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# **mgatk Documentation**

***Release 0.1.0***

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**Aug 19, 2017**



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# CHAPTER 1

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About

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**mgatk** is a blah blah blah



content/media/overview.png

## CHAPTER 2

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### Installation

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## CHAPTER 3

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### Dependencies

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## CHAPTER 4

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### Trimming

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## CHAPTER 5

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Alignment

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## CHAPTER 6

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Annotating peaks

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### Single end reads?

In the current implementation, **proatac** only supports paired-end reads. There's some support on [Biostars](#) that explains what one should do given single-end sequencing data.

### I found a bug / error; what do I do?

Please let us know if you find any errors/inconsistencies in the documentation or code by filing a new [GitHub Issue](#).

### I ran proatac; now what do I do?

A non-exhaustive list of ideas / resources includes:

- Perform nucleosome calling with [NucleoATAC](#)
- Identify variable transcription factors using [chromVAR](#)
- Compare peaks called from **proatac** to existing datasets. [CistromeDB](#) is a particularly useful resource for this.



## CHAPTER 8

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Author

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The primary developer is Caleb Lareau in the *Aryee Lab* <<http://aryeelab.org>> and the Buenrostro Lab.



## CHAPTER 9

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### Citation

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If you use **proatac** in your research, please cite our tool at the following URL:

<http://aryeelab.org/mgatk>



## CHAPTER 10

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### Bugs / Errors

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Please let us know if you find any errors/inconsistencies in the documentation or code by filing a new [GitHub Issue](#).