

Citation

How to cite GREAT

- If you use GREAT in the context of **human or mouse**, please cite:
Cory Y McLean, Dave Bristor, Michael Hiller, Shoa L Clarke, Bruce T Schaar, Craig B Lowe, Aaron M Wenger, and Gill Bejerano. "GREAT improves functional interpretation of *cis*-regulatory regions". *Nat. Biotechnol.* **28**(5):495-501, 2010. PMID 20436461
- If you use GREAT in the context of **zebrafish**, please cite:
Michael Hiller, Saatvik Agarwal, Jim H. Notwell, Ravi Parikh, Harendra Guturu, Aaron M. Wenger, Gill Bejerano. "Computational methods to detect conserved non-genic elements in phylogenetically isolated genomes: application to zebrafish". *Nucleic Acids Res.*, 2013. PMID 23814184

Why Cite GREAT

Over the long run, the best way to assure the continued availability and development of GREAT is for us to be able to show its relevance and contribution to biomedical research. We thank you for your support!

Publications & Reprints

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Some of the papers that cite GREAT

See [Google Scholar](#) for a more up to date list.

1. Amit, I., Regev, A., and Hacohen, N. (2011). Strategies to discover regulatory circuits of the mammalian immune system. **Nature Reviews Immunology** 11, 873--880.
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Testimonials

We really appreciate people's supportive e-mails and re-cap a handful of them here to encourage folks to take the plunge.

Date: April 21, 2011

Hi Gill,

Just wanted to let you know that we tried GREAT on a new kind of genomic data set after your talk. It worked amazingly well and made sense with respect to known biology.

Keep up the good work!

Subject: your tool is cool

Date: October 19, 2010

Dear GREAT developers

I find this tool very useful in analyzing my ChIP-seq peaks, especially after being quite frustrated using other tools to get insight into the functions/pathways associated with my TF. ...

Subject: Re: great

Date: May 5, 2010

Hey guys, I had a chance to try out GREAT for a bit with our ... chip-seq data. It looks like an amazing tool and it's way ahead of anything else out there for chipseq-related functional analysis. My favorite part is being able to click through each annotation and seeing the actual genes that were assigned.. very fancy and cool. That and the integration with the mouse phenotype ontologies--a big thing that other tools dont' have. Anyway we'll definitely be using it and I'll be sure to spread the word!

Date: May 4, 2010

Hi ...

This is not a ... ad. GREAT is awesome, we have been playing around with it quite a bit.

...

you certainly will be referenced in a paper that we want to submit by the end of this month. And I suspect many more after that.