

June 8<sup>th</sup>, 2016

Ann Loraine, Ph.D.  
Department of Bioinformatics and Genomics  
600 Laureate Way, UNC Charlotte  
North Carolina Research Campus  
Kannapolis, NC 20801

Dear Ann,

I am writing to express my enthusiastic support for your upcoming grant application requesting funding to develop and maintain the Integrated Genome Browser. This browser, or "IGB", has played a key role in numerous projects in my laboratory, including the 5 publications below. We have used IGB for analyses of RNAseq datasets of total RNA, as well as small RNAs involved in gene silencing. In addition, we find that the IGB platform easily integrates with our in-house software to visualize RNA editing sites, a particular interest of my laboratory.

High-throughput methods yield reams of data, and global analyses can point to trends. However, just what these analyses mean is not always clear, and a crucial part of such analyses is the ability to zoom in on a particular gene and its associated sequencing reads. The ability to simultaneously view and compare small RNAs, transcriptome coverage, and ChIP data, is critical to gain a fuller understanding of the types of gene regulation we study.

As you know, the IGB platform also provides robust tools for fine-tuning how data is visualized (e.g. data labels, colors), which makes creating figures for our publications, usually a laborious process, very easy. The IGB Quickload function makes sharing analyzed data sets with collaborators simple and intuitive.

IGB is the browser that my lab turns to for this task time and time again.

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Welker NC, Pavelec DM, Nix DA, Duchaine TF, Kennedy S, Bass BL. (2010). Dicer's helicase domain is required for accumulation of some, but not all, *C. elegans* endogenous siRNAs. *RNA*. **16**, 893–903. PMID: PMC2856884

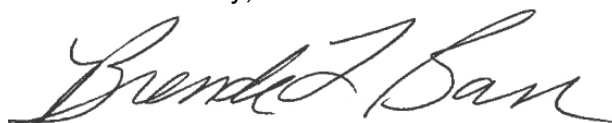
Warf MB, Shepherd BA, Johnson WE, Bass BL. (2012). Effects of ADARs on small RNA processing pathways in *C. elegans*. *Genome Research*. **22**, 1488–98. PMID: PMC3409262

Youssef OA, Safran SA, Nakamura T, Nix DA, Hotamisligil GS, Bass BL. (2015). Potential role for snoRNAs in PKR activation during metabolic stress. *Proc Natl Acad Sci USA*. **112**, 5023–8. PMID: PMC4413318

Whipple JM, Youssef OA, Aruscavage PJ, Nix DA, Hong C, Johnson WE, Bass BL. (2015). Genome-wide profiling of the *C. elegans* dsRNAome. *RNA*. **21**, 786–800. PMID: PMC4408787

Blango MG, Bass BL. (2016). Identification of the long, edited dsRNAome of LPS-stimulated immune cells. *Genome Research*. **26** (6), 852-862.

Sincerely,



Brenda L. Bass