The origin and evolution of release factors: implications for translation termination, ribosome rescue and quality control pathways

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SUPPLEMENTARY MATERIAL

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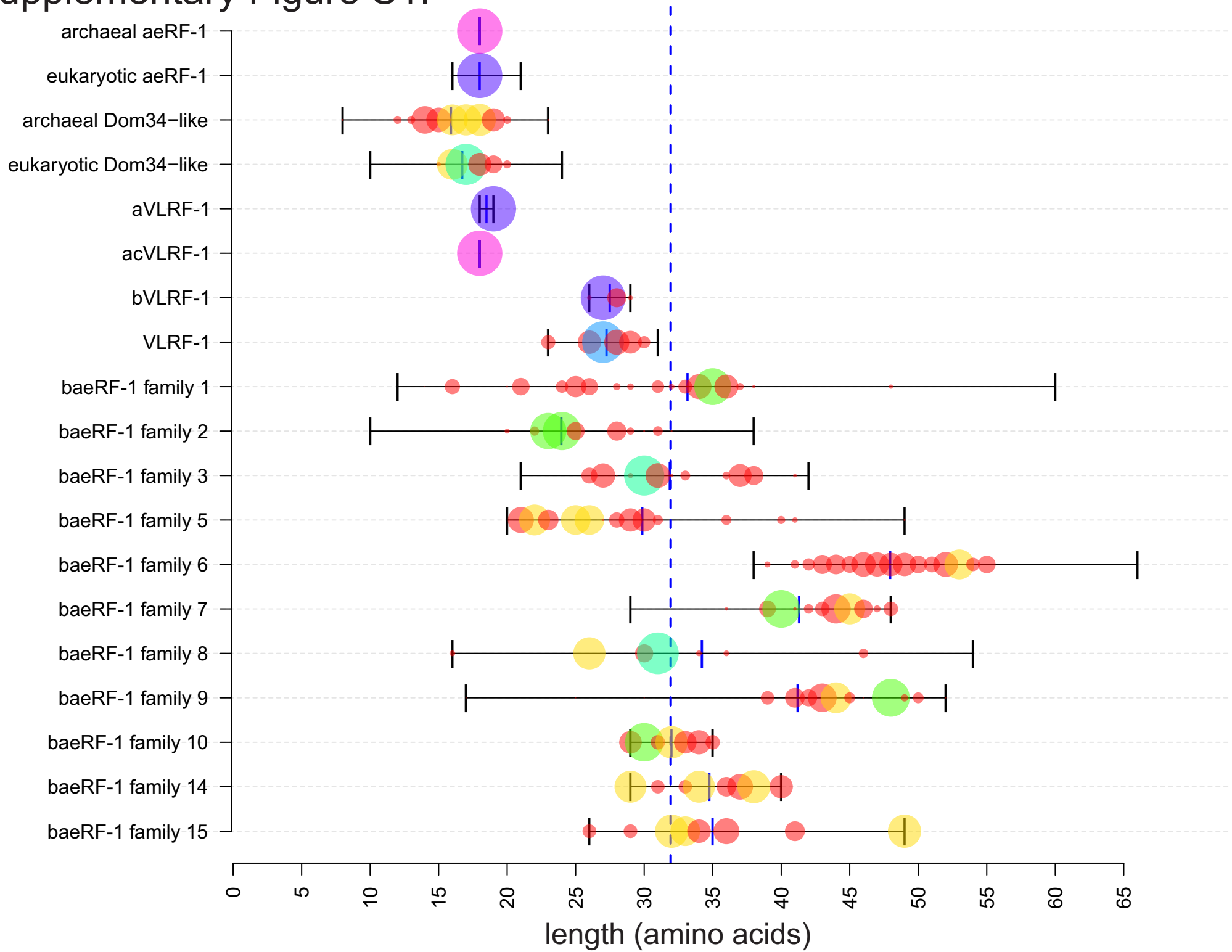
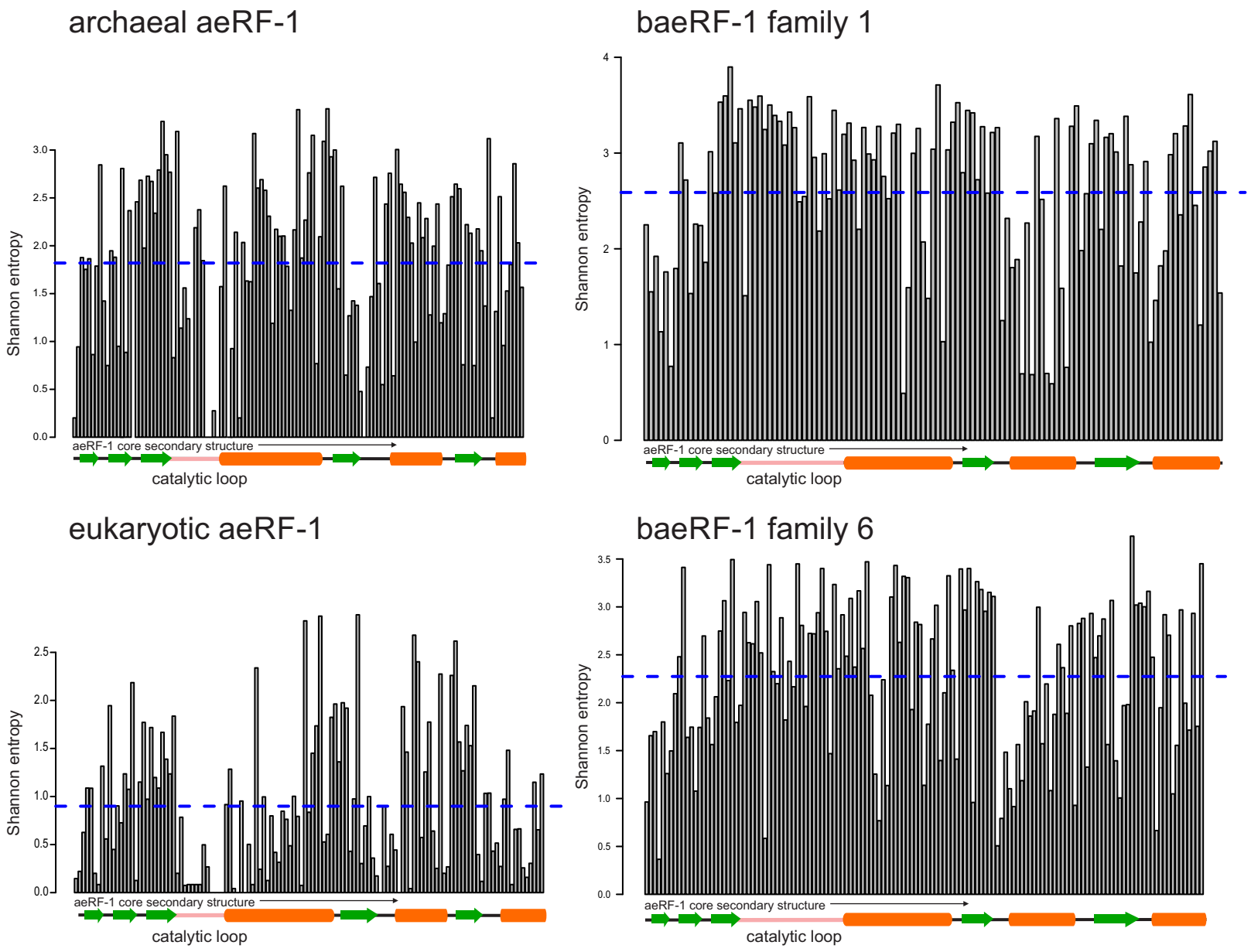
Supplementary Figure S1. Length diversity of catalytic loop in aeRF-1 families. Families are labeled on the *y*-axis and length of catalytic loops are plotted by total amino acid number on the *x*-axis. Sequences within a family corresponding to a specific length are depicted as a circle centered at that length, with circle radius scaled by the number of sequences in the family with that length, normalized by the total sequence count for the family. Loop sequence lengths which are unique (only a single sequence is observed at that length) within a family are not assigned circles. Coloring of circles within a family is based on an automatically-generated rainbow spectrum with red coloring for smaller numbers of sequences and violet coloring for larger numbers of sequences. Black lines depict the range of loop lengths across a family. Blue vertical bars in each family provide the median length in a family. Dotted blue vertical line indicates the median for all loop lengths across all plotted families.

Supplementary Figure S2. Positional entropy values for baeRF-1 families (right column) compared to the classical aeRF-1 families (left column). Mean entropy values within a family are plotted as blue horizontal lines and secondary structures are provided at bottom of plots. Catalytic loop region is labeled and shown as pink line in the secondary structure. Entropy was calculated using the Shannon entropy formula $-\sum_{i=1}^{M} P_i \log 2 P_i$ where P_i is the fraction of a given amino acid i and M is the total number of different amino acids.

Supplementary Figure S1.



Supplementary Figure S2.



SUPPLEMENTARY DATA

The origin and evolution of release factors: implications for translation termination, ribosome rescue and quality control pathways

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ABSTRACT

The evolution of the release factor-peptidyl hydrolase (RF-PH): which catalyze the breakage of the final tRNA-peptide bond during translation termination, is central to understanding the origin and early evolution of the translation apparatus. Here we report the identification of a large number of archaeo-eukaryotic RF-PHs emerged from distinct prokaryotic folds on the base of their respective lineages. Recent computational surveys and targeted experimental studies have revealed that several of these RF-PHs are involved in ribosome rescue and quality control pathways, including the eukaryotic quality control pathway.

This recent work is distilled into an accounting of the diversification of these RF-PH domains, and this is in turn placed into the broader evolutionary framework of the evolution of the translation apparatus. We review the deep evolutionary ancestor for the origins of these RF-PH domains in light of this new comprehensive survey. Subsequently, we focus on the evolutionary trajectories of the various RF-PH domains in archaeo-eukaryotes. We also review the evolutionary trajectories of the several offshoots involving release and the ribosome, including pathways activated in response to ribosomal stalling such as the ribosome quality control pathway. Finally, we report on a novel domain architecture for a release factor in which the RF-PH domain is fused to a GTPase domain. Such solutions were subsequently transferred across superkingdoms. We report the first global survey of one such solution, prototyped by the recently-characterized HBS1-PELO system in eukaryotes, in which the GTPase domain is fused to a release factor-like domain in a vast majority of bacteria and archaeo-eukaryotes. Finally, we report on an under-appreciated aspect that appears to have frequently driven innovation in rescue pathways: biological conflict with genic entities likely to evolving to disable translation directly at the ribosome. At least three rescue pathways clustered on the RFa, ArfA/PrfJ, and eIF3j/HBS RF-PH domains; were likely involved in response to such conflict.

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DATA

I. List of sequences for novel archaeo-eukaryotic release factors

A. ImmA/IrrE clade

1. Family 1

##Family 1 is a standalone ImmAF1, there are no N- or C-terminal fusions

WP_097419297.1	-	152	bacteria\proteobacteria\alphaproteobacteria	Salipiger mucosus DSM 16094
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WP_085293302.1	-	152	bacteria\proteobacteria\alphaproteobacteria	Roseovarius indicus
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WP_098570962.1	-	152	bacteria\proteobacteria\alphaproteobacteria	Leisingera daeponensis
WP_013290423.1	-	152	bacteria\proteobacteria\alphaproteobacteria	Leisingera methylohalidivorans
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WP_013290423.1	-	152	bacteria\proteobacteria\alphaproteobacteria	Leisingera methylohalidivorans
WP_013290423.1	-	152	bacteria\proteobacteria\alphaproteobacteria	Leisingera sp. MED145
WP_013290423.1	-	152	bacteria\proteobacteria\alphaproteobacteria	Leisingera sp. MED145
WP_013290423.1	-	152	bacteria\proteobacteria\alphaproteobacteria	Leisingera sp. MED145
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WP_053682583.1	-	157	bacteria\proteobacteria\alphaproteobacteria	Jannaschia seosinensis
WP_053682583.1	-	157	bacteria\proteobacteria\alphaproteobacteria	Jannaschia aquimarina
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WP_013693464.1	-	152	bacteria\proteobacteria\alphaproteobacteria	Maricaulis maris
WP_053683420.1	-	151	bacteria\proteobacteria\alphaproteobacteria	Jannaschia rubra

frequent family of fairies the standard zone microsystems index. description. measurement. frequently.

chemistry

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chemistry 2

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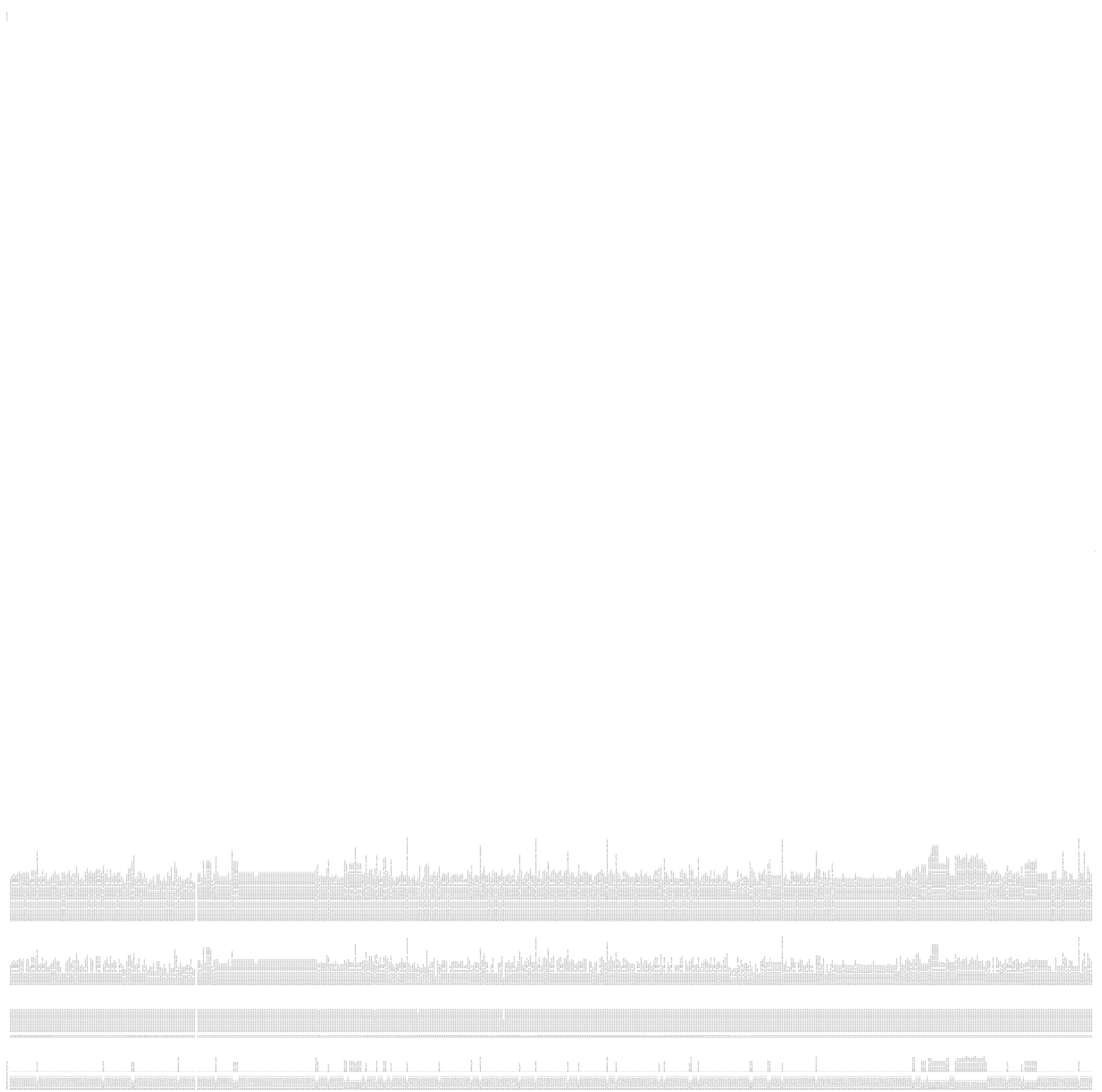

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Academic Library Acquisitions

Acquisitions Librarian	Cataloging Librarian	Interlibrary Loan Librarian	Reference Librarian	Serials Librarian	Systems Librarian

Committee Report: Annual Review of Operations

Chapter 1: Introduction

Section 1.1: Background

Section 1.2: Methodology

Chapter 2: Findings

Section 2.1: Overview

Section 2.2: Details

Chapter 3: Recommendations

Section 3.1: Short Term

Section 3.2: Long Term

Chapter 4: Conclusion

Section 4.1: Summary

Section 4.2: Next Steps

Appendix A: Data Tables

Appendix B: Bibliography

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NP_001190394.1      aspa55                                  eukaryota>metazoa>chordata>vertebrata                   Oenopus leavis                                  mitochondrial ribosomal protein S55 L homolog (Oenopus leavis)
NP_001077648.1      MRPS22                                  eukaryota>metazoa>chordata>vertebrata                   Mareba fasciicularis                            28S ribosomal protein S22, mitochondrial (Mareba fasciicularis)
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NP_001178944.1      LOC100200092                            eukaryota>metazoa>chordata>vertebrata                   Xenopus (Silurana) tropicalis                   28S ribosomal protein S22, mitochondrial precursor (Xenopus (Silurana) tropicalis)
NP_001178944.1      LOC100200092                            eukaryota>metazoa>chordata>vertebrata                   Xenopus (Silurana) tropicalis                   28S ribosomal protein S22, mitochondrial precursor (Xenopus (Silurana) tropicalis)
NP_001178944.1      LOC100200092                            eukaryota>metazoa>chordata>vertebrata                   Xenopus (Silurana) tropicalis                   28S ribosomal protein S22, mitochondrial precursor (Xenopus (Silurana) tropicalis)
XP_004084019.1      GSTEG:GSTEG004141-PC                    eukaryota>metazoa>chordata>vertebrata>actinopterygii>perciformes  Gasterosteus aculeatus aculeatus  unnamed protein product (Gasterosteus aculeatus aculeatus)
XP_004084019.1      GSTEG:GSTEG004141-PC                    eukaryota>metazoa>chordata>vertebrata>actinopterygii>perciformes  Gasterosteus aculeatus aculeatus  unnamed protein product (Gasterosteus aculeatus aculeatus)
XP_011674782.1      LOC105937431                            eukaryota>metazoa>mollusca>cephalopoda                  Octopus bimaculoides                            PREDICTED: 28S ribosomal protein S22, mitochondrial isoform X2 (Octopus bimaculoides)
XP_014779053.1      LOC106327815                            eukaryota>metazoa>mollusca>cephalopoda                  Octopus sinensis                                PREDICTED: 28S ribosomal protein S22, mitochondrial isoform X1 (Octopus sinensis)
XP_011674782.1      LOC105937431                            eukaryota>metazoa>mollusca>cephalopoda                  Octopus bimaculoides                            PREDICTED: 28S ribosomal protein S22, mitochondrial isoform X2 (Octopus bimaculoides)
XP_011674782.1      LOC105937431                            eukaryota>metazoa>mollusca>cephalopoda                  Octopus bimaculoides                            PREDICTED: 28S ribosomal protein S22, mitochondrial isoform X2 (Octopus bimaculoides)
XP_014779053.1      LOC106327815                            eukaryota>metazoa>mollusca>cephalopoda                  Octopus sinensis                                PREDICTED: 28S ribosomal protein S22, mitochondrial isoform X1 (Octopus sinensis)
XP_014779053.1      LOC106327815                            eukaryota>metazoa>mollusca>cephalopoda                  Octopus sinensis                                PREDICTED: 28S ribosomal protein S22, mitochondrial isoform X1 (Octopus sinensis)
NP_788763.2         DAPI3                                   eukaryota>metazoa>chordata>vertebrata                   Mus musculus                                    28S ribosomal protein S36, mitochondrial precursor (Mus musculus)
NP_001165282.1      LOC100627381                            eukaryota>metazoa>chordata>vertebrata                   Xenopus (Silurana) tropicalis                   28S ribosomal protein S36, mitochondrial precursor (Xenopus (Silurana) tropicalis)
XP_002923181.1      LOC100370781                            eukaryota>metazoa>chordata>vertebrata                   Ailuropoda melanoleuca                          PREDICTED: 28S ribosomal protein S36, mitochondrial-like (Ailuropoda melanoleuca)
XP_005082695.1      LOC101930214                            eukaryota>metazoa>chordata>vertebrata                   Myotis brandtii                                 PREDICTED: 28S ribosomal protein S36, mitochondrial-like (Myotis brandtii)
NP_001240196.1      LOC100506809                            eukaryota>metazoa>chordata>vertebrata                   Bos taurus                                      28S ribosomal protein S36, mitochondrial precursor (Bos taurus)
XP_001919896.1      LOC100124553                            eukaryota>metazoa>chordata>vertebrata                   Equus caballus                                  PREDICTED: 28S ribosomal protein S36, mitochondrial-like (Equus caball
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