A comprehensive online resource for Candida tropicalis,

Candida shehate and Candida boidinii

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ABSTRACT

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1 INTRODUCTION

DNA sequencing is now routine for most research laboratories thanks to the current high throughput instruments available? Making sense of this data has been made easier by analysis pipelines such as Prokka which identify and label the relevant feature of a DNA sequence outputted GFF3 format?? However, inspecting the results is impractical and researchers prefer a queryable web based user interface. Many existing approaches to solve this problem include (Intermine, Trupal, GenomeHubs GFFView etc) require a long list of software dependencies which make it difficult to install and maintain. This results in sequence data persisting in FASTA files, being under used for much of it's useful life.

$$\sum x + y = Z \tag{1}$$

2 APPROACH

3 METHODS

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Table 1. This is table caption

head1	head2	head3	head4
row1	row1	row1	row1
row2	row2	row2	row2
row3	row3	row3	row3
row4	row4	row4	row4

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Fig. 1. Caption, caption.

Fig. 2. Caption, caption.

4 DISCUSSION

5 CONCLUSION

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- 3. this is item, use enumerate

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