

# Overview

TGAC Browser is a new open-source Genomic Browser under development at TGAC.

It is often the case that genomic browser customisations are required between different research groups, with the need to tailor tracks and features on a frequent basis. Many popular browsers use on-the-fly server-side track rendering which is not efficient in terms of performance, scalability or browsing experience. They often rely on specific library dependencies, where writing plugins or modifying existing code can be troublesome and resource-expensive. We focus on functionality which, although potentially available in other browsers more suited to internet architectures, concentrates on improved, more productive interfaces and analytical capabilities:

- **User-friendly:** Live data searching, track modification, and drag and drop selection; actions that are seamlessly powered by modern web browsers
- **Responsiveness:** Client-side rendering and caching, based on JSON fragments generated by server logic, helps decrease the server load and improves user experience
- **Analysis Integration:** The ability to carry out heavyweight analysis tasks, using tools such as BLAST, via a dedicated extensible daemon
- **Annotation:** Users can edit annotations which can be persisted on the server, reloaded, and shared at a later date
- **Off-the-shelf Installation:** The only prerequisites are a web application container, such as Jetty or Tomcat, and a standard Ensembl database to host sequence features
- **Extensible:** Adaptable modular design to enable interfacing with other databases, e.g. GMOD

For more information, or to try out a demo instance, please visit <http://tgac-browser.tgac.ac.uk>