



METAREP

JCVI Metagenomics Reports

website www.jcvi.org/metarep

source code <http://github.com/jcvi/METAREP>

blog <http://blogs.jcvi.org/tag/metarep>

contact metarep-support@jcvi.org

An open source tool for high-performance comparative metagenomics

JCVI Metagenomics Reports (METAREP) is a new open source tool for **high-performance comparative metagenomics**. It provides a suite of web based tools to help scientists to **view, query, browse, and compare metagenomics** annotation data derived from ORFs called on metagenomics reads or assemblies.

METAREP supports browsing of functional and taxonomic assignments. Users can either specify fields, or logical combinations of fields to **filter and refine datasets**. Users can compare multiple datasets at various functional and taxonomic levels applying statistical tests as well as hierarchical clustering, multidimensional scaling and heatmaps.

For each of these features, **tab delimited files can be exported** for downstream analysis. The web site is optimized to be user friendly and fast.

▼ View

top summaries by data type

▼ Query

use SQL-like query syntax

▼ Browse

NCBI Taxonomy, GO, Kegg pathways

▼ Compare

datasets using plots and statistical tests

Data	Species (Blast)	Gene Ontology	En
Top 20 Hits			
#Rank	Class		
1	Burkholderia sp. 383		
2	Burkholderia sp.		
3	Candidatus Pelagibacter ubique HTCC1062		
4	unassigned		
5	Shewanella sp. ANA-3		
6	Burkholderia cenocepacia H12424		
7	Burkholderia cenocepacia AU 1054		
8	Shewanella sp. MR-4		
9	Shewanella sp. MR-7		
10	Burkholderia xenovorans LB400		

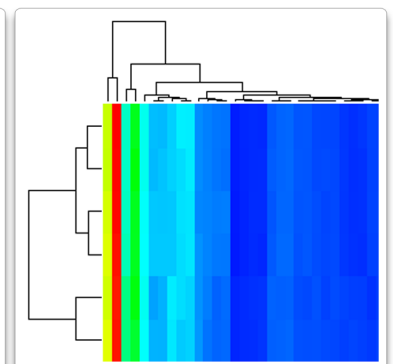
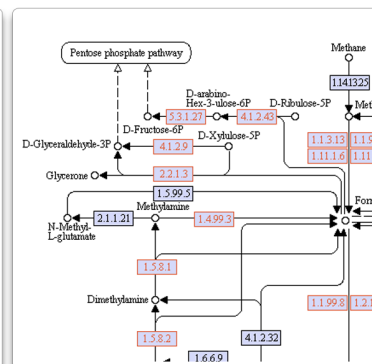
Enter Search Term

Found 843978 hits in GS-00a-01-01-2P5KB for

blast_evalu_exp:{50 TO *} AND blast_s

Top Ten Functional Classifications

Blast Species	Common Name
1. Burkholderia sp. 383 (190912) (22.62%)	1. hypothetical protein
2. Burkholderia sp. (190656) (22.59%)	2. protein of unknown
3. Candidatus Pelagibacter ubique HTCC1062 (83721) (9.92%)	3. transcriptional regu (1.25%)
4. unassigned (76884) (9.11%)	4. major facilitator sup (3815) (0.45%)



Feature Summary ▶

- **Handle extremely large datasets.** Uses scalable high-performance search engine (we have indexed 300 million annotation entries, but much larger volumes can be handled).
- **Compare 20+ datasets at the same time.** Use various compare options including statistical tests and plot options to visualize dataset difference at various taxonomic and functional levels.
- **Use statistical tests** such as METASTATS (White et al.), a modified non-parametric t-test to compare two sample populations (e.g. metagenomics samples from healthy and diseased individuals).
- **Export publication-ready graphics.** Export heatmaps, hierarchical clustering and multi-dimensional scaling plots in PDF format.
- **Analyze KEGG metabolic pathways.** Summaries include enzyme highlights on KEGG maps, pathway enzyme distributions and statistics about pathway coverage at various pathway levels.
- **Search using a SQL-like query syntax.** Build your query using 14 different fields that can be combined logically.
- **Drill down into data** using METAREP's NCBI Taxonomy, Gene Ontology, Enzyme Classification or KEGG Pathway browser.
- **Install your own METAREP version.** Flexible central configuration, METAREP and 3rd party code base is completely open source.
- **Cross-link function with phylogeny.** Slice your data at various taxonomic and/or functional levels. For example, search for all bacteria or exclude eukaryotes or search for a certain (GO/EC ID)/taxonomic combination.
- **Generic data format.** Data types that can be populated include a free text functional description, best BLAST hit information, as well as GO ID, EC ID, and HMMs.