 cu50 cu39595 cu50 cu39595 cu50 cu39505 cu50 cu39505 cu50 cu39505 cu50 cu39505 cu50 cu39595 cu50 cu39595 cu50 cu39595 cu50 cu39595 cu50 cu39595 cu50 cu39505 cu50 cu39505 cu50 cu39595 cu50 cu39505 cu50 cu39595 cu50 cu39595 cu50 cu39595 cu50 c	2 ZBBSR206	GacGggagggcaCCACCa-ggaguGGagccuguggcUVAAuuugACUCAACAcgggAAAACUVAccaggUCCGGAcauagUAAGGAUUgaCagauuGAAa	ZBBSR206
 4 ZBSK718 GacGgaaggcacCAACa -ggaguGdagccugrggUUAAkuugAUUCAACAcgggAAAACUUA.ccaggUCCGGAcauggGAAGGAUUGACagauuGAAA ZBSSR217 5 ZBSSR211 GacGgaagggcaCCAACCa -ggaguGdagccugGaggCUVAAkuugAUUCAACAcgggAAAACUUA.ccaggUCCGGAcauggGAAGGAUUGACAgauuGAAA ZBSSR211 5 ZBSSR211 GacGgaaggggcaCCAACCa -ggaguGdagccugGaggCUVAAkuugAUUCAACAcgggAAAACUUA.ccaggUCAGGAcuugGGAAGAUUGACAgauuGAAG Pehroma BUGACUM 7 PChroma GacGgaaggggcaCCAACCa -ggaguGdagccugGaggCUVAAkuugAUUCAACAcgggAAAACUUA.ccaggUCAGGAcuugGGAAGUUGACGaguuGAAG Pehroma BUGACUM 8 ENNOGSING GacGgaagggcaCCAACCa -ggaguGGagCUUAAkuugACUCAACAcgggAAAACUUA.ccaggUCAGGAcuugGAAGGAUUgaCagauuAAAg Pehroma GacGgaaggggca-CAACAa-gguguGGaaAcuugGAagCUUAAkuugACUCAACACGggAAAACUUA.ccaggUCAGGACUUGACGAGauuGAAG GAGUGAGGAUUGACAgauuAAUA M 2071 9 ENNOGSING GacGgaaggggcaCCACAa -gUuguGGauAcuugGAQCUCAACACGggAAAACUUA.ccagGUCAGACauugUAAGGAUUGACGggaugggcaCGACAA -gUuguGGauAcuugGAQCUCAACACGGggAAAACUUA.ccagGUCAGACauugUAAGGAUUGACGAGauAUUAUA M 10273 9 M10271 GacGgaaggggcaCCACAA -gUuguGGauAcuugGAQCUCAACACACGggAAAACUUA.ccagGUCCAGACauugGAAGGAUUGACUGACAA-gUUGUGGauAcuugGGAUACUCAACACUGGGAAAGGUCAAACACUGGGAAAGGGAUUGACUCAACAA-gUUGUGGauAcuugGGGUAAUUGACUCAACACUGGGAAAGGUCAAAACUUA.ccagGUCCAAAA-gUUUGGAUAcuUGAACUCAACACACGGGAAAGGUCUAACAA-gUUUGGAUAcuUGAACUCAACACUGGGAAAGGUCUAACAA-gUUUGGAUACUUGAACUUGAACUCAACACUGGGAAAGGGAUUGAUAU M 10270 10072 GacGgaaagggcaCCACAA -gUUUGGauAcuugggCUUAAkuUGACUCAACACACGGGAAAGGUCUAACAA-gUUUGGAUUCUGAACACUGGGAAGGGGCCAAA -gUUUGGAUUCUUGACCUCAACACACGGGAAAGGUCUAACAA-gUUUGGAUUCUUGACUCAACACACGGGAAAGGUCAACAACAGUGAUCGAACAAACA	 ZEBSRIB RecGgaagggracCACCa-ggagucGagccug cgcrUthAuuugAUUCAACAcggggAAAACUUA.ccaggUCCGGA.cauggGAAGGAUUgaC ZEBSRIS RecGgaaggggracCACCCa-ggagucGagccug cggcrUthAuuugAUUCAACAcggggAAAACUUA.ccaggUCCGGA.cauggGAAGGAUUgaC ZEBSRIS RecGgaaggggaGCCACCA-ggagucGagccug cggcrUthAuuugAUUCAACAcggggAAAACUUA.ccaggUCCGGA.cauggGAAGGAUUgaC RecGgaaggggaGCCACCA-ggagucGagccug cggcrUthAuuugACUCAACAcggggAAAACUUA.ccaggUCCGGA.cauggGAAGGAUUgaC RecGgaaggggaGCCACCA-ggagucGagccug cggcrUthAuuugACUCAACA.ccggggAAAACUUA.ccaggUCCGGA.cauggGAAGGAUUgaC Renoma RecGgaaggggaCCCACCA-ggagucGagcCug cggcrUthAuuugACUCAACA.ccggggAAAACUUA.ccaggUCCGGA.cauggGAAGGAUUgaC Renoma RecGgaaggggaCCCACAa-gUuguGGauAcuguggCUUAAuuUgACUCCAACA.cCggggAAAACUUA.ccaggUCCCGAA.cauagUGAGGAUUgaC RecGgaaggggaCCCACAa-gUuguGGauAcuguuggCUUAAuuUgACUCCAACA.cCggggAAAACUUA.ccagGUCCAGA.cauagUGAGGAUUgaC RecGgaaggggaCCCACAa-gUuguGGauA.cuguuggCUUAAuuUgACUCCAACA.cCggggAAAACUUA.ccagGUCCAGA.cauagUGAGGAUUgaC RecGgaaggggaCCCACAa-gUuguGGauA.cuguuggCUUAAuuUgACUCCAACA.cCugggAAAACUUA.ccagGUCCAGA.cauagUGAGUUAGAUUUgACCCAACA.cUgggAAAACUUA.ccagGUCCAGA.cauagUGAGUUAU RecGgaaggggaCCCACAa-gUuguGGauA.cuguuggCUUAAuuUgACUCCAACA.cUggAAAACUUA.ccagGUCCAGA.cauagGUAGAUUgaC Ru10271 RacGgaaggggaCCCACAa-gUuguGGauU.cuguuggCUUAAuuUgACUCCAACA.cUggAAAACUUA.ccagGUCCAGA.cauagGUAGAUUgaC Ru10271 RacGgaaggggaCCCACAa-gUuguGGauU.cuguuggCUUAAuuUgACUCCAACA.cUggAAAACUUA.ccagGUCCAGA.cauagGUAGAUUgaC RacGgaaggggaCCCACAa-gUuuGGaUU.cuguuggCUUAAuuUgACUCCAACA.cUggAAAACUUA.ccagGUCCAGA.cauaggUAGAUUgaC RacGgaaggggaCCCACAa-gUuuGGaUU.cuguuggCUUAAuuUgACUCCAACA.cUggGAAAACUUA.ccagGUCCAGA.cauaggUAGAUUgaC RacGgaaggggaCCCACAA-gUuuuGGaUU.cuguuggCUUAAuuUgACUCAACA.cUggAAAACUUA.ccagGUCCAGA.cauaggUAGAUUGAU RacGgaagggaCaCCACAA-gUuuuGGaUu.cuguuggCUU	3 ZBBSR235	GacGggagggcaCCACCa-ggaguGGagccuguggcUVAuuugACUCAACAcggrAAACUVAccaggUCCGGAcauagVAGGAUUgaCagauuGAAa	ZBBSR235
 BESK111 GacGggaaggeacCAACa-ggaguGGagccugcggcUDAAuuugAUUCAACAcgggAAAACUUAccaggUCCGGAcauggGAAGGAUUgaCagauuGAAa ZBBSR211 ZEBSR211 GacGggaaggeacCAACa-ggaguGGagccugcggcUDAAuuugAUUCAACAcgggAAAACUUAccaggUCAGGAUUgaCagauuGAag ZBBSR211 ZEDSR211 GacGggaagggeacCAACa-ggaguGGagccugcggcUDAAuuugAUUCAACAcgggAAAACUUAccaggUCAGGAUUgaCagauuGAag ZUGROTUN ZEDSR211 GacGgaagggeacCAACa-ggaguGGagcCugcggcUDAAuuugAUUCAACAcgggAAAACUUAccaggUCAGGAUUgaCagauuGAag ZUGROTUN BENTOOING GacGgaagggeacCAACa-ggaguGGagcCugcggcUDAAuuugACUCAACAcgggAAAACUUAccaggUCAGAcauagUGAGAUUgaCagauuAAg ZNTOCING BENTOOING GacGgaagggeacCAACa-gUugGGaucugGagcUDAAuuUgACUCAACAcgggAAAACUUAccaggUCAGAcauagUGAGAUUgaCagauuAAg ZNTOCING BENTOOING GacGgaagggeacCAACa-gUuguGGauAcuguggcUDAAuuUgACUCAACAcgggAAAACUUAccaggUCCGAAcauagUGAGAUUgacagauuAAU M10270 ZM10279 GacGgaaggggacCCACAa-gUuguGGauAcuguggcUDAAuuUgACUCAACAcUggAAAACUUAccaggUCCGAAcauagUUAGGAUUgacagAUUAAU M10270 M10279 GacGgaaggggacCCACAa-gUuguGGauAcuguggcUDAAuuUgACUCAACACUggAAAACUUAccaggUCCGAAcauagUUAGAUUgacagAUUAAU M10270 M10279 GacGgaaggggacCCACAa-gUuguGGauAcuguggcUDAAuuUgACUCAACACUggAAAACUUAccaggUCCGAAcauagUUAGAUUgacagAUUAAU M10270 M10279 GacGgaaggggacCCACAa-gUuguGGauAcuguggcUDAAuuUgACUCAACACUggAAACUUAccaggUCCGAAcauagUUAAU M10270 M10279 GacGgaagggggacCCACAA-guuguGGaUU-uuugggCUDAAuuUgACUCAACACUggAAACUUAccaggUCCGAAcauagUUAAU M10270 GacGgaaggggacCCACAA-guuguGGGUU-cuguuggcUDAAuuUgACUCAACACUggAAACUUAccaggUCCGAAcauaggUAGAUUGAAUUGAAUUGAAUUGAAUUGAAUGAAUGAAU	 ZBBSR211 GacGgaagggcacCACCa-ggagudGagccugcggcUUTANuugAUUCAACAcgggAAAACUUAccaggUCCGGAcauggGAAGGAUUgaC ZBBSR211 GacGggaagggcacCACCa-ggagudGagccugcggcUUTANuugAUUCAACAcggggAAAACUUAccaggUCCGGAcauggGAAGGAUUgaC Fehroma GacGgaagggcacCACCa-ggagudGagccugcggcUUTANuuugAUUCAACAcggggAAAACUUAccaggUCCGGAcauagUGAGGAUUgaC BENTODING GacGgaagggcacCACCa-ggagudGagccugcggcUUTANuuugAUUCAACAcggggAAAACUUAccaagGUCCGGAcauagUGAGGAUUgaC BEUGROTUN GacGgaagggcacCACCa-ggagudGagccugcggcUUTANuuugACUCAACAcggggAAAACUUAccaagGUCCGGAcauagUGAGGAUUgaC DICDISCO GacGgaagggcacCACCa-gguguGGauAcuguggCUUANuuugACUCAACAcGggggAAAACUUAccaagGUCCGGAcauaAgUAGGAUUgaC M10219 GacGgaagggcacCACCa-gUuguGGauAcuguggCUUAAuuUgACUCAACAcUgggAAAACUUAccaagGUCCAGAcauaAUUUAGGAUUgaC M10219 GacGgaaggggcacCACCAa-gUuguGGauAcuguggCUUAAuuUgACUCCAACAcUgggAAAACUUAccaagGUCCAGAcauaGUUAGGAUUgaC M10219 GacGgaaggggcacCACAa-gUuguGGauAcuguggCUUAAuuUgACUCCAACAcUgggAAAACUUAccaagGUCCAGAcauagUAGGAUUgaC M10219 GacGgaaggggcacCACAa-gUuguGGauAcuguggCUUAAuuUgACUCCAACAcUgggAAAACUUAccaagGUCCAGAcauagGUAGGAUUgaC M10210 GacGgaaggggcacCACAa-gguuGGaUcuguggCUUAAuuUgACUCCAACAcUgggAAAACUUAccaagGUCCCAGAcauagGUAGGAUUgaC M10212 GacGgaaggggcacCACAa-gguuGGaUcuguggCUUAAuuUgACUCCAACAcUGggAAAACUUAccaagGUCCCAGAcauagGUAGGAUUgaC M10213 GacGgaaggggcacCACAa-gguuGGaUcuguggCUUAAuuUgACUCCAACAcUGggAAAACUUAccaagGUCCCAGAcauagGUAGGAUUgaC M10213 GacGgaaggggcacCACAa-gguuGGaUcuguggCUUAAuuUgACUCCAACAcCGgggAAAACUUAccaagGUCCCAGAcauagGUAGGAUUgaC M10213 GacGgaaggggcacCACAa-gguuGGaUcuguggCUAAuuUgACUCCAACAcACGgggAAAACUUAccaagGUCCCAGAcauagGUAGGAUUgaC M10213 GacGgaaggggcacCACAa-gguuGGaUcuguggCUAAuuUgACUCCAACAcACGgggAAAACUUAccaagGUCCCAGAcauaggUAGGAUUgaC M10213 GacGgaaggggcacCACAa-gguuGGaUcuguggCUAAuuUgACCAACACACGGggAAAACUUAccaagGUCCCAGAcauaggUAGGAUCUGACCAA-GAUGGGGCCAACA-GAGGGAAgggGCCCACAA-gguuGGGGCUCAAA-ACACGGggGGGGCCACAA-gguuGGG	4 ZBBSR218	GacGsgagggcaCCACCa-ggaguGGagccugcggcUUAAuuugAUUCAACAcgggAAAACUUAccaggUCCGGAcauggGAAGGAUUgaCagauuGAAa	ZBBSR218
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 M10774 GecGgaagggcacCACAA-gbugudGauAcueguggCUTAAuUUGACCAACACUGggAAAACUUAAccagGuCCAAACAUAUUAGGAUUAGUAMAUA M10272 GacGgaagggcacCACAA-gbugudGauAcueguggCUTAAuUUGACUCAACACUGggAAAACUUAccagGUCCAACAACAUAUUAGGAUUAGCAACUUAAUA M10272 GacGgaagggcacCACAA-gbugudGauAcueguggCUTAAuUUGACUCAACACUGggAAAACUUAccagGUCCAGAAcauagGUUAAUA M10272 GacGgaaggggcacCACAA-gguudGauAcueguggCUTAAuUUGACUCAACACUGggAAAACUUAccagGUCCAGAAcauagGUUAGAUUAUA M10270 GacGgaaggggcacCACAA-gguudGauAcueguggCUTAAuUUGACUCAACACUGgAAAACUUAccagGUCCAGAAcauaggUAGGAUUAUA M10270 GacGgaaggggcacCACAA-gguudGaUucuguggCUTAAuUUGACUCAACACUGgAAAACUUAccagGUCCAGAacauaggUAGGAUUAUA M10270 GacGgaaggggcacCACAA-gguudGaUucuguggCUTAAuuUGAACACUGgAAAACUUAccagGUCCAGAacauaggUAGGAUUAUA M10270 GacGgaaggggcaCCACAA-gguuGGaUucuguggCUTAAuuUGAACACUGgAAAACUUAccaGGUCCAGAacauaggGUAGGAUUGAUA ZBBSR2 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUTAAuuUGAACUCAACAUGgAAAACUUAccaGGUCCAGAacauaggUAGGAUUGAUA ZBBSR2 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUTAAuuUGAACUCAACAUGgAAAACUUAccacgGUCCAGAacauaggUAGGAUUGAUU ZBBSR2 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUTAAuuUGAACUCAACAUGgAAAACUUAccacgGUCCAGAacauagGUAGAUUGAUUAGUA ZBBSR2 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUTAAuuUGAACACUGgAAAACUUAccacgGUCCAGAacauagGUAGAUUGAUUAAU ZCR6 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUTAAuuUGAACACGggAAAACUUAccacgGUCCAGAAcauagGUAGAUUGAUUAGUAGUAA ZCR6 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUTAAuuUGAACUCAACACGggAAAACUUAccacagGUCCAGAAcauagUAGAUUUGAUUCAUCAACACGGGAAACCAACACGGGGUCCAGAAcauagUAGAUUGAUUA ZCR6 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUTAAuuUGAACUCAACACAGGgAAAACUCAACAGGGGUCCAGAAcauagUAAUA ZCR6 GacGgaagggcaCCACAA-gauguGGaUucuguggCUTAAuuUGAACUCAACACGGGAAACAACUCAACAGGGGAAGCAAAGGAUUGAUU	 M10274 GacGgaagggcacCACAA-gruguGGauAcuguggCUDAAuUGgACCAACACUGggAAACUUAccagGUCAAAACUGAC M10272 GacGgaagggcacCACAA-gruguGGauAcuguuggCUDAAuUGgACUCAACACUGggAAAACUUAccagGUCCAGAcauagCUAGGAUUgac M10272 GacGgaaggggcacCACAA-gruguGGauAcuguuggCUDAAuUGgACUCAACACUGggAAAACUUAccagGUCCAGAcauagCUAGGAUUgac M10273 GacGgaaggggcacCACAA-gruguGGauAcuguuggCUDAAuUGgACUCAACACUGggAAAACUUAccagGUCCAGAcauagCUAGGAUUgac ZBBSR73 GacGgaaggggcacCACAA-gruguGGaUccuguuggCUDAAuUUGAACACUGggGAAAACUUAccagGUCCAGAcauagCUAGGAUUgac ZBBSR73 GacGgaaggggcacCACAA-gguuGGaUucuguugGCUUAAuuUgACUCAACACUGgGAAAACUUAccagGUCCAGAcauaggUAGGAUUgac ZBBSR173 GacGgaaggggcacCACAA-gguuGGaUucuguugGCUUAAuuUgACUCAACAcagggAAAACUUAaccagGUCCAGAcauaggUAGGAUUgaC ZBBSR173 GacGgaaggggcacCACAA-gguuGGaUucuguugGCUUAAuuUgACUCAACAcagggAAAACUUAaccagGUCCAGAcauaggUAGGAUUgaC ZBBSR12 GacGgaaggggcacCACAA-gguuGGaUucuguugGCUUAAuuUgACUCAACAcagggAAAACUUAaccagGUCCAGAcauaggUAGGAUUgaC ZCR4 GacGgaaggggcacCACAA-gauguGGaUucuguggCUUAAuuUgACUCAACAcagggAAAACUUAaccaggUACGAAUgaC ZCR6 GacGgaaggggcacCACAA-gauguGGaUucuguggCUUAAuuugACUCAACAcaGgggAAAACUUAacagGUCCAGAcauaggUAGGAUUgaC ZCR6 GacGgaaggggcacCACAA-gauguGGGUucuguggCUUAAuuugACUCAAACAcagggAAAACUUAacagGUCCAGAcauaggUAGGAUUgaC ZCR6 GacGgaaggggcacCACAA-gauguGGGUucuguggCUUAAuuugACUCAACAcagggAAAACUUAacacGGGUAAGGUAacgGUAAAGUC ZCR6 GacGgaaggggcacCACAA-gauguGGGUucuguggCUUAAuuugACUCAACAcagggAAAACUUAacacgGGUCCGGAcauagUACCAAAACACGGGGAAggggaCUUAAAU ZCR6 GacGgaaggggcacCACAA-gauguGGGUucuguggCUUAAuuugACUCAACAcagggAAAACUUAacAcagggUACGAUUGAAAUCA ZCR6 GacGgaaggggcacCACAA-gauguGGGUucuguggCUUAAuuugACUCAAACAcagggAAAACUUAacAcaggUACCAAACAA-gauguGGGAUCugGAUUUGAAACACACAGGGGAAGGGAACGGAA-acagGUCCAAA-ACACAGGGGAAGGGAACGGAA-ACAA-ACACAGGGGGAAGGGAACGGAAACAA-GACGAGGAAGGA	2 W10279		TODUT7
 M10272 GacGgaagggcaCCACAa-gUuguGGauAcuguggCUDAAuuUgACUCAACacUggAAAACUUAccagGUCCAAAcauaggCUAGAUUgacagAUUAAUA M10272 M10210 GacGgaagggcaCCACAa-gUuguGGauAcuguggCUDAAuuUgACUCAACAcUggAAAACUUAccagGUCCAGAacuuggacagAUUAAUA M10210 BBSR7 GacGgaagggcaCCACAa-gUuguGGaUAcuguggCUDAAuuUgACUCAACAcUggAAAACUUAccagGUCCAGAacuuggacaGUUAGAACUACACAGGAUUGacagAUUAAUA M10210 BBSR7 GacGgaagggcaCCACAa-gGuuguGGaUucuguggCUDAAuuUgACUCAACAcUggGAAACUUAccagGUCCAGAacuuggacaGUUAGAGACUGACAGAGUUAUA ZBBSR7 GacGgaagggcaCCACAa-guuguGGaUucuguggCUDAAuuUgACUCAACAcUggGAAACUUAccagGUCCAGAacuuggagCUCAGACagGGCUGAGACUGACAGAGUUAUUAUA ZBBSR7 GacGgaagggcaCCACAa-gauguGGaUucuguggCUDAAuuUgACUCAACAcUggGAAACUUAccagGUCCAGAacuuggaagUUAUUAUA Sibhcyan BacGgaagggcaCCACAa-gauguGGaUucuguggCUDAAuuUgACUCAACAcUggGAAACUUAccagGUCCAGAacuuggaaGUUAUUAUA Sibhcyan BacGgaagggcaCCACAa-gauguGGaUucuguggCUDAAuuUgACUCAACAcUggAAACUUAccagGUCCAGAacuuggaaGUUAAUUGAU ZBBSR2 GacGgaagggcaCCACAa-gauguGGaUucuguggCUDAAuuUgACUCAACACUggAAACUUAccagGUCCAGAacuugguaGUUAGUUAUU ZBBSR2 GacGgaagggcaCCACAA-gauguGGaUucuguggCUDAAuuUgACUCAACACUggAAACUUAccagGUCCAGAacuuaggUAGGAUUGAUUAUA ZCR6 GacGgaagggcaCCACAA-gauguGGaUucuguggCUDAAuuUgACUCAACACUggAAAACUUAccaggUCCAGAacuuaggUAGGAUUGAUUAGAU ZCR6 GacGgaagggcaCCACAA-gauguGGaUucuguggCUDAAuuUgACUCAACACGagAAAACUUAccaggUCCAGAacuuaggUAGGAUUGAUUAGACUGAAUA ZCR6 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUDAAuuUgACUCAACAcaggAAAACUUAccaggUCCAGAAcuuaggUAGGAUUGAUUA ZCR6 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUDAAuuUgACCACACAAAACUCAccaggAAAACUUAccaggUACGAAUAGAUUAGACUUAAU ZCR6 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUTAAuuUgACCAACAACACACGAGGAUAAACUCAACAAGGGUCCAGAAcuuaggUAGGAUUAGUUAGAAUUGAAU ZCR6 GacGgaagggcaCCACAA-gauguGGaUucuguggCUTAAuuugAAACUCAACAACAAGGAACUCAACAAGGGUCCAGAACUAAGACUUAAUAAAU A0	 M10272 GacGgaagggcacCACAA-gUuguGGauAcuguggcUNAuuUgACUCAACAcUggAAACUUAccagGUCCAGAcauagCUAGGAUUgac M10210 GacGgaaggggcacCACAA-gUuguGGaUAcuguggcUUAAuuUgACUCAACAcUggAAACUUAccagGUCCAGAcauagCUAGGAUUgac M20210 GacGgaaggggcacCACAA-gguugGGaUccuguggcUUAAuuUgACUCAACAcUggAAACUUAccagGUCCAGAcauagCUAGGAUUgac M202110 GacGgaaggggcacCACAA-gguugGGaUccuguggCUAAuuUgACUCAACAcUggAAACUUAccagGUCCAGAcauagGUAGGAUUAAC M20213 GacGgaaggggcacCACAA-gguugGGaUucuguggCUAAuuUgACUCAACAcUggAAACUUAccagGUCCAGAcauagGUAGGAUUAAC M20213 GacGgaaggggcacCACAA-guugGGaUucuguggCUUAAuuUgACUCAACAcUggAAACUUAccagGUCUAGAcauagGUAGGAUUAAC Siphcyan GacGgaagggcacCACAA-guugGGaUucuguggCUUAAuuUgACUCAACAcUGggAAAACUUAccagGUCCAGAcauagGUAGGAUUGGC M20214 GacGgaagggcacCACAA-guugGGaUucuguggCUUAAuuUgACUCAACAcUGggAAAACUUAacGgUCCAGAcauagGUAGGAUUGGC ZCR4 GacGgaagggcacCACAA-guugGGaUucuguggCUUAAuuUgACUCAACAcCGggAAAACUUAacGgUCCGGAcauagGUAGGAUUGGC ZCR6 GacGgaagggcacCACAA-gauguGGaUucuguggCUUAAuuUgACUCAACAcGggAAAACUUAacGgUCCGGAcauagGUAGGAUUGAC ZCR6 GacGgaagggcacCACAA-gauguGGaUucuguggCUUAAuuugAUUCAACAcGggAAAACUUAacGgUCCGGAcauagGUAGAUUGACUCAACACGGgaAggggcacCACAA-gauguGGaUucuguggCUUAAuuugAUUCAACAcGggAAAACUUAacGgUCCGGAcauagGUAGAUUGAAUUGAU ZCR6 GacGgaagggcacCACAA-gauguGGaUucuguggCUUAAuuugAUUCAACAcGgggAAAACUUAacGGAAcauaggUAGAAUUGAAUCAACACGGgaAggggcacCACAA-gauguGGaUucuguggCUUAAuuugAUUCAACAcGggAAAACUUAacGggUCCGGAcauagGUAAACUUAAACACGGGAAGGGAAGGACCACAA-gauguGGaUucuguggCUUAAuuugAUUCAACAcGggAAAACUUAacGGGAAcauaggUAAACUUAAAACAGGGAAGGAACCACAA-gauguGGaUucuguggGUUAAuuugAUUCAACACGGgAAAACUUAACACGGGAAGGUAAGGCACACAA-gauguGGaUucuguggGUUAAuuugAUUCAACACGGgAAAACUUAACACAGGAACAACAGGAACACAGGAAGGAAGG	3 W10274	GacegaaagggcacCAcAaaaguuuruuuuuuuuuuuuuuuuuuuuuuuuuuuuuuu	6/70LM
5 M10210 GacGgaagggcacCACAa-gfuguGGauAcuguggcUUAAuuUGACUCAACAcUggAAAACUUAccaggUCCAGAcauagcUAGGAUUgacagAUAAUW ZBBSR7 GacGgaagggcacCACAa-gguuuGGaUccuguggcUUAAuuUGACUCAACAcUggGAAACUUAccaugggaACUAUAUAGAcauaggUAGGACUGACAGagauuGAUA ZBBSR7 ZBBSR173 GacGgaagggcacCACAa-gguuuGGaUccuguggcUUAAuuUGAAUCAGACGUggGAAAACUUAAccaugggAACUAUAGAcauaggUAGGAUUGACGAGAGUGACUGACAG Sibheyan GacGgaaggggcacCACAa-guuuGGaUccuguggcUUAAuuUGAAUCAGACGUggAAAACUUAAccaugggAAUAUUUUAU Sibheyan B Sibheyan GacGgaaggggaaCCACAa-guuuGGaUccuguggCUUAAuuUGAAUCAGACGUggAAAACUUAAccaugggAAUUAUUGACGAGAUUGACGAGGAUUGACGAGAUUGACGAGAUUGACGAGAUUGACGAGAUUGACGAGGAUUGACGAGGAUUGACGAGAUUGACGAGAUUGACGAGAUUGACGAGAUUGACGAGAUUGACGAGAUUGAUCAGACGAGAUUGAUCAGACGAGAUUGACUCAACAGUGAGUUCAGAA-guuuGGaUucuguggCUUAAuuUGAACUCAACACUggAAAACUUAaccagGUCCAGAA-auagGUAGGAUUGAGUCAGAA-gauuGGaUucuguggCUUAAuuUGAACUCAACACUGgAAACUUAaccagGUCCAGAAcauagGUAGGAAUUGACUGAGAUUGAUUAGAU 2CR16 GacGgaagggcaCCACAA-gauguGGaUucuguggCUUAAuuUGAACUCAACACGggAAAACUUAaccugGUCCAGAAcauagCUAGAAUUGAUUGAUUGAUUAGACGAGAUAGAUU 2CR16 GacGgaaggggaaCCCACAA-gauguGGaUucuguggCUUAAuuUGAACCAACACGggAAAACUUAaccaggUCCGGAAcauaGUAACUUAGAUAGAUU 2CR6 GacGgaaggggaaCCCACAA-gauguGGaUucuguggCUCAAAacuugGAAACUCAACAGGgAAAACUUAacuagGUCCAGAAcauaGUAACUUAAUAUAA 2CR6 GacGgaaggggaaCCACAA-gauguGGaUucuguggCUCAAAauuGAAACUCAACAGGGGAAGGGCCACAA-gauguGGaUucugGGCUCAAAACAGCACGGGAAAACUCAAccaggUCCAGAAacauaGUAAAUAUAAAUAA 2CR6 GacGgaaggggaaCCACAA-gauguGGaUucuguggCUCAAAAuuUGAAACUCAACCAGGGAAACCACACGAGGUCCAGAAacaaaGUUUGAAUQACGAGAUAAA 41 41 42 42 4400000000000000000000000000	5 M10210 GacGgaagggcacCACAa-gUuguGGauAcuguggcUUAAuUGACUCAACAcUggAAACUUAccagGUCCAGAcauagCUAGGAUUgac SIBBSR17 GacGgaagggcacCACAa-gGuuGGaUucuguugGCUUAAuUGACUCAACACUGgGAAACUUAccagGUCCAGAcauagguAGGACUGaC 7 ZBBSR17 GacGgaagggcacCACAa-gauguGGaUucuguugGCUUAAuUGACUCAACACUGgGAAAACUUA.ccagGUCUGAGacauaggaAUUAAU 8 Sipheyan GacGgaagggcacCACAa-gGuuGGaUucuguugGCUUAAuUUGAUUCAACACUGgGAAAACUUA.ccagGUCUGAGacauaggaAUUAAU 9 ZBBSR12 GacGgaagggcacCACAa-gGuuGGaUucuguugGCUUAAuuUGAUUCAACACUGgAAAACUUA.ccagGUCGAGAcauaggUAGGAUUgaC 9 ZBBSR2 GacGgaagggcacCACAa-gGuuguGGaUucuguugGCUUAAuuUGACUCAACACACUGgAAAACUUA.ccagGUCGAGAcauaggUAGGAUUgaC 9 ZCR4 GacGgaagggcacCACAa-gGuugGGaUucuguugGCUUAAuuUGACUCAACACUGgAAAACUUA.ccagGUCGAGAcauaggUAGGAUUgaC 1 ZCR4 GacGgaaggggcacCACAa-gauguGGaUucuguugGCUUAAuuUGAUCCAACACGUGGAAACACUAACAACUGAGAcauagGUAGAUUgaC 2 ZCR6 GacGgaaggggcacCACAa-gauguGGaUucuguugGCUUAAuuUGAUCCAACACGUGGAAAACUUA.ccuagGUCCGGAAcauaGUUAGUAGU 2 ZCR6 GacGgaaggggcacCACAa-gauguGGaUucuguggCUUAAuuUGAUCCAACACGUGggAAAACUUA.ccaggUCGGGAAauaGUAAUUGAU 3 FHXPOLXC GacGgaaggggcacCACAa-gauguGGaUucuguggGCUAAuuugAUUCAACACGgggAAAACUUA.ccaggUCGGGAaagggcacCAACAa-gauguGGaUucugcggGCUAAuuugAUUCAACACGgggAAAACUUA.ccaggUCGGGAaagggCaCAACAA-gauguGGaUucuguggGCUUAAuuugAUUCAACACGgggggAAAACUUA.ccaggUCGGGAaacaGUAUUAAUUGAC 3 FHXPOLXC GacGgaaggggcacCAACAa-gauguGGGUUCugGggGUUAAUUUAAUUGACCGggggggAAAACUUAACACGGggggggGAAAACUCAACAACGGAAGGAAGGGAAG	4 W10272	GacGgaagggcaCCACAa-gUuguGGauAcuguggcUUAAuuUgACUCAACA-cUggAAAACUUAccaaGGUCCAGAcauaacUJAGGAUTeacaaabuAUA	W10272
 5 ZBBSR7 6 ZZBSR7 6 GacGgaagggcacCACAA-gguguGGaUccuguggcUTAAuuUGAUCCACACACUggGAAACUCAccauaggUAGGACUGACGAaaGGGUCGAUA 7 ZEBSR113 6 acGgaagggcacCACAA-guguGGaUucuguggcUTAAuuUGAUCCAACACUggGAAACUUTAAccauuggaAUUAAUCAGCAAGGAUGAUA 8 Ziphcyan 6 acGgaaggggcacCACAA-gUuguGGaUucuguggcUTAAuuUGAUCCAACACUggGAAAACUUAccauuggaAUUAUAUGAGCGAGGAUGAUA 8 Ziphcyan 6 acGgaaggggcacCCACAA-gUuguGGaUucuguggcUTAAuuUGAUCCAACACUggGAAAACUUAuccagGUCCAACAauuggGAAUUAUUGAU 8 Ziphcyan 6 acGgaaggggcacCCACAA-gUuguGGaUucuguggcUTAAuuUGACCAACACAGggAAAACUUAuccagGUCCAACAacuuggGAAUGAUUGAU 8 Ziphcyan 6 acGgaaggggcacCCACAA-gUuguGGaUucuguggcUTAAuuUGACUCAACAcUgggAAAACUUAuccagGUCCAACAacuuggGAAUUGAUU 8 Ziphcyan 6 acGgaaggggcacCCACAA-gAuguGGaUucuguggcUTAAuuUGACUCAACAcUgggAAAACUUAuccagGUCCAGAcauaggTAGGAUUGAU 8 Zicki 8 CacGgaaggggcacCCACAA-gauguGGaUucuguggcUTAAuuUGACUCAACAcUGggAAAGCUUAuccagGUCCAGAcauaggTAGGAUUGAU 8 Zicki 8 CacGgaaggggcacCCACAA-gauguGGaUucuguggCUTAAuuUGACUCAACAcGgggAAAGCUUAuccagGUCCAGAcauaggTAGGAUUGAUU 8 Zicki 8 CacGgaaggggcacCACAA-gauguGGaUucuguggCUTAAuuugAUUCAACAcGgggAAAGCUUAuuagGUCCCGAAcauagGUCCAGAauaGUAAU 8 Zicki 8 CacGgaaggggcacCACAA-gauguGGaUucuguggCUTAAuuugAUUCAACAcGgggAAAGCUUAuuagGUCCCGAAcauagGUCCAGAAuagGuaGCGAUCAAACAACAAGAAACUAACAAACUAAACUAAACU	 5 ZBBSR7 6 ZZBSR7 6 GacGgaaggGcaCCACAA-ggugGGaUccuguggCUTAuuUGACUCAACACUGgGAAACUCAccagGUCCGGAcauaggUAGGACUgAA 7 ZEBSR1173 6 GacGgaagggGcaCCACAA-gauguGGaUccuguuggCUTAAuuUGAUCCAACACUGgGAAACUTA.ccagGUCUTAGAcauugggaaCUTAUTAAC 8 Sipheyan 6 GacGgaagggGcaCCACAA-gauguGGaUccuguuggCUTAAuuugACUCCAACACUGggAAAACUTA.ccagGUCUTAGAcauugggaaCUTAUTGAC 8 ZBSR12 6 GacGgaagggGcaCCACAA-gAuguGGaUccuguuggCUTAAuuugACUCAACACCGggAAAACUTA.ccagGUCUTAGAcauaggAAUTGGAC 8 ZBSR12 6 GacGgaagggGcaCCACAA-gAuguGGaUccuguuggCUTAAuuugACUCCAACACUGggAAAACUTA.ccagGUCCAGAcauaggUAGGAUUGGA 7 CR16 6 GacGgaagggGcaCCACAA-gauguGGaUccuguggCUTAAuuUgACUCAACACUGgAAAAUUTA.ccugGUCCAGAcauagGUTCAGAcauagGUTCAGACUTAAUUGAACUCAACAACACUGgAAAAUUTA.ccUgGUCCAGAcauagGUTCAGACUTAAUGAGUUGAGUUGAUUGACUCAACAACACUGGAAAUGAUUAuuagGUCCAGAcauagGUUCCAGACUTAAUUGAAUTAAUU 7 ZCR6A 6 GacGgaagggcaCCACAA-gauguGGGUUcuuuggGCUCAAuuugGUUCCAACACGGGAAAGGUUAuuagGUCCAGAcauagGUUCCAGACAUAGACUTAUAGG 7 ZCR6A 6 GacGgaagggcaCCACAA-gauguGGGUUcuguggCUTAAuuugAUUCAACACGGgAAAGCUUAuuagGUCCAGAcauaGUUACUAUAgaC 7 A0 8 THYPOLYC 7 GacGgaagggcaCCACAA-gauguGGGGUCugGGGUUCUGGGGGUCCAACACAGGGGAAGGUCCAGACauaGUUAGUAUAGACUAUAAGUC 7 41 4 1 	5 W10210	GacGgaagggcaCCACAa-gUuguGGauAcuguggcUUAAuuUgACUCAACAcUgaAAACUUAccaaggUCCAGAcauaaccUAGGAUUgacaaaAUuAAUA	0120LM
 ZEBSR173 GacGgaagggcaCCACAa-gauguGGaUucuguggcUCAAuuUgAUUCAACAcUggAAAGCUUAucagGUCUAGAcauuggaaCUAUAACagACuGAUA ZEBSR173 Bipheyan GacGgaaggggcaCCACAa-gbuguGGaUucuguggCUTAAuuUgACUCAACACaggAAAACUUAccauaggaUUAUUUGAGGGAUUAUA Sibheyan ZEBSR2 GacGgaaggggcaCCCACAA-gbuguGGaUucuguggCUTAAuuUgACUCAACacgggAAAACUUAccagGUCUAAAcauaggaUUAGUUUGAU ZERS12 GacGgaaggggcaCCCACAA-gbuguGGaUucuguggCUUAAuuUgACUCAAACaCgggAAAACUUAccagGUCCAAAcauaggaUAGGAUUGAUCGAA ZCR4 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUUAAuuUgACUCAAACaCgggAAAACUUAccagGUCCAAAcauaggUAGGAUUGAUGAU ZCR4 GacGgaaggggcaCCACAA-gauguGGaUucuguggCUUAAuuUgACUCAAACacgggAAAACUUAAccagGUCCGAAAcauaggUAGGAUUGAUUGAU ZCR6A GacGgaaggggcaCCACAA-gauguGGaUucuguggCUUAAuuUgAACUCAACacgggAAAACUUAAccagGUCCGGAAcauaggUAGGAUUGGUA ZCR6A GacGgaaggggaacGCACAA-gauguGGaUucuguggCUUAAuuUgAACUCAACacgggAAAACUUAAccaggUCCGGAAcauaggUAGGAUUGGUA ZCR6A GacGgaaggggaacGCACAA-gauguGGaUucuguggCUUAAuuUgAACUCAACACagggAAAACUUAAccugGUCCGGAAcauaggUCCGGAAcauaggGUCGGGAAacgaGuGGAUUGGAUUGGUA ZCR6A GacGgaaaggggaaCCACAA-gauguGGaUucuguggCUUAAuuUgAACUCAACagggAAAACUCAAccaggUCCGGAAcauaggUCCGGAAcauaggGUCGGAAacagaCuGGAUUGAUUGAUUGGUA ZCR6A GacGgaaaggggaaCCACAA-gauguGGaUucugggCUUAAuuugACUCAACAcggggAAAACUUCAAcaaggUCCGGAAcacaagUUUGAUUGAUUGAUUAAUUGGUA ZCR6A GacGgaaaggggaaCCACCA-agauguGGaUucugggCUUAAuuugACUCAACAcggggAAAACUCAAcaaggUCCGGAAacacaagUUUGAUUGAUUGAUUAAUUGAACUCAACACGGgGAAAGGAACCUGAGGAAACAGAGGGAAGCACAGGGAAGCCAGAACACACAACA	 ZEBSR173 GacGgaagggcaCCACAA-gauguGGGUucuguggcUCAAuuUgAUUCAACACUGgAAAGCUUAucagGUCUAGAcauuggaaCUAUAAaC B sipheyan GacGgaagggcaCCACAA-gauguGGUUcuguggcUUAAuuugACUCAACACUGgAAACUUA.ccagGUUCUAGAcauugggaAUUAUUGaC BESR2 GacGgaaggggcaCCACAA-gauguGGUUcuguggcUUAAuuugACUCAACACUGgAAAACUUA.ccagGUUCAAGAcauaggUAGGAUUGaC CR4 GacGgaaggggcaCCACAA-gauguGGUUcuguggcUUAAuuUgACUCAACACUGgAAAACUUA.ccagGUCCAGAcauaggUAGGAUUGGC CR4 GacGgaaggggcaCCACAA-gauguGGGUUcuguggcUUAAuuUgACUCAACACUGgAAAACUUA.ccagGUCCAGAcauaggUAGGAUUGGC ZCR4 GacGgaagggcaCCACAA-gauguGGGUUcuguggcUUAAuuUgACUCAACACUGGAAAUGGUCAAGAcauagGUACGAUUGAC ZCR6A GacGgaagggcaCCACAA-gauguGGGUUcuguggcUUAAuuugAUUCAACACAGGgAAAGCUUA.uuagGUCCAGAcauagGUACUAUUGACUAACACACGGGAagggaagggcaCCACAA-gauguGGGUUcugugggCUUAAUuugAUUCAACACAGGggAAAGCUUA.uuagGUCCAGAcauagGUACUAUUGAGUGAGUUAAUA ZCR6A GacGgaagggcaCCACAA-gauguGGGUUucugugggCUUAAuuugAUUCAACACACGGggAAAGCUUA.uuagGUCCAGAcauaGUUACUAUAgaCU ZCR6A GacGgaagggcaCCACAA-gauguGGGUUucugugggCUUAAuuugAUUCAACACACGgggAAAGCUUA.uuagGUCCAGAcauaGUUACUAUAgaCU ZCR6A GacGgaagggcaCCACAA-gauguGGGUUucugugggCUUAAuuugAUUCAACACAGGggAAAGCUUA.uuagGUCCAGAcauaGUUACUAUAgaC RHYPOLYC GacGgaagggcaCCACAA-gauguGGGGUUcugugggCUUAAuuugAUUCAACACAGggggAAAACUUA.ccagggUCCAGAcauaGUUAGAAGACUAAAGACUAAAACACAGGGGAAGGUAACACACAGGAACACUAAAAGUC RHYPOLYC GacGgaagggcaCCACAA-gauguGGGgUUcugGggUUUAAuuugACUCAACACAGggggAAAACUCAACACACGGAAAGGCUAACACAGACAAAGACUAAAAGUCAACAACACACAC	6 ZBBSR7	GacGgaagggcaCCACAa-gguguGGaUccuguggcUUAAuuUgACUCAACAcUggGAAACUCAccagGUCCGGAcauaqqUAGGACUqaaCaqauuQAUA	ZBBSR7
8 siphcyan GacGgaagggcacCACAa-gUuguGTaUucuguggcUUAauuugACUCAACAcaggAAAACUUAccagGUCUAGAcauaggaAUUAUUgaCgggAUUAUA Siphcyan 9 ZEBSR2 GacGgaagggcacCACAa-gAuguGGaUucuguggcUUAauuUgACUCAACAcUggAAAACUUAccagGUCCAGAcauaggUAGGAUUgaCagauuGAUA ZEBSR2 0 ZCR4 GacGgaaggggcacCACAa-gauguGGaUucuguggcUUAauuUgACUCAACAcUggAAAACUUAucagGUCCAGAcauagGUUAGAUUgaCagauuGAUA ZCR4 1 ZCR16 GacGgaaggggcacCACAA-gauguGGaUucuguggcUUAAuuUgACUCAACAcUggAAAACUUUAccUgGUCCGAGAcauagGUUAGAUUGAGCagauuGGU 2 ZCR5 GacGgaagggggcacCACAA-gauguGGaUucuguggcUUAAuuugACUCAACAcUgggAAAACUUAucagGUCCAGAcauagUUAACUUUAgQCagaCugGU 2 ZCR5 GacGgaagggggagggggggggggggggggggggggggg	 8 siphcyan GacGgaagggcaCCACAa-gUuguGGUUcuguggCUUAkuuugACUCAACAcagggAAAACUUAccagGUCUAGAcauaggaAUUAUUgaC 8 2EBSR2 GacGgaagggcaCCACAa-gUuguGGUUcuguuggCUUAkuuUgACUCAACAcuggAAAACUUA.ccagGUCCAGAcauaggUAGGAUUgaC 9 2EBSR2 GacGgaaggggcaCCACAa-gAuguGGGUucuguuggCUUAkuuUgACUCAACACUggAAAACUUA.ccagGUCCAGAcauaggUAGGAUUgaC 9 2CR6 GacGgaaggggcaCCACAA-gauguGGGUucuguggCUUAkuuUgACUCAACAcuggAAAACUUA.ccagGUCCAGAcauaggUAGGAUUgaC 2 2CR6A GacGgaaggggcaCCACAA-gauguGGGUucuguggCUUAkuuUgACUCAACAccaggAAAACUUA.ccagGUCCAGAcauagGUAGGAUUAGU 2 2CR6A GacGgaaggggcaCCACAA-gauguGGGUucuguggCUUAkuuugAUUCAACAccagggAAAACUUA.ccaggUCCGGAcauagGUAGGAUUGAUGAC 2 2CR6A GacGgaagggcaCCACAA-gauguGGGUucuguggCUCAAuuugAUUCAACAccagggAAAACUCA.ccaggUCCGGAcauagGUACGAUUGAAGGU 2 2CR6A GacGgaagggcaCCACCA-gaaguGGGUucuguggCUCAAuuugAUUCAACAccagggAAAACUCA.ccaggUCCGGAcauagGUACGAAUGAGU 2 2CR6A GacGgaagggcaCCACCA-gaaguGGGUucuguggCUCAAuuugAUUCAACAccaggggAAAACUCA.ccaggUCCGGAuacaCGUAUGAAguC 4 NABRUBE GacGgaagggcaCCACCA-gaaguCuGGgguCuGGggUCuGGggUCUCAACAcGGgggggAAAACUCA.ccaggUCAGGAAcacaCUUAAGUC 5 auk hali>>	7 ZBBSR173	GacGgaagggcaCCACAa-gauguGGaUucuguggcUCAAuuUgAUUCAACAcUggAAAGCUUAucagGUCUAAcauuggaagUAUAAAaCagACuGAUA	ZBBSR173
 2 ZBBSR2 3 ZBBSR2 6 acGgaagggcaCCACAa-gAuguGGaUccuguggcUUAAuuUgACUCAACACUggAAAACUCAccagGUCCAGAcauaggUAGGAUUgaCagauuGAUA 2 ZBR4 2 ZCR4 6 acGgaaggggcaCCACAA-gauguGGaUccuguggCUUAAuuUgACUCAACACUggAAAACUUUAccugGUCCAGAcauaggUAGGAUUGAUA 2 ZCR5 6 acGGgaaggggcaCCACAA-gauguGGaUucuguggCUUAAuuugAUUCAACACUggAAAACUUUAccugGUCCCAGAcauagUAACUUAGAUUGAUGAUUA 2 ZCR5 6 acGGgaaggggcaCCACAA-gauguGGaUucuguggCUUAAuuugAUUCAACACACUgaAAAUUUAccUgGUCCCAGAcauagUAACUUAGAUUGAUGAUA 2 ZCR5 6 acGgaagggggacaCCACAA-gauguGGaUucuguggCUUAAuuugAUUCAACACCagggAAAGCUUAuuagGUCCAGAcauaGUAACUUAGAUUAGAUGAU 2 ZCR5 3 PHYPOLYC 6 acGgaagggggacaCCACCA-ggauGGGAUCugeggGUUAAuuugAUUCAACACGaggAAAGCUUAuauagGUCCAGAcacuaGUAACUUAAUUGAUUAAUUUGAUUAACUCAACACGggGAAAGCUUAAuuagGUCCAGAAcaaguuGAAU 7 A1 4 A1 4 A1 4 A1 4 A1 	 BZBSR2 GacGgaagggcaCCACAa-gAuguGGaUccuguggcUUAAuuUgACUCAACACUggAAAACUCAccaggUCCAGAcauaggUAGGAUUgaC CZR4 GacGgaaggggcaCCACAa-gAuguGGaUccuguggcUUAAuuUgACUCAACACUggAAAACUUAcagGUCCAGAcauaggUAGAUUgaC IZCR16 GacGgaaggggcaCCACAA-gauguGGaUccuguggcUUAAuuUgACUCCAACACUggAAAAAUUUAccUgGUCCGAAcauagGUAGAUUGAUUGAC IZCR16 GacGgaaggggcaCCACAA-gauguGGaUccuguggcUUAAuuUgAUUCAACACUggAAAAAUUUAccUgGUCCGAAcauagGUAGAUUGAUUGAUUGAUUGAUUGAU IZCR16 GacGgaaggggcaCCACAA-gauguGGaUccuguggcUUAAuuugAUUCAACAcGgggAAAACUUAcuagGUCCGGAcauaGUAAUUAJUAG PHYPOLXC GacGgaaggggcaCCACAA-gauguGGaUccugugggCUUAAuuugAUUCAACAcGggggAAAACUCAccaggUCCGGAcauaCUAAUUAGAUG PHXPOLXC GacGgaagggcaCCACAA-gauguGGaUccugcgggCUUAAuuugAUUCAACAcGggggAAAACUCAccaggUCCGGAcaacaCGUAUGAAQUC ANBGRUBE GacGgaagggcaCCACCAA-gauguGGaUCugcgggCUUAAuuugAUUCAACAcGggggAAAACUCAccaggUCCGGAuacaCGUAUUGAAUGUC A NABRUBE GacGgaagggcaCCACAA-gauguGGaUCugcgggCUUAAuuugAUUCAACAcGgggggAAACUCCAccaggUCGGGAuacaCGUAUGAAQUC A NABRUBE acggaagggcaCCACAA-gauguGGaguCugcgggCUUAAuuugAUUCAACAcGgggggAAACUCAccaggUCGGGAuacaCGUAUUGAUUGAUUGACUCAACAcGgggggAAACUCAcGagguCCGGAuacaCGUAUUGAUUGAUUCAACAccGgggggAAACUCAACAccGgggggaAACCUCAACACACGGAuacaCGUAUUGAUUGAUUCAAUAACACACGGGGGggggGAAACCUCAACACACGAGGGaaggGUCACAACACACGGaaggaGUCAGGAACACACAACACACGGGGGGGGGUCCGGAuacaCGUAUUGAUUGAUUCAACACACGGgggggAAACUCAACACACACACACACACACGGGAAGgUCGGAUACACACAACACA	8 Siphcyan	GacGgaagggcaCCACAa-gUuguGUaUucuguggcUUAAuuugACUCAACAcaggAAAACUUAccagGGUCUAGAcauaggaAUUAUUGUGGaCggaUuAUAU	Siphevan
 0 ZCR4 GacGgaagggcaCCACAa-gAuguGGaUucuguggCUUAAuuUgACUCAACAcUggAAAACUUAucagGUCCAGAcauagGUAGGAUUgaCagaUuGAUA ZCR4 1 ZCR16 GacGgaaggggcaCCACAA-gauguGGaUucugugGCUCAAAuuUgACUCAACacUggAAAAUUUAcCUGGUCCGGAcauagGUAGAAUUGAUGAUA ZCR6A 2 ZCR6A GacGgaaggggcaCCACAA-gauguGGaUucugugGCUCAAAuuugAUUCAACAcGgggAAAACUUAucagGUCCGGAAcauagUAACUUAGAUGAUA ZCR6A 3 PHYPOLYC GacGgaaggggcaCCACAA-gauguGGaUucugugGCUCAAAuuugAUUCAACAcGgggAAAACUUAaccaggUCCGGAAcauaGUAACUAUAAGCGGAUAAUAUA 3 PHYPOLYC GacGgaaggggcaCCACCA-ggaguGGaguCugGggCUCAAAAuuugAUUCAACAcggggAAAACUCAccaggUCCGGAAcauaGUAACUAAAuaguUGAAUAAUA 4 NAERUBE GacGgaaagggcaCCACCA-ggaguGGaguCugGggUUAAUuuGAUUGAUAguUAAUAAU 4 A1 41 43 43 440 440 440 440 440 440 440 441 441 441	 2CR4 GacGgaagggcaCCACAa-gAuguGGaUucuguggcUUAAuUUGACUCAACACUGgAAAACUUAucagGUCCAGAcauaggUAGGAUUgaC 1 2CR16 GacGgaaggggcaCCACAa-gauguGGaUucuguggcUUAAuuUgACUCAACAcUggAAAAUUUAccUgGUCCGGAcauagGUUAGAUUGAU 1 2CR6A GacGgaagggggcaCCACAa-gauguGGaUucugugggCUUAAuuugAUUCAACAcCagggAAAACUUAuuagGUCCGGAcauagGUUAGAUUGAU 2 2CR6A GacGgaagggggacCACAAa-gauguGGaUucugugggCUUAAuuugAUUCAACAcacgggAAAACUCAccaggUCCGGAuacGUAACUUAGAUGAA 2 2CR6A GacGgaagggggacCACAAa-gguuGGGaUucugugggCUUAAuuugAUUCAACAcacgggAAAACUCAccaggUCCGGAuacaCUUAGAUUGAAGUC 3 PXPDLYC GacGgaaggggcaCCACCA-ggaguGGaguGGggUUGGggCUUAAuuugACUCAACAcGggggGAAAACUCAccaggUCCGGAuacaCGUUGAUUGAC 4 NAEGRUBE GacGgaaagggcaCCACCCA-ggaguGGgguGGggGUUAAuuugACUCAACAcGggggGAAACUCAccaggUCCGGGAuacaCGUUGAUUGAUUGGC 5 euk heli 37>>>	9 ZBBSR2	GacGgaagggcaCCACAa-gAuguGGaUccuguggcUVAAuuUgACUCAACAcUggAAAACUCAccagGUCCAGAcauaggUAGGAUVgaCagauuGAUA	ZBBSR2
I SCR16 GacGgaagggcacCACAA-gauguGGaUccuguggCUUAAuUUGACUCAACAcUgaAAAAUUUAccUgGUCCGGAcauagCUUAGAUUgAUagauuGGUA ZCR16 ZCR6A GacGgaagggggcacCACAA-gauguGGaUucuggGUCAAAAagggAAAGCUUAuuagGUCCAAAcauggGUCCAAAcaugGUCCAAACaugGggcaCagaCagaCagaCagaCaga PHYPOLYC GacGgaagggggracCAACA-agguuGGaQucugggGUCAAAACagggAAAGCUUAuuagGUCCAAAcagguCAAAguCAAAGGUGAUA PHYPOLYC GacGgaaggggracCAACA-agguuGGaQuCUGAGUgggGUCAACAACAGggGAAACCUCAccaggUCCGAAacaagguCAAAGUUGAAUUA NAEGRUBE GacGgaaaggggracCAACA-gGguuGGaguCugcggCUUAAuuugAUUCAACAcgggAAAACUCAccaggUCCGAAacacaggUCAGGAAaguCaagguCAAAAU A NAEGRUBE GacGgaaaggggracCAACA-gGguuGGaguCugcggCUUAAuucgACUCAACAcgggAAAACUCAccaggUCAGGAAcacaAGUUUGAUUGACAgguuAAU A NAEGRUBE GacGgaaagggacCCACCA-ggauGGaguCugcggCUUAAuucgACUCAACAcgggAAAACUCAccaggUCAGGAAcacacaggUCAGGAAcacagguCAAGAGUGA A bala bala a a a a a a a a a a a a a a a a a a	 ZCR16 GacGgaagggcaCCACAA-gauguGGaUccuguggcUUAAuuUgACUCAACAcUgaAAAUUUAccUgGUCCGGAcauagCUUAGAUUGAU ZCR6A GacGgaaggggcaCCAAA-gauguGGaUccugugggCUCAAuuugAUUCAACAcuggAAACCUUAuuagGUCCAGAcauagCUAACUAUAgaC ZCR6A GacGgaaggggca-CACAA-gauguGGaUccugugggCUCAAuuugAUUCAACAcaggAAAACUCAccaggGUCCGGAuacaCUUAAUUAgaC PHYPOLYC GacGgaaggggca-CACAA-gauguGGaUCucgggGUUAAuuugACUCAACAcagggGAAAACUCAccaggUCCGGAuacaCUUAGAAGuC NXEGRUBE GacGgaagggca-CACAA-ggaguGGagUCgggGUUAAuuugACUCAACAcggggGAAAACUCAccaggUCCGGAuacaCUUAGAAGuC NXEGRUBE GacGgaagggca-CACAA-ggaguGGagUCgggGUUAAuuugACUCAACAcggggGAAAACUCAccaggUCAGGAcaacaGUUUGAUUGAC NXEGRUBE GacGgaagggca-CACAA-ggaguGGagUCgggGUUAAuuugACUCAACAcggggGAAAACUCAccaggUCAGGAcaacaAGUUUGAUUGAC NXEGRUBE GacGgaagggca-CACCA-ggaguGGagUCgggGUUAAuuugACUCAACAcggggGAAAACUCAccaggUCAGGAcacaAGUUUGAUUGACUGaC NXEGRUBE GacGgaagggca-CACCA-ggaguGGagUCggggUUAAuucgACUCAACACGgggGggGAAACUCAACAGggGGAAACUCAACAACAGgggGAAACUCAACAACAGggggGaAAACUCAACAACAACAACAGggggGaAAACUCAACAACAGGAACAACAACAACAACAGGGGaaggacaCAACAACAACAACAACAACAACAACAACAACAACAACAA	0 2CR4	GacGgaagggcaCCACAa-gAuguGGaUucuguggcUUAAuuUgACUCAACAcUggAAAACUUAucagGUCCAGAcauaggUAGGAUUgaCagaUuGAUA	2CR4
² ZCR6A GacGgaagggcaCCACAa-gauguGGaUucuguggCUCAAuuugAUUCAACAcaggAAAGCUUAuuagGUCCAGAcauaGUAACUAUAgaCagaCuGAUA ZCR6A ³ PHYPOLYC GacGgaaggggca-CACAa-agaguGGAACCugcggGUUAAuuugACUCAACAcgggAAAACUCAccaggUCCGGAuacaCGUAUGAAAguCaagcuGAAa PHYPOLYC ⁴ NAEGRUBE GacGgaaagggca-CACAc-aggaguGGaguCugcggcUUAAuuugACUCAACAcggggAAAACUCAccaggUCAGGAacaaguUGAAuacaaguuAAUa NAEGRUBE ⁵ cuk heli ³⁷ 42 43 ⁶ cuk heli ⁴¹ 42 43	2 ZCR0A GacGgaagggcacCACAA.gauguGGaUucuguggcUCAAUuugAUUCAACAcaggAAACCUUAuuagGUCCAGAcauaGUAACUADAgaC 3 PHYPOLYC GacGgaaggggca-CACAA.agaguGGAACCUgcgggGUUAAuuugACUCAACAcggggAAAACUCAccaggUCCGGAuacacGUAUGAAGuC 4 NAEGRUBE GacGgaaggggca-CACCA-gaguGGaguCGuggggUUAAuuugACUCAACAcggggAAAACUCAccaggUCAGGAcacaAGUUUGAUUgaC 5 euk heli 37 42	1 2CR16	GacdgaagggcacCACAA-gauguGGaUccuguggcUUAAuUGACUCAACAcUgaAAAAUUUAccUgGUCCGGAcauagCUUAGAUUgAUagauuGGUA	ZCR16
3 PHYPOLYC GacGgaagggca-CACAa-agaguGGAACCugcggcUUAAuuugACUCAACGgggAAAACUCAccaggUCGGGAuacaCGUAUGAAAguCaagcuGAAa PHYPOLYC 4 NAERUBE GacGgaaagggcaCCACCA-ggaquGGaguCugcgggcUUAAuucgACUCAACGgggGAAACUCAccaggUCAGGAacacaAGUUUGAUUGAUUgACA 4 NAERUBE GacGgaaagggcaCCACCA-ggaquGGaguCugcgggcUUAAuucgACUCAACGggGAAACUCAccaggUCAGGAacacaAGUUUGAUUGAUUGAAA 4 NAERUBE GacGgaaagggcaCCACCA-ggaquGGaguCugcgggcUUAAuucgACUCAACGggGAAACUCAccaggUCAGGAacacaAGUUUGAUUGAUUGAAA 4 NAERUBE GacGgaaagggcaCCACCA-ggaquGGaguCugcgggcUUAAuucgACUCAACGgggGAAACUCAccaggUCAGGAacacaAGUUUGAUUGAUUGAUUAAU 5 Cuca 4 NaERUBE GacGgaaagggcaCCACCA-ggaquGGaguCugcgggGaCAACUCAACCAGGgGACGAcacaAGUUUGAUUGAUUGAUUAAUA NAEGRUBE 5 Cuca 4 NaERUBE GacGgaaagggcaCCACCA-ggaquGGAgUCAGGggGGAACUCAACCAGGGGGGGACACACAGGGAACUCAACAGGGGUCAGGAAAGUCAACUCAACAGGGAAACUCAACAGGGACUCAACAGGGAGGG	3 FHYPOLYC GacGgaagggca-CACAa-agaguGGAACCUgcggcUUAAUUgACUCAACAcggggAAAACUCAccaggUCCGGAuacaCGUAUGAAguC 4 NAEGRUBE GacGgaagggcaCCACCA-ggaguGGaguCugcgggGUUAAUucgACUCAACAcggggGAAACUCAccaggUCAGGAcacaAGUUUGAUUgaC 5 euk hali 37	2 ZCR6A	GacGgaaggcaCCACAa-gauguGGaUucuguggcUCAAuuugAUUCAACAcaggAAAGCUUAuuagGUCCAGAcauaGUAACUAUAgaCagaCuGAUA	2CR6A
w MADANDE WAGAGAAAGGAGCUAACUA-GGAGUUAAGUGGGGGUUAAUUGGACUCAACAGGGGGAAAACUCAAcaaggUCAGGACaaCaAGUUUGAUUGACUGGGGGGUUAAUA 5 uuk heli 37 43 43 43 34 40 40 40 40 40 40 41 41 42 43 43 43 43 44 41 42 43 43 43 43 43 43 44 44 44 44 44 44 4	* MADENDE GAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	3 PHYPOLYC	gacdgaaggggaa-CACAa-agagucGAACCuggggcUTAAuuugACUCAACAcggggAAAACUCAacaaggUCCGGAuacaCGUAUGAAAguCaagcuGAAa	PHYPOLYC
2 euch liett 3/ 33 39 40 40 41 42 43 euch helt	5 tad	A NAEGRUBE	GacegaaaggcaccAccA-ggaguedagucugcggcUUAAuucgAcUCAACAcgggGAAACUCAccaggUCAGoAcacaAGUUUGAUUgaCagguuAAUa	NAEGRUBE
			5/ 50 59 40 40 41 41 42 43	euk heli

Posi- tion:	Sequence identity:	Data:	
2313 2313	1 1369mask 2 MNELEIDY	11111111111111111111111111111111111111	1369mask Mneleidy
2313 2313	3 DIAGRAND 4 ATHBOMBA	gCucutuctUcdAUTCuaugGGuggDggugcauugguggugguggggggggggggggggggg	DIAGRAND ATHBOMBA
2313	5 BLAEMERS	gCucuthcUVGAUVCuaugGOuggOggougeregunCuuAguuCauggaUVGAuuuguCuggUV-AAUVccgAUAACGaacGAQAccuugaucu-Gc	BLAEMERS
2313	6 CHLREINH	gCucuUucUUGAuucugugGougGUggugcauuggcguugcuuAguugguggUUGCcuugucAggUU-GAUUccGGUAACGaacGAGAccucagccu-Gc ACumuturitintiititaittiteuumdaumdraumdraunaanumaanumaanumaanumaanumaanumaanuma	CHLREINH
2313	8 PORAERUG	າຍ ແລະ	PORAERUG
2313	9 ACACAST1	gCucuUucUU0AUUcuaugGGuggUggugcauggccguuCuuAguugguggaGUGAuuugucuggUU-AAUUccgUUAACGaacGAGAccuuaaccu-Gc	ACACAST1
2313	10 PHRBALAM	gCueuture/MaguagGouggOrgerogeregeregeregue/Undanuegeu/Ordanuege/Ordanuege/OrdArdaaacon-Ge	PHRBALAM
2313	12 EMIHUXLE	gcuccuuscoussousgeusgeugguggesesuggeceguucuusguugguggageevesuuugguu-AAvuocegousAAceaaceaaceuaaeceu-ee gCuccuuscUUGAUUcgauggGuggUggugeauggecguuCuuAguugguggagguggaGUGAuuugucuggUU-AAUUccgUUAACGaacGAGAcegeageceu-Ge 1	STIALSIU
2313	13 OCHDANIC	gCucuDucUDGAUDcuaugGGauggUggugcauggccguuCuuAguugguggaGUGAuuugucuggUD-AAUDccgUDACGaacGAGAccccugccu-Gc	OCHDANIC
5112	15 LARMINIT	guerous obvious augestages danges cauges cause causa danga ange ange ange ange ange ange ange	LAFAUEND
2313	16 OXYGRANU		OXYGRANU
2313	17 BLEAMERI	gCucuUucUUGAUUcuaugGGuggUggugcauggccguuCuuAguugguggaGUGAuuugucuggUV-AAUUccgAUAACGaacGAGAccuuaaccu-Gc	BLEAMERI
2313	18 HARVERMI	gCucuUucUUGAUUcagugGGuggUggugcauggccguuCuuAguugguggaGUGAuuugucuggUU-AAUUccgUUAACGaacGAGAccuuaaccu-Gc	HARVERMI
2313	19 THEANNUL	gCucuUucUUGAUUcuuugGGuggUggugcaUuggucguuCuuAguuGguggaGUGAuuuguCuggUU-AAUUccgUUAACGaacGAGAccuuaaccu-Gc	THEANNUL
2313	20 SYMPILOI	gCucudu cUDGAUCuaugGGuggUgguggaegueguegguggaeggueggaeggaeggaegaegaegaegaegaegaegaegaegae	SYMPILOI
2313	ZI ZBBSRZUS	קרט ברטעה כויטרפארטרפאטקפרטפטרפטרפטרפארט באינויים איניינים איניינים איניינים איניינים איניינים איניינים אינייני היניינייניים איניינים	ZBBSR205
2313	23 ZBBSR235	a university of the second s The second sec	ZBBSR235
2313	24 ZBBSR218	gCueutuet00A00euaug909ugeaugeeaugeeguucuuAguuggag000Auuugueugg00-AA00eeg00AAccueageeu-Ge	ZBBSR218
2313	25 ZBBSR217	gCucuUucUUGAUUcuaugGGuggUggugcauggccguuCuuAguugguggaGUGAuuugucuggUU-AAUUccgUUAACGaacGAGAAccucagccu-Gc	ZBBSR217
2313	26 ZBBSR211	gCucuUucUUGAUUcuaugGGuggUggugcauggccguuCuuAguugguggaGUGAuuugucuggUU-AAUUccgUUAACGaacGAGAccucagccu-Gc	ZBBSR211
2313	27 Pchroma	A-ucutu.c00A00cuaugedugeugeugeugeugeucgueguugguggag06A00Auuugucugg00-AA00ccg00AAcGaac6A6AccucgAccu-Gc	Pchroma
5155	28 EUGROTUR	a ucuoucuousouceungeseggeggeggeaugeneggeggegegegegegegegegegegegegegegeg	EUGROTION ENTOGTNO
2313	30 DICDISCO	ער היא מער היא	DICDISCO
2313	31 ZTnucl	gCCcugucC0GAUT0ugugGCuggUggugcauggccguuCuuAguuggugaaGUGAuuugucuggUU-UAUT0ccgUUAACGaacGAGACUauuAccA-A-	ZTnucl
2313	32 W10279	gCCcugucCUGADuuugugGCuggUggugcauggccguuCuuAguuggugaaGUGAuuugucuggUD-UAUUccgUDAACGaacGAUAcUauAcCA-A- 1	W10Z79
2313	33 W10Z74	gCCcugucCUGAUUUugugCCuggUggugcaguuCuuAguuggugaaGUGAuuugucuggUU-UAUUccgUUAACGaacGAGAcUauuAccA-A-	W10274
2313	35 W10210	gccongree.cugangregesingregesingregesentungrungeregegesensamungrengegu - vauregeguaadesaacelaanaeeea - arteringregesensensensensensensensensensensensensen	7/201M
2313	36 ZBBSR7	survey and a second	ZBBSR7
2313	37 ZBBSR173	ອັດຕິອາເດີນແດ້ນດີອີການທີ່ເຊື້ອງຄາຍອີດຈາກອີດຈາກຄຸ້ມແອບລາຍອີກາຍອີກາຍອີການອີການອີການອີການອີການອີການອີການອີການ	ZBBSR173
2313	38 Siphcyan	gCucutucUTANuuugugGGUUguggugcaugguggugguuggugggggggggggggggg	Siphcyan
2313	39 ZBBSR2 40 7794	adiuutukutatta kuutukuta adigaaga adga egundukuta ugga edekununuu uugu euggu kutu kutu eguntuka kuta ada eda ka atiuutukutatta kuta ada ada ada ada ada ada ada ada ada a	ZBBSR2 7/P4
2313	41 ZCR16	ggueuriCertragangagagggggggegegugunAgungggggggganungurunggunggun - AnthreegUnAACGaacGAAAcuanuaCu-Ge	ZCR16
2313	42 2CR6A	gCucuCucUUGAUUGugugGGuggUggaugcauggccguuGuuAguugguggUGUGAUuugucuggUU-AAUUccgUUAACGaacGAGAcuauCUAuu-Au	ZCR6A
2313	43 PHYPOLYC	gacuutactCaMtGauguaAougd/groups/drguceguecturofgeuceguegat/tofauucuge/ungfUr-th/th/cegat0AdACcecgeGGGU/Ce	PHYPOLYC
2313	45 euk heli	greenourooroorooggaagagaagagaagagaacaaareegaggaacaaareegagaacaaareegaxaxacaaacaaaggaagagear- 1 43 43 42 48 44 45 46 47 47 45 48 4-9 1	euk heli
2313	46 rad		rad

Posi- Sequence

ACACAST1 PHRBALAM STYALSID Pchroma EUGROTUN ENTOGING DICDISCO Siphcyan ZBBSR2 OXYGRANU BLEAMERI THEANNUL SYMPILO1 1369mask MNELEIDY DIAGRAND ATHBOMBA BLAEMERS CHLREINH ORYSATIV PORAERUG EMIHUXLE CAFROENB LABMINUT HARVERMI ZBBSR205 ZBBSR206 ZBBSR235 ZBBSR218 ZBBSR217 ZBBSR211 BBSR173 PHYPOLYC NAEGRUBE uk heli OCHDANIC ZTDUCL W10Z74 W10Z72 W10Z10 ZBBSR7 W10Z79 2CR16 ZCR6A ZCR4 uaa-AUAugcC-gcgcuaacccGUCCAUCAAAACCCAUGGGUGgcucacgcgguccgCUgcgggggugguggugguggucgcu----UCGC-----UCGC uaa-AVaAuGUVGGGC--AGAGGCCUVVGGUVUgauuAAguuucuuuuuUGGGGGCAACUCGGUuagagggggauGGagucUVAUCAAACUCUAGUucaaa uaa-uuaguUGcauuugAaauggAAAUGCA------uða-aŭaguaa--guacugu--------uaa-Aŭagcagd---Daauuuuu-------UVa-UVCgcaU---C-auaaU------uaa-AUaguaC----auuuuuU------auuuuuU------au uaa-AUaguau----aaucAC-----aaucAC-----uaa-CUaguCGAAc-c-aaUCUC------A 2-0 Data: <u>^</u> CAFROENB LABMINUT ZBBSR235 ZBBSR218 identity: 1 1369mask EUGROTUN ENTOGING DICDISCO ZBBSR173 Siphcyan DIAGRAND ATHBOMBA BLAEMERS ORYSATIV PORAERUG ACACAST1 PHRBALAM STYALSID EMIHUXLE OXYGRANU BLEAMERI HARVERMI THEANNUL SYMPILO1 ZBBSR205 ZBBSR206 ZBBSR217 ZBBSR211 PHYPOLYC NAEGRUBE euk heli MNELEIDY CHLREINH OCHDANIC Pchroma ZTnucl W10279 W10274 W10272 W10210 ZBBSR2 ZBBSR7 ZCR16 **ZCR6A** ZCR4 rad 33 2 ŝ v æ σ 2 님 12 13 14 15 16 5 18 61 20 527 33 24 25 26 28 29 30 33 37 34 35 35 35 37 38 6 40 41 42 43 46 tion: 2413 2413 2413 2413 2413 2413 2413 2413 2413 2413 2413 2413 2413 2413

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uuu-gu-gu-gu-------GUCUAacgcaaggAAGUu uAc-uu-gUGA------ACAACcaagCggAAGCu uAc-uu-gUGA-------hACAAccaagG99AAGCu uAc-gc-guC-------UACAAcgaagG99AAGCu ACG-ua-ucAAUCucuuuuuUAuacaGuaGauaauAAUUUGUGUUAUUUUGAAUAauaaaAauuauAuaGuguaUCaaaaagaAAAgauaAAGGAAGCG ugg-ug-auh------CaUAAgunacuggAOGCA ugg-ug-auh------CAUAAguuacuggAGGCA ugg-cu-uug-------CuaaaungenggAacuu uag-Au-uug------CUuaaaAAGcuggAAGcuggAAGUg uag-uu-uug-------CGuaaaAAgeuggAAgeu ugg-uu-uug-----UhuaaaWigcuggAAGUu ugg-cu-uug------CAuaaaUUgcuggACGAu uuc-auuceddaa------acUagaaugaggaAgau uau-ug-gc-------GUUUAgccaauggAAGUa uge-ugCge--------eccuagesgaAgou uau-uu-gcUC------CCAgcaaauggAAGUu uau-ccguGAU------UACCAacggauggAAGUu åac-uu-gu------CUUCAacaaguGgAAGUu uuu-gu-gg-------GCCAAAcacaaggAAguu uau-ucgcACCCG------CCAgcgaauggAAGUu uAc-uu-gUGA-----AACAACcaagCggAAGCu uAc-ga-guC------UACAAacgcgAggAAGCu uAc-gu-gaCC-----UACAAGcgcgcgAggAAGCu uAccugeCV-------CAAgeaggCggAAGUe 1gg-ug-auÀ------CÀUAAguuacuggAGGCA uuu-ug-gu------cACUAaccaaaggAAGUu Sept4aln" on 5-SEP-96 15:33:41 Data: 51 EUGROTUN ENTOGING DICDISCO ATHBOMBA BLAEMERS CHLREINH ACACAST1 PHRBALAM CAFROENB LABMINUT OXYGRANU BLEAMERI HARVERMI THEANNUL ZBBSR206 ZBBSR235 ZBBSR218 ZBBSR217 ZBBSR217 identity: NAEGRUBE euk heli 1369mask PORAERUG EMIHUXLE ZBBSR211 ZBBSR173 Siphcyan DIAGRAND ORYSATIV STYALSID OCHDANIC PHYPOLYC MUELEIDY SYMPILO1 ZBBSR205 Sequence Pchroma ZTnucl W10Z79 W10Z74 W10Z72 W10Z10 ZBBSR7 ZBBSR2 ZCR4 ZCR16 ZCR6A to su н r 8 0 0 2 ŝ v 40 42 43 4545 Position: 2613 2613 2613

ZBBSR205 ZBBSR206 ZBBSR235

SYMPILO1

ZBBSR218 ZBBSR217 ZBBSR211 EUGROTUN

STYALSID EMIHUXLE OCHDANIC

CAFROENB LABMINUT OXYGRANU BLEAMERI HARVERMI THEANNUL

MUELEIDY DIAGRAND ATHBOMBA BLAEMERS HUISALHC PORAERUG PHRBALAM

ORYSATIV ACACAST1

l369mask

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ENTOGING DICDISCO

ZTDUC1 W10Z79 W10Z74

Pchroma

Siphcyan ZBBSR2

ZBBSR173

W10272 W10210 ZBBSR7

PHYPOLYC NAEGRUBE

ZCR16 ZCR6A ZCR4

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Posi- Sequence

1369mask 1369mask 1186ma	CHLREINH CHLREINH CRXSATIV CRXEAUG BGCGGAUG-CC ACACAST1	Acuuuuuccuug PHRBALAM STYALSID EMIHUXLE OCHDANIC	CAFROENB CAFROENB CAFROENB LABMINUT CAFROENB CAFROENB CAFROENB	HARVERMI HARVERMI HARVERMI HARVILL HARVILL	The second sec	ZBSR211 Pchroma EUGROTUN JGGGAUUUUUAU ENTOGING	DICDISCO	M102/2 010210 2BBSR17 2BSR173	
111111111111111111111	cuACACugacgcgACCAACGAGCCUAU cuACACugaugUaUCCAACGAGUAUAUAG cuACACugaugcauGCAGCGAGUGUA cuACACugauuaaUCCAGCGAGUCUCAAUCGAC	cuACACugauugguchACUAGCANguguuACACaCo CuCACugaugaugcaUTCAACGAGUA	cuACACugGcuggUGCAACAAGUGCUACA cuACAAugaugaaUGCAACGAGUUAUAA cuACAAugacgcauACAGCGAGUAGUC	uuACACugaeggagUCAACGAGGUUUU cuACACugaugeguUCAAUCGAGUUA cuACACugaugegUUCAACGAGUUUGCAA cuACACuggugeaUUCAACAUGAUUAUA	cuACACuggugeaUUCAACAAGCAUAAUCA cuACACuggugeaUUCAACAAGCAUUAUAA cuACACugguguuUUCAACAAGCCUUAUUU cuACACugguguuUUCAACAAGCCUUAUUU	cuACACugguguuUUCAACAAGCCUAGUAC cuACACugacacguUCAUCAAGUUUACAAC cuACACugauacguUCAUCGAGCUCUA cuACAAugAaauACUAUAGUAGUAUACUACUUACUAG	cuxCaAuguaggaaACAAAAAGGCU	aukoAacaggggAgAyAaxuouxaauuraanusaanu aukoAacaggggAgAbAAxuoUxAAUU-AAA cuAcaAUaggagAgUAACUGAGUUUGUU-CAA cuAcAAUAggaGaaUUAGUACGCUUACCAU	CUNCAAUNGGAGAAUNACUNUUUCACDAT CUNCAAUBGGAGAUAQUAGUAGUUUUCACDAT CUNCAAUBGGAGAUAAUUAGCUUGO-UDA CUNCAAUBGGAGAUAAUUVAGCUUACU-CUA CUNCAAUBGGAGAUCAGUNCOCUUACVAU UUACAAUBGAGAAUCAGUNCOCUUGAACAAGGCC CUNCAAUBGUUAUAAAACGAGCGCUAUGGUUUUUAU CUNCAAUBGGUACCAGCGAGCGCUAUGGUUUUUAU
11111111111111111111111111111111111111	ggUcugugAugecCuuaGAUGUucuggGCCgcAcgcgCgC ggUcugugAugecCuuaGAUGUucuggGC-gcAcgcgCgC ggUcugugAugecCuuaGAUGUucuggGCCgcAcgcgCgC ggUcugugAugecCuuaGAUGUucuggGCCgcAcgcgCgC	gguedgugaugoccuuegAUGCeuggGCCGCAegegGG ggUeugaugaugacceuuagAUGUueuggGCCgcAegegGG ggUeugugAugoccuuaGAUGUueuggGCCgoAegegCG ggUeugugAugoccuuaGAUGUceuggGCCgoAegeGGG	ggÜcugugAugocCuuaGAUGUccuggGCCgcAcgogCgC ggÜcugugAugocCuuaGAUGUcuuggGCCgcAcgoGgCg ggÜcugaugacccuuaGAUGUccuggGCCgcAcgoGgG gdÜcugaugaccCuuaGAXG-ccugaGCCgcAcgoGG	໘໘Ⴎຬຩ໘ຆຌໞຆຬຬຬຒຆຨຨຆໟໟຆຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬ ໟໟຎຩຏຆໞຆໟຬຬຬຒຆຨຨຆໟຏຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬ ໟໟຏຬຩໟຏຌໞຆຬຬຬຒຆຨຨຆໟຏຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬຬ	ggDougugAugoochuaGAUGCuouggGoCCgoAcaugggg ggDougwgAugoochuaGAUGUuouggGoCCgoAcaugggg ggDougugAugoochuaGAUGUuouggGCCgoAcaogggg ggDougugAugoochuaGAUGUuouggGCCgoAcgogggg	ggUcugugAugeccUutaGAUGUucuggGCCgcAcgcggg ggucUgugAugecCuutaGAUGUucuggGCCgcAcgcgCg ggUcugugAugecCuutaGAUGUucuggGCUgcACgcgCg ggucugugAUgeCCUUAGAAUcuuggGCUgcAcgcgCg	ggrougugAugecctuuaGAUGACcuuggGoCg6cg5ggg ggrougugAugecctuuaGAUGUAeuggGoCg6cgeGeaegg6 ggrougugAugecctuuaGAUGUAeuggGCUg6Geaeggg6 ggrougAugeCcuuaGAUGUAeuggGCUg6Geaegg6	systements of the contraction of the control of the	sgfccugugAugeccaucGAVGUTuuggCAgeGeaeggg ggfbcugugAugeccuuaGAVGUTuuggGCAgeGeaeggg ggfbcugugAugeccuuaGAVGUTucuggGCAgeGeaeggg ggfbcugugAugeccuuaGAVGUTucuggGCAgeGeaegggg ggfbcugugAugeccuuaGAUGUTuuggGCAgeGeaegggg ggueugugAUGeccuuaGAUGUTucuggGCAgeGeaeggg ggueugugAUGeccuuaGAUGUTucuggGCCgeAegegGa gaueugugAUGeccuuaAAUGUTucuggGCCgeAegegGa gaueugugAUGeccuuaAAUGUTucuggGCCgeAegegGa at a to the
111111111111 ugaggCaaUaacA ugaggCaaUaacA ugaggCaaUaacA ugaggCaaUaacA	ຆ໘ຘ໘໘ຒຌຆຎຌຨຬໞ ຆໟຌໟໟຒຨຘຬໞ ຆໟຌຌໟຒຨຌຬຬຨ ຆໟຌຌຬຬຨຨຒຨຨຬຨ	ຆ໘ຘ໘໘ຒຘຆຒຨຘຒຨ ຆໟຌຏຌຒຨຏຒຨຬຒ ຬຌຬຌຌຒຨຏຒຨຬຒ ຨຌຌຌຌຒຨຏຒຨຨຒຨ	ggaggCaaUaacA ugaggCaaUaacA ugaggCaaUaacA uaaqqCaaUaacA	ຆ໘ຘ໘໘ຓຨຆຏຌຌຬຬ ຆຌຘຌໟຒຨຨຒຨຨຬຨ ຆ໘ຘຌໟຒຨຨຒຨຨຬຨ ຆຌຨຨຌຬຬຨຨຆຨຨຬຨ	ມຕອດດູດີCaaUaacA ນດູຂດງດີCaaUaacA ນດູຂດງດີCaaUaacA ນດູຂດງດີCaaUaacA	ຆໟຌໟໟຬຨຨႮຨຨຬໞ ຬໟຌໟໟຬຨຨຆຨຨຬໞ ຬໟຌໟໟຬຨຨຆຨຨຬໞ ຆຆຨຨຬຬຨຏຬຨຬຨ	cgaggcaauaacA aguUgCaaUgacA aguUgCaaUgacA aguUgCaaUgacA	aguugcaaugaca aguugcaaugaca gguagcaauaaca Uguagcaauaaca	gguagcaAuaacA gguagcaAuaacA aguagcaatbaacA gguagcaatbaacA gguagcaatbaacA uuaggccAUaatbaacA uuaggccAUaacA 48
1 1369mask 2 MNELEIDY 3 DIAGRAND 4 ATHBOMBA 5 BLAEMERS	6 CHLREINH 7 ORYSATIV 8 PORAERUG 9 ACACAST1	10 PHRBALAM 11 STYALSID 12 EMIHUXLE 13 OCHDANIC	14 CAFROENB 15 LABMINUT 16 OXYGRANU 17 BLEAMERI	18 HARVERMI 19 THEANNUL 20 SYMPILO1 21 ZBESR205	22 ZBBSR206 23 ZBBSR235 24 ZBBSR218 25 ZBBSR217	26 ZBBSR211 27 Pchroma 28 EUGROTUN 29 ENTOGING	JU DICDISCO 31 ZTNUC1 32 W10279 33 W10274 33 W10274	35 W10210 35 W10210 37 ZBBSR173 37 ZBBSR173	18 Siphcyan 19 ZBBSR2 41 ZCR4 42 ZCR66 43 PHYPOLYC 43 PHYPOLYC 44 NAEGRUBE 45 euk heli 46 rad
2713 2713 2713 2713 2713	2713 2713 2713 2713	2713 2713 2713 2713	2713 2713 2713 2713	2713 2713 2713 2713 2713	2713 2713 2713 2713	2713 2713 2713 2713	2713 2713 2713 2713	2713 2713 2713 2713	2712 2713 2713 2713 2713 2713 2713 2713

Posi-	Sequence		
tion:	identity:	Data:	
2813	1 1369mask		1369mask
2813	2 MNELEIDY		MNELEIDY
2813	3 DIAGRANE		DIAGRAND
2813	4 ATHBOMBA	1	ATHBOMBA
2813	5 BLAEMERS	UUCGGCUCGGCCUGAGCUUAAGCUGGGAUU	BLAEMERS
5182	6 CHLREINE		CHLREINH
5187	V ORYSATIV		ORYSATIV
CT07	B PUKAEKUC	1	PORAERUG
5182	9 ACACASTI	-GU-UGGGGUCAAACCCAACUGUGUC-GCUGUC-GCUGUCGCGCGCGGGGGGGG	ACACAST1
5182	11 CHKBALAN	uucuucucdaaAAgggagggggggggggggggggggggggg	PHRBALAM
2813	TICHTIC IL		STYALSID
2813	13 OCHDANIC		EMIHUXLE
2813	14 CAFROENB		CARDENE
2813	15 LABMINUT		L'ARMTNITT
2813	16 OXYGRANU		OXYGRANU
2813	17 BLEAMERI		BLEAMERI
2813	18 HARVERMI		HARVERMI
2813	19 THEANNUL		THEANNUL
2813	20 SYMPILOI		SYMPILO1
5182	20232882 12	. URAGANAU-UNGANAU-SGAGGAAGGGAGGGAAGGGAGGCGAAGGGAU-AAUCU-UVGANAU	ZBBSR205
CT07	JUZNEBERZUE		ZBBSR206
CT07	CLANCERS LL		ZBBSR235
CT07	CICUMARA NC		ZBBSR218
2813	26 ZRRSP211	Coudaace-Odahaggucugggucugggucugggucugggucuuuoaaace-	ZBBSR217
2813	27 Debroma		ZBBSR211
2813	28 FUCEOTIA	20000000000000000000000000000000000000	Pchroma
2813	29 ENTOGING	Tronting	EUGROTUN
2813	30 DTCDTSCO	UCCAUDA	ENTOGING
2813	31 ZTnucl		DICDISCO
2813	32 W10Z79		Tonutz
2813	33 W10Z74		6/70TM
2813	34 W10Z72	2014.001-001-001-001-001-001-001-001-001-001	W10272
2813	35 W10Z10		OIZOIM
2813	36 ZBBSR7	gagaA-gaacUgugg-AAUCUUAAAAC	ZBBSR7
2813	37 ZBBSR173		ZBBSR173
2813	38 Siphcyan		Siphcyan
2813	39 ZBBSR2		ZBBSR2
5137 2111	40 20K4	2	ZCR4
2813	42 20P64	UUAAAAAUgcuaUgaauga-AAUgcuUUAAAC	ZCR16
2813	43 PHYPOLYC		ZCR6A
2813	44 NAEGRUBE		ЭХТОАХНА
2813	45 euk heli		NAEGRUBE
2813	46 rad		EUK DELL
			rac

Siphcyan ZBBSR2 ENTOGING ZBBSR7 ZBBSR173 STYALSID EMIHUXLE NAEGRUBE EUGROTUN DIAGRAND BLAEMERS PORAERUG CAFROENB OXYGRANU ZBBSR206 ZBBSR218 ZBBSR211 PHYPOLYC euk heli **1369mas**k MNELEIDY ATHBOMBA CHLREINH PHRBALAM OCHDANIC BLEAMERI HARVERMI THEANNUL ZBBSR205 ZBBSR235 ZBBSR217 ORYSATIV ACACAST1 LABMINUT SYMPILO1 Pchroma W10Z74 W10Z72 ZTnucl W10279 W10Z10 ZCR16 ZCR6A CR4 rad ugcaucgUGAVGGGAVUgacuCUVGGAAVUAVUAUVAGCGAGGAAuuccuAGUAa-aCgca-agUCAVCAAcuugcAuuGACUACGUGCcu UgcaucgUGAUGGGAUAgaucaUUGCAAUUAUugaucUUCAACGAGGAauuccUAGUAa-gcgcg-aguCAUCAgcucgugcuGAUUACGUCCCUgccc ugcaaccgUGCUUGGGAUAgacuaUUGCAAUUUUuagucUUCAACGAGGAAuuccuAGUAa-aCgca-agUNAUCAGcuugcAuuGAUUACGUCCCugccc инАиАсаЮЗАСАОGФАИиааидаИИФААИЙАИиидииаИФААСФАФСААФСААШиссиЙФИАа-аАиид-иgUCAUИААсаиааФииGAAUACGUCCCиgccc uccua cgUAACUGGGCUugau cUUUGUAAUUAUUgau caUAAACGAGGAauu ccUUGUAa-gcgua-agUCAUUACcuu aug cu GAAUAUGUCCCug cc uGucuu u AUAUAUGGAAUugCACu aUGCAAUUUu - aCAcaUAAACUAGGAau aU cu UGUAa-gU gu a-agU CAUAAU cgugu U cu GAAUGCGUCCCu gu cc uGccuuuAAVAVGGAAVugCgCuaVGCAAVVVu-acAcaVAAACVAGGAauaVcuVGVAa-gVaca-ugVCAVAAVcguguuVcuQAAVGCGVCCCugucc uucau cgUGCUGGQGAUAgaccaUUGCAAUUAUuggucUUGAACGAGGAauuccUAGUAa-gcacg-agUCAUCAAcucgugcuGAUVACGUCCCUgccc cuugycgUGCUGGGGCUAgaucUUUGUAAUUUUCgaucUUCAACGAGGAauuccuAGUAa-gcgug-auUCAUCAGaucgcguuGAUUACGUCCCugccc cuuau cgUGAUGGGGAUUGaCcUUUGUAUUAUUAUGACGAGGAAU accuAGUAa - gugug - ggUCAUCAAcccacgcuGAUUACGUCCCugccc ulcaucgUQAUGGGANagaucaUUGCAAUUGUuggucuUCAACGAGGAaugccuAGUAa-gcgcg-agUCAUCAGcucgcguuGACUACGUCCCugccc ugcaucgUGCUGGGGAUagauuaUUGUAAUUAUuaaucuUCAACGAGGAaugccuUGUAa-gcgca-agUCAUCAGcuugcguuGAAUACGUCCCugccc uucgUcgUGaUGGGGCUAgaccCUUGCAAUUAUUggucUCCAACGAGGAauuccUAGUAa-aCgca-agUCAUCAGcuugcAuuGAUUACGUCCCUgccc ugcgucgUGAUGGGANAgaucuUVGGAAUVAVagaucUVGAACGAGGAauuccuAGVAa-gcgca-agVCAUVACcuugcgcuGAUVAAGVCCCugccc uccgucgUGAUGGGGAUagaucaUUGCAAUUAUugaucuUGAACGAGGAauuccuAGUAa-gcgcg-agUCAUCAAcucgcgcuGAUUACGUCCCugccc cgcaucgUGAUGGGAUCGauuaUVGCAAUUGUuaaucGUGAACGAGGAugccUAGUAu-gcgca-agUCAUCAGcuugugcaGAAUVACGUCCCugccc ugcaccg0Gc0UGGGAUAgacuaUUGCAAUUUUagucUUCAACGAGGAauuccuAGUAa-aCgca-agUCAUCAGcuugcAuuGAUUACGUCCCugccc ugcaccgVGcVVGGGAVAgacuaVVGCAAVVVVuagucVVCAACGAGGAuuccuAGVAa-aCgca-agVCAVCAGcuugcAuuGAVVACGVCCCugccc aacaccgUGCUUGGGAUAgacuaUUGCAAUUUUuagucUUCAAGGAauuccuAGUAa-aCgca-agUCAUUAGcuugcAuuGAUUACGUCCCugccc aacaccg1dGCUUGGAUAgacuaUVGCAAUUUUuagucUUCAACGAGGAuuccuAGUAa-acgca-agUCAUVAGcuugcAuuGAUVACGUCCCugccc aacaccgUGCUUGGGAUAgacuaUUGCAAUUUUuagucUUCAACGAGGAAuuccuAGUAa-aCgca-agUCAUUAGcuugcAuuGAUUACGUCCCugccc cgugucgUGAUGGGAUAgauuaUUGUAAUUAUugaucUUCAACGAGGAauuccUAGUAa-aCgcg-ggUCAUCAAcccgnAuuGAUUACGUCCCugccc cguaucgUGAUGGGGAUagauuaUUGUAUUUUugaucuUCAAGGAGuuccuAGUAa-aCgcg-cguCAUUAacgcgcgAuuGAUVACGUCCCugccc uGccuuuAAUAUGGAAUugGgCuaUGCAAUUU-acAcaUAAACUAGGAauaUcuUGUAa-gUaca-ugUCAUAAUcguguUcuGAAUGGGUCCCugucc uGccuuuAAUAUGGAAUugCACuaUGCAAUUUu-aCAcaUAAACUAGGAauaUcuUGUAa-gUaca-ugUCACAAUcguguUcuGAAUGCGUCCCugucc uGccuuuAAUAUGGAAUugCgCuaUGCAAUUUu-acAcaUAAACUAGGAauaUcuUGUAa-gUaca-ugUCAUAAUcguguUcuGAAUGCGUCCCugucc uCuucuuVAVAGAAVcacgCuVVGCAACVVVaCcgugVAAACVAGGAauaccuAGVAa-guguU-uguCAVCAacgVacgcuGAAVACGVCCCugccc uuàuuuAUAAUUGGGCUuacgCaUuGAAGUUGUAuguaCAAACCAGGAauaucuAGUAa -auAga-uguCAUUAacauuGauuGAAUAUGUCCCugccu uGAcuuAUAAUUGGGCUuacaCaUUGAAUUUUuuguaUAAACCAGGAauaUcuAGUAa-gUcaa-gguCAAUAacAuugUuuGAAUGCGUCCCUgccu uuuvuuVAUAVGGAAVcasgCUVUGAAAUUVUVAcgugVAACUAGGAauaCcuAGVAa-gugua-uguCAVCAacgugcauuGAAVAUGVCCCugccc uGuucuAUAUGGAAUuacGCuUuGAAAUVaUaCGguaUAAACCAGGAauaCcuAGUAa-guguA-uguCACUAacgCguacuGAAUACGUCCCugccc GAuucuUVAUVVOUAAVcaugcuUVGAAAVVUVUAAcaugVAAACVAGGAauaucCAGUAa-guguV-UguCAVCAacUVgcacuGAAVACGVCCCugccc ---ucugucgUGCUGGGAUAgagcaUVGCAAUVAUugcucUVCAACGAGGAauaccuAGUAa-gcgca-agUCAUCAGcuugcguuGAUVACGUCCCugccc cgcgucgUGAUGGGQAUagauuaUUGCAAUVAJuagucuUCAACGAGGAaugccuAGUAa-gcgcg-agUCAUCAGcucgcguuGAUVACGUCCCugccc uuaaucgUGCUGGGGAUagaucaUUGUAAUUAUugaucuUCAACGAGGAauuccuAGUAa-gcgcg-agUCAUCAGcucgcguuGAUUACGUCCCugccc cuaaucgUdAUGGGAAUaggccUUVGCAAUUAVUggccuUAAACGAGGAauuccuAGUAggcCGCCUAGUCAUC - - MKUGCgccGACGUCCCUgccc ugcaucgUGCUGGGGAUagauuaUUGGAAUUAUuaaucuUGAACGAGGAauuccuUGUAa-gcgug-agUCAUCAGcucgcguuGAAUACGUCCCugccc ugcaUcgUGAUGGGAUAgauuaUUGCAACUAUuaaucUUCAACGAGGAauuccUAGUAa-gogug-ugUCAUCAGegcacguuGAUUACGUCCCugccc ugugUcgUdgUdgAUAGGGAUAgauuaUUGCAAUUAUuaaucUUGAACGAGGAauuccUAGUAa-augcg-ggUCAUCAGcucgcguuGAUUACGUCCCugccc ccagCcgUGAUGGGAUAgguuCUUGCAAUUUUUaauCUUCAACGAGGAuuccUAGUAa-aCgca-arUCAUCAGcuugcAuuGAUUACGUCCCugccc uuACuuACAAUUGGGCUuacgCaUuGAAUUaUuAuguaCAAACCAGGAauaucuAGUAa-aUaga-uguCAUUAacauugCuuGGAUAUGUCCCugccu cCugcuUUGACUGGGACAgaucUUUGCAAUUAUUggucUCAAACGAGGAuuuuuAGUAa-Ucgca-ggUCAUUAAccugcgUuGAAUGCGUCCCugccc accguuAUGACAGGGAUcgaggaUUGGAAC-Au-ccucgUGAACGAGGAuuccUAGUAa-gCgug-guUCAUGAUaccacAuuGAUVACGUCCCUgccu ----ŝ ·---ŝ -----80 54 <u>....</u> 54 ----Data: 22 identity: 1369mask MNELEIDY DIAGRAND ATHBOMBA BLAEMERS CHLREINH PORAERUG PHRBALAM EMIHUXLE CAFROENB OXYGRANU EUGROTUN DNIDOLNE DICDISCO ZBBSR173 PHYPOLYC ORYSATIV STYALSID OCHDANIC LABMINUT BLEAMERI THEANNUL ZBBSR205 ZBBSR206 ZBBSR235 ZBBSR218 ZBBSR217 ZBBSR211 Siphcyan NAEGRUBE euk heli HARVERMI SYMPILO1 Sequence ACACAST: Pchroma W10Z72 ZTnucl W10Z79 W10274 W10210 ZBBSR7 ZBBSR2 ZCR16 **ZCR6A** 2CR4 rad 20 m 39 40 41 ÷ 44 32 46 Position: 2913 2913 2913 2913 1913

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	1 1369mar 1 1369mar 2 2 MAELBII 2 2 MAELMER 2 2 MELMER 2 2 2 MELMER 2 2 2 2 MELMER 2 2 2 MELMER 2 2 2 MELMER 2 2 2 MELMER 2 2 2 2 MELMER 2 2 2 MELMER 2 2 2 2 MELMER 2 2 2 2 2 MELMER 2 2 2 2 2 MELMER 2 2

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tion:	identity:	Data:	
3114	1 1369mask	11111111111111111111111111111111	1369mask
3114	2 MNELEIDY	aCggcgCcgcc-gaGAAC-UUgC-ucAAa-cuUdaucauuuuAGAggAaguaAAAGUCGUAACAAGGuuucCguaqquGAaccuqcAqaaqqGAUCAAG	MNELEIDY
3114	3 DIAGRAND	CgccugAguu-ggGAAC-UUgC-ucAAa-cuUGaucauuuAGAggAaguaAAAGUCGUAACAAGGuuucCguagguGAaccugcAgaagGAUCAAG	DIAGRAND
3114	4 ATHBOMBA	A-Cccgc-gUUgcu-gadAAG-CUga-ucAAa-cuUGgucauuuAGAggAaguaAAAGUCGUAACAAGGuuucCguaaggUGAAccugcAgaagGAUCAAG	ATHBOMBA
3114	5 BLAEMERS	Acac-uuggcga@AAA-UUgC-ucAAa-cuUggucaucuAGAggAaguaAAAGUCGUAACAAGuuuccguaggUGAAccugcggaagGAUCAUU	BLAEMERS
3114	6 CHLREINH	ccUVgcuu-gaGAAG-UVca-uuAAa-ccCVcCcaccuAGAggAaggaGAAGUCGUAACAAGuuuccguaggVGAAccugcgggaagGAVCAVV	CHLREINH
3114	7 ORYSATIV	c-ccccgAcgucgc-gaGAAG-UCca-uuGAa-ccUuaucauuuAGAggAaggaGAAGUCGUAACAAGuuuccguaggUGAAccugcggaagGAUCAUU	ORYSATIV
3114	8 PORAERUG	cgagugcggAAAG-UUca-uuAAa-ccUuaucaucuAGAggAaggaGAAGUCGUAACAAGGuCucCguagguGAaccugcAggAAgGAUCAAG	PORAERUG
3114	9 ACACAST1	CUCCCCUTUUu-GgcggAGGAAG-UCga-uuGAa-ccUTaccauuuAGAggAaggaGAAGUCGUAACAAGGucuccguaggUGAAccugcggaggGAUCAUT	ACACAST1
3114	10 PHRBALAM	gguuuuauauuuuc-caQAAG-UUau-cuAAa-ccUUauuaucuAGAggAaggaqAAGUCGUAACAAGGuuucuguagguGAaccugcagaagGAUCAAG	PHRBALAM
3114	11 STYALSID	gcGauTcgucccgaGAAG-UUca-uuAAa-ccUUaucauuuAGAgGAaggaGAAGUCGUAACAGGuuucCguagguGAaccugcAgaagGAUAGA	STYALSID
3114	12 EMIHUXLE	CgcgAcgccgc-rgGAAG-CUgU-ccGAa-ccUTaucauuuAGAggAaggaQAAGUCGUAACAAGGuuucCguaggUGAAccugcAgaagGAUCAAG	EMIHUXLE
3114	13 OCHDANIC	ggagAaucgu-ggAAAG-UUaU-uuAAa-ccUCaucauuuAGAggAagguGAAGUGGAACGGAAGGuuuccguaggUGAAccugcggaagGAUCAUU	OCHDANIC
3114	14 CAFROENB	ggugAlaggAc-gaGAAg-cuAAa-ccUdaccaucuAGAggAagguGAAGUGUAACAAGguuucCguaggUGAAccugcAgaagGAUCAA	CAFROENB
3114	15 LABMINUT	aacgCUgruuu-aaAAAG-UUga-uuAAa-ccUUaccauuuAGAggAagguGAAGUCGUAACAAGGuuucCguaggUGAAccugcAgaagGAUCAAG	LABMINUT
3114	16 OXYGRANU	gccuugugc-gggAAAA-CCAA-guAAa-ccAuaucacuuAGAggAaggaGAAGUCGUAACAAGGuuuccguaggUGAAccugcAgaagGAUCAUU	OXYGRANU
3114	17 BLEAMERI	gugugu-ggGAAG-UUGA-guAA-ccUUaucacuuAGAggAaggaGAAGUCGUAACAAGGuAucuguaggUGAAccugcagaAgGAUCAAG	BLEAMERI
5114	18 HARVERMI	ccuguguccg0gccaGAAG-CUgu-ucGAA-ccUUaccguuuAGAggAaggaAgGAAGUCGUAACAAGGUauccGua-gUGAAaCcugCAgaAgGAUCAAG	HARVERMI
3114	19 THEANNUL	gggaacgucUA-ggGAAG-UUUV-guGAa-ccUUaucacuuAAAggAaggaGAAGUCGUAACAAGGuuucCguaggUGAAccugcAgaagGAUCAAG	THEANNUL
3114	20 SYMPILO1	gAcguugcguu-ggAAAG-UUuC-auGAa-ccUUaucacuuAGAggAaggaGAAAUCGUAAGGuuuccguaggUGAAccugcAgaagGAUCAAG	SYMPILO1
3114	21 ZBBSR205	acgguacauUuuaaCAAc-uuaa-UcAAa-ccUaaucaucuAGAggAaggaGAAGUCGUAACAAGGuuucCguaggUGAAccugcAgaagGNUCAAG	ZBBSR205
3114	22 ZBBSR206	acaUugcguUuuaaCAAc-uuaa-VcAAa-ccUaaucaucuAGAggAaggaGAAGUCGUAACAAGGuuucUguaggUGAAccugcAgaagGAUCAAG	ZBBSR206
3114	23 ZBBSR235	acgguacauUuuaaCAAc-uuaa-ccUaAucaucaucuAGAggAaggaGAAGUCGUAAGGuuucYguaggUGAAccugcAgaagGAUCAAG	ZBBSR235
3114	24 ZBBSR218	AcgG-A-UUuc-gaCAAc-uuga-UCAAa-ccUaaucaucuAGAggAaggaGAAGUCGUAACAAGGuuucCguaggUGAAccngcAgaagGAUCAAG	ZBBSR218
3114	25 ZBBSR217	AcgG-A-UUuc-gaCAAc-uuga-UCAAa-ccUaaucaucuAGAggAaggaGAAGUCGUAACAAGGuuucCguaggUGAAccugcAgaagGAUCAAG	ZBBSR217
3114	26 ZBBSR211	ugAAUuuUuc-gaAAAc-uuga-UcAAa-ccUaaucaucuAGAgGAaggaGAAGUCGUAACAAGGuuucCguaggUGAAccugcAggaagGAUCAAG	ZBBSR211
3114	27 Pchroma	cacugcgggcAugc-auGAAC-UgaA-AcAAa-ccUGagcgucuAGAggAaguaAAAUCGUAACAAGGuuuccgua-gUGAACcugcAgaagGAUCA	Pchroma
3114	28 EUGROTUN	UUU9gcaUacU-g-QAAG-Ugac-CCAAa-cuUGaucaucuA6AggAaguaAAAGUCGUAACAAGGuuucCgua-gUGAACcugcAgaagGAUCA	EUGROTUN
3114	29 ENTOGING	caauugaaaaUgaAAA-uagaUGuGAa-ccUCCuuauuuAGAggAaggaGAAGUCGUAACAAGGuuuccguaggUGAAccugcgggaagGAUC	ENTOGING
3114	30 DICDISCO	GAUauaaau-UaAAAuuaVuuAAa-uuCCauuguuuAGAggAaggaGAAGUCGUAACAAGGuaucoguaggUGAAccugoggaugGAUCAUU	DICDISCO
3114	31 ZTnucl	UGAAKGucaguu-auAUaU-auuu-gcAAa-cuAAAcuauuuAGAggAaggaGAAGUCGUAACAAGGuuuccguaggUGAAccugcAgaa	ZTnucl
3114	32 W10Z79	UAAAGGuuaguu-auAUaU-auuu-gcAAa-cuAAAcuauuuAGAggaAggaGAAGUCGUAAGGuuuccguaggUGAAccugcAgaaggAUCAAG	0279 W
3114	33 W10274	UGAAGGucaguu-auAUsU-auuu-gcAAa-cuAAAcuauuuAGAggAaggaGAAGUCGUAACAAGGuuucuguaggUGAAccugcagaagGAUCAAG	W10274
3114	34 W10272		W10272
3114	OTZATA SS	Ανάλαθασασμάμα - αμάμα - ανάμα - στάλα - στάλλο τα μυμάθασα βαδάδα στα δάλο Αλολολλολογία στο μαράδο στα σ	W10210
3114	36 ZBBSR7	0000guaCUuuuuuAAa-auuu-gcAAa-uuAAAuuuuuuAAAggAaggAAGAAGUCGUAACAAGGuuucCguaggUGAAccugcAgaagGAUCAAG	ZBBSR7
3114	S/LASBEZ /S	AUCAAAAGGGuaAAc-auuu-gaAAa-cuAGAuuauuuAGAggAaggaGAAGUCGUAACAAGGuuucCguaggUGAAccugcAgaagGAUCAAG	ZBBSR173
3114	38 Siphcyan	acchuudugGuUdAg-auuu-gCUAa-cuAGAuuauuuAGAggAaggaGAAGUGUCGUAACAAGGuuucCguaggNGAAccugcAgaagGAUCAAG	Siphcyan
3114	39 ZBBSR2	UGUUGuhUuu-UuAAA-auuu-gcAAa-cuAGAuuaucuAGAggAaggaGAAGUCGUAACAAGouuucCguagguGAAccugcAgaagGAUCAAG	ZBBSR2
3114	40 ZCR4	DAUDguGADuu-DuuAa-auuU-acAAa-cuAGAuuauuuAGAggAaggaGAAGUCGUAACAAGGuuucCguaggUGAAccuNcAgaagGNUCAaN	ZCR4
3114	41 ZCR16	guAGUACAauuuuuAAa-aUuu-gcAAg-cuAGAuuaucuAGAggAaggaGAAGGUCGUAACAGGuuucCguaggNGAAccugcAgaagGAUCAAG	ZCR16
3114	42 ZCR6A	uaGCAAAGGGGuaAAC-auuu-gUAAa-cuAGAuuauuuAGAggAaggaGAAGUCGUAACAAGGuuucCguaggUGAAccngcAgaagGAUCAAG	ZCR6A
3114	43 PHYPOLYC	ggggggggucggccAAAGG-UCUA-ACUacuGUaCggccuAGAggAagcaGAAGUCGUAACAAGGuaaUcguaggUGAAccugcgUuugGAUCAUU	PHYPOLYC
3114	44 NAEGRUBE	CAAgguAA-ggGAAA-ceag-uuAa-ucUCuucgucuGUAggAaggAAgGUCUVACAAGGucuUcguaggUGAAccugcgUaggGAUCAUU	NAEGRUBE
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