

KBase's App Catalog

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<http://kbase.us>

Project Goals: The DOE Systems Biology Knowledgebase (KBase) is a free, open-source software and data platform that enables researchers to collaboratively generate, test, compare, and share hypotheses about biological functions; analyze their own data along with public and collaborator data; and combine experimental evidence and conclusions to model plant and microbial physiology and community dynamics. KBase's analytical capabilities currently include (meta)genome assembly, annotation, comparative genomics, transcriptomics, and metabolic modeling. Its web-based user interface supports building, sharing, and publishing reproducible, annotated analysis workflows with integrated data. Additionally, KBase has a software development kit that enables the community to add functionality to the system.

KBase apps are analysis tools that you can use in KBase. Currently, KBase has over 160 apps (see narrative.kbase.us/#appcatalog) offering diverse scientific functionality for (meta)genome assembly, contig binning, genome annotation, sequence homology analysis, tree building, comparative genomics, metabolic modeling, community modeling, gap-filling, RNA-seq processing, and expression analysis. Apps interoperate seamlessly to enable a range of scientific workflows (see <http://kbase.us/apps/>). For example, a user could predict species interactions from metagenomic data by assembling raw reads, binning assembled contigs by species, annotating genomes, aligning RNA-seq reads, and reconstructing and analyzing individual and community metabolic models.

The KBase [App Catalog](#) lists all of the currently available apps. Each app links to a reference page (which includes technical details about the inputs and outputs) called an App Details Page, and (when available) to a [tutorial](#) that walks step by step through an example. You can click the star at the lower left of any app to add it to your “favorites.” The options in the “Organize by” menu let you sort the apps by My Favorites, Run Count, Category (the default sort), and more. A “Version” menu enables toggling between those apps that are in production, and those that are currently under development by members of the community.

The App Catalog is also available in an abbreviated form in the Narrative Interface. This allows users to directly add apps to their workflow and execute them in place, while also browsing or searching the list of apps and managing their favorites.

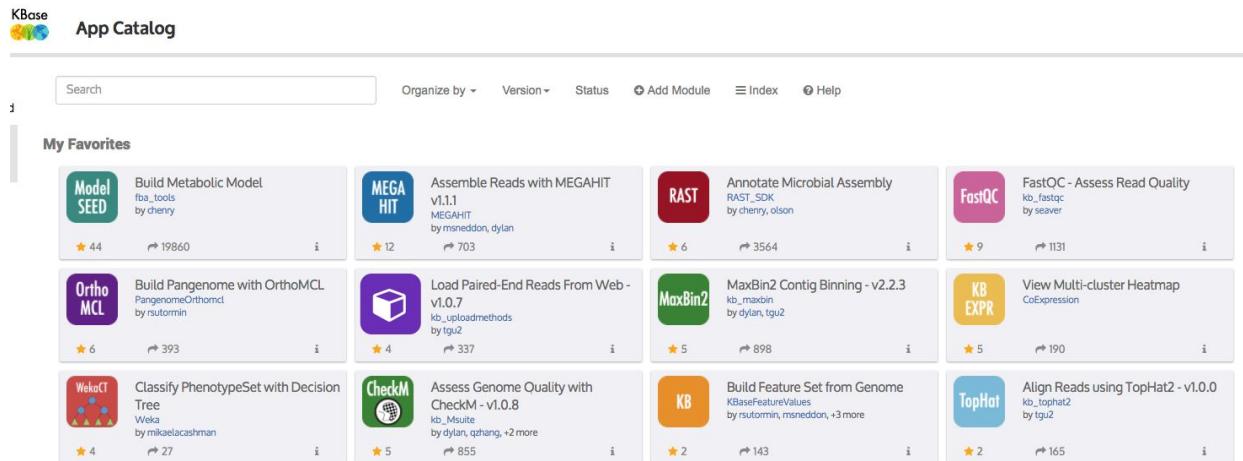


Figure 1. A portion of the KBase App Catalog (narrative.kbase.us/#appcatalog) showing the apps that a particular user has “favorited”.

KBase was designed to be an extensible community resource. This extensibility is supported by the KBase [Software Development Kit \(SDK\)](#), which is a set of command-line tools and a web interface (part of the App Catalog) that allow any developer to build, test, register, and deploy new or existing software as KBase apps, thereby extending the platform's scientific capabilities. The number of apps available in KBase is expected to increase rapidly as members of the community use our SDK to add their analysis tools to the KBase platform.

KBase is funded by the Genomic Science program within the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research under award numbers DE-AC02-05CH11231, DE-AC02-06CH11357, DE-AC05-00OR22725, and DE-AC02-98CH10886.