

# Functional Database HMP

**Authors:** HMP Consortium, HMP Metabolic Reconstruction Working Group, HMP Genes of Interest Working Group

**Version:** 1.0

**Effective Date:** 10/11/11

---

## 1 Abstract

## 2 Introduction

This SOP describes creation and use of a functional database used by the HMP Data Analysis Working Group for metabolic reconstruction and identification of genes of interest from metagenomic WGS reads.

## 3 Requirements

### 3.1 Software requirements

mblastx (<http://www.multicorewareinc.com/>)

## 4 Procedure

### 4.1 Map reads

Illumina metagenomic WGS reads were mapped against a functional database consisting of genes downloaded from the following sources:

- Antibiotic Resistance Genes (n=7,828), <http://ardb.cbcb.umd.edu/>
- KEGG EC/KO (n=2,000,708), <http://www.genome.jp/kegg/>  
This includes all KEGG entries with either an EC or KO number.
- MetaCyc/ENZYME (n=189,903), <http://metacyc.org/> and <http://enzyme.expasy.org/>  
This is a combined dataset consisting of all unique sequences found in metacyc & enzyme
- Proteases (n=184,066), <http://merops.sanger.ac.uk/>
- Transporters (n=5,729), <http://www.tcdb.org/>
- Virulence Factors (n=2,294), <http://www.mgc.ac.cn/VFs/>
- Carbohydrate-active enzymes db (n=86,122), <http://www.cazy.org/> (\*\*not publicly available for download)

### 4.2 Run searches

Searches were run using mblastx (<http://www.multicorewareinc.com/>) using default parameters, up to a maximum of 20 hits, and a maximum E-value of 10.

## 5 Implementation

## 6 Discussion

## 7 Related Documents & References

# Functional Database HMP

**Authors:** HMP Consortium, HMP Metabolic Reconstruction Working Group, HMP Genes of Interest Working Group

**Version:** 1.0

**Effective Date:** 10/11/11

---

## 8 Revision History

Version	Author/Reviewer	Date	Change Made
1.00	HMP Consortium	10/11/11	Establish SOP