

# Citation

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- 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

The Nature Biotechnology paper is currently the inaugural GREAT publication. Reprints are available at <http://bejerano.stanford.edu/publications.html#ref27>.

## Some of the papers that cite GREAT

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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.
2. Benson, C.C., Zhou, Q., Long, X., and Miano, J.M. (2011). Identifying functional single nucleotide polymorphisms in the human CArGome. **Physiological Genomics** 43, 1038--1048.
3. Buske, O.J., Hoffman, M.M., Ponts, N., Le Roch, K.G., and Noble, W.S. (2011). Exploratory analysis of genomic segmentations with Segtools. **BMC Bioinformatics** 12,.
4. Capellini, T.D., Handschuh, K., Quintana, L., Ferretti, E., Di Giacomo, G., Fantini, S., Vaccari, G., Clarke, S.L., Wenger, A.M., Bejerano, G., et al. (2011a). Control of Pelvic Girdle Development by Genes of the Pbx Family and Emx2. **Developmental Dynamics** 240, 1173--1189.
5. Capellini, T.D., Zappavigna, V., and Selleri, L. (2011b). Pbx Homeodomain Proteins: TALEnted Regulators of Limb Patterning and Outgrowth. **Developmental Dynamics** 240, 1063--1086.
6. Chu, C., Qu, K., Zhong, F.L., Artandi, S.E., and Chang, H.Y. (2011). Genomic Maps of Long Noncoding RNA Occupancy Reveal Principles of RNA-Chromatin Interactions. **Molecular Cell** 44, 667--678.
7. Cullum, R., Alder, O., and Hoodless, P.A. (2011). The next generation: Using new sequencing technologies to analyse gene regulation. **R espirology** 16, 210--222.
8. Diep, D., Plongthongkum, N., Gore, A., Fung, H.L., Shoemaker, R., and Zhang, K. (2012). Library-free methylation sequencing with bisulfite padlock probes. **Nature Methods** 9, 270-U69.
9. Donaldson, I.J., Amin, S., Hensman, J.J., Kutejova, E., Rattray, M., Lawrence, N., Hayes, A., Ward, C.M., and Bobola, N. (2012). Genome-wide occupancy links Hoxa2 to Wnt-?-catenin signaling in mouse embryonic development. **Nucleic Acids Research**.
10. Dozmorov, M.G., Cara, L.R., Giles, C.B., and Wren, J.D. (2012). GenomeRunner: automating genome exploration. **Bioinformatics** 28, 419--420.
11. Fernández, M., and Miranda-Saavedra, D. (2012). Genome-wide enhancer prediction from epigenetic signatures using genetic algorithm-optimized support vector machines. **Nucleic Acids Research**.
12. Fujita, P.A., Rhead, B., Zweig, A.S., Hinrichs, A.S., Karolchik, D., Cline, M.S., Goldman, M., Barber, G.P., Clawson, H., Coelho, A., et al. (2011). The UCSC Genome Browser database: update 2011. **Nucleic Acids Research** 39, D876--D882.
13. Gao, Z., Zhang, J., Bonasio, R., Strino, F., Sawai, A., Parisi, F., Kluger, Y., and Reinberg, D. (2012). PCGF Homologs, CBX Proteins, and RYBP Define Functionally Distinct PRC1 Family Complexes. **Molecular Cell** 45, 344--356.
14. Giannopoulou, E.G., and Elemento, O. (2011). An integrated ChIP-seq analysis platform with customizable workflows. **BMC Bioinformatics** 12.
15. Goeke, J., Jung, M., Behrens, S., Chavez, L., O'Keeffe, S., Timmermann, B., Lehrach, H., Adjaye, J., and Vingron, M. (2011). Combinatorial Binding in Human and Mouse Embryonic Stem Cells Identifies Conserved Enhancers Active in Early Embryonic Development. **PLoS Computational Biology** 7.
16. Hutchins, A.P., Poulain, S., and Miranda-Saavedra, D. (2012). Genome-wide analysis of STAT3 binding in vivo predicts effectors of the anti-inflammatory response in macrophages. **Blood**.

17. Karczewski, K.J., Tatonetti, N.P., Landt, S.G., Yang, X., Slifer, T., Altman, R.B., and Snyder, M. (2011). Cooperative transcription factor associations discovered using regulatory variation. **Proceedings of the National Academy of Sciences of the United States of America** 108, 13353--13358.
18. Kong, L., Wang, J., Zhao, S., Gu, X., Luo, J., and Gao, G. (2012). ABrowse-a customizable next-generation genome browser framework. **BMC Bioinformatics** 13, 2.
19. Lee, B.K., Bhinge, A.A., Battenhouse, A., McDaniel, R.M., Liu, Z., Song, L., Ni, Y., Birney, E., Lieb, J.D., Furey, T.S., et al. (2012). Cell type specific and combinatorial usage of diverse transcription factors revealed by genome wide binding studies in multiple human cells. **Genome Research** 22, 9-24.
20. Liu, Z., Scannell, D.R., Eisen, M.B., and Tjian, R. (2011). Control of embryonic stem cell lineage commitment by core promoter factor, TAF3. **Cell** 146, 720.
21. Lowe, C.B., Kellis, M., Siepel, A., Raney, B.J., Clamp, M., Salama, S.R., Kingsley, D.M., Lindblad-Toh, K., and Haussler, D. (2011). Three Periods of Regulatory Innovation During Vertebrate Evolution. **Science** 333, 1019--1024.
22. Luo, G. (2012). Gabriel Etienne Zentner Doctor of Philosophy. Case Western Reserve University.
23. Ma, Z., Swigut, T., Valouev, A., Rada-Iglesias, A., and Wysocka, J. (2011). Sequence-specific regulator Prdm14 safeguards mouse ESCs from entering extraembryonic endoderm fates. **Nature Structural & Molecular Biology** 18, 120--U175.
24. Maienschein-Cline, M., Zhou, J., White, K.P., Sciammas, R., and Dinner, A.R. (2012). Discovering transcription factor regulatory targets using gene expression and binding data. **Bioinformatics** 28, 206--213.
25. Marban, C., Su, T., Ferrari, R., Li, B., Vatakis, D., Pellegrini, M., Zack, J.A., Rohr, O., and Kurdiani, S.K. (2011). Genome-Wide Binding Map of the HIV-1 Tat Protein to the Human Genome. **PLoS One** 6.
26. Martin, D.I.K., Singer, M., Dhabhi, J., Mao, G., Zhang, L., Schroth, G.P., Pachter, L., and Boffelli, D. (2011). Phyloepigenomic comparison of great apes reveals a correlation between somatic and germline methylation states. **Genome Research** 21, 2049--2057.
27. May, D., Blow, M.J., Kaplan, T., McCulley, D.J., Jensen, B.C., Akiyama, J.A., Holt, A., Plajzer-Frick, I., Shoukry, M., Wright, C., et al. (2012). Large-scale discovery of enhancers from human heart tissue. **Nature Genetics** 44, 89--U125.
28. McLean, C.Y., Reno, P.L., Pollen, A.A., Bassan, A.I., Capellini, T.D., Guenther, C., Indjeian, V.B., Lim, X., Menke, D.B., Schaar, B.T., et al. (2011). Human-specific loss of regulatory DNA and the evolution of human-specific traits. **Nature** 471, 216--219.
29. McLean, C.Y. (2011). Computational analysis of the mammalian cis-regulatory landscape (Stanford University).
30. Nanda, V., and Miano, J.M. (2012). Leiomodulin 1, a New Serum Response Factor-dependent Target Gene Expressed Preferentially in Differentiated Smooth Muscle Cells. **Journal of Biological Chemistry** 287, 2459--2467.
31. Novershtern, N., Subramanian, A., Lawton, L.N., Mak, R.H., Haining, W.N., McConkey, M.E., Habib, N., Yosef, N., Chang, C.Y., Shay, T., et al. (2011). Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. **Cell** 144, 296--309.
32. Patel, M., Simon, J.M., Iglesia, M.D., Wu, S.B., McFadden, A.W., Lieb, J.D., and Davis, I.J. (2012). Tumor-specific retargeting of an oncogenic transcription factor chimera results in dysregulation of chromatin and transcription. **Genome Research** 22, 259--270.
33. Rada-Iglesias, A., Bajpai, R., Swigut, T., Brugmann, S.A., Flynn, R.A., and Wysocka, J. (2011). A unique chromatin signature uncovers early developmental enhancers in humans. **Nature** 470, 279--.
34. Rödelberger, C., Vingron, M., and Robinson, P.D.P. (2011). Computational Characterization of Genome-wide DNA-binding Profiles.
35. Ryu, S.H., Yoo, T., Kang, K., Park, S.Y., Joe, C.O., and Chung, J.H. (2011). Transcriptional changes of secreted Wnt antagonists in hindlimb skeletal muscle during the lifetime of the C57BL/6J mouse. **Mechanisms of Ageing and Development** 132, 511-514.
36. Sakabe, N.J., Aneas, I., Shen, T., Shokri, L., Park, S.Y., Bulyk, M.L., Evans, S.M., and Nobrega, M.A. (2012). Dual transcriptional activator and repressor roles of TBX20 regulate adult cardiac structure and function. **Human Molecular Genetics**.
37. Sandve, G.K., Gundersen, S., Rydbeck, H., Glad, I.K., Holden, L., Liestol, K., Clancy, T., Drablos, F., Ferkingstad, E., et al. (2011). The differential disease regulome. **BMC Genomics** 12.
38. Soccio, R.E., Tuteja, G., Everett, L.J., Li, Z., Lazar, M.A., and Kaestner, K.H. (2011). Species-Specific Strategies Underlying Conserved Functions of Metabolic Transcription Factors. **Molecular Endocrinology** 25, 694--706.
39. Stroud, H., Feng, S., Kinney, S.M., Pradhan, S., and Jacobsen, S.E. (2011). 5-Hydroxymethylcytosine is associated with enhancers and gene bodies in human embryonic stem cells. **Genome Biology** 12.
40. Sullivan, A.L., Benner, C., Heinz, S., Huang, W., Xie, L., Miano, J.M., and Glass, C.K. (2011). Serum Response Factor Utilizes Distinct Promoter- and Enhancer-Based Mechanisms To Regulate Cytoskeletal Gene Expression in Macrophages. **Molecular and Cellular Biology** 31, 861--875.
41. Tijssen, M.R., Cvejic, A., Joshi, A., Hannah, R.L., Ferreira, R., Forrai, A., Bellissimo, D.C., Oram, S.H., Smethurst, P.A., Wilson, N.K., et al. (2011). Genome-wide Analysis of Simultaneous GATA1/2, RUNX1, FLI1, and SCL Binding in Megakaryocytes Identifies Hematopoietic Regulators. **Developmental Cell** 20, 597--609.
42. Trompouki, E., Bowman, T.V., Lawton, L.N., Fan, Z.P., Wu, D.C., DiBiase, A., Martin, C.S., Cech, J.N., Sessa, A.K., Leblanc, J.L., et al. (2011). Lineage regulators direct BMP and Wnt pathways to cell-specific programs during differentiation and regeneration. **Cell** 147, 577--589.
43. Tuteja, G. (2012). DNA-Protein Interaction Analysis (ChIP-Seq). **Bioinformatics for High Throughput Sequencing** 127-149.
44. Yoon, S.J., Wille, A.E., Chuong, E., Gupta, R., and Baker, J.C. (2014). HEB and E2A function as SMAD/FOXP1 cofactors. **Genes & Development** 28, 1664-1661.
45. Zentner, G.E., Tesar, P.J., and Scacheri, P.C. (2011). Epigenetic signatures distinguish multiple classes of enhancers with distinct cellular functions. **Genome Research** 21, 1273--1283.

## 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.