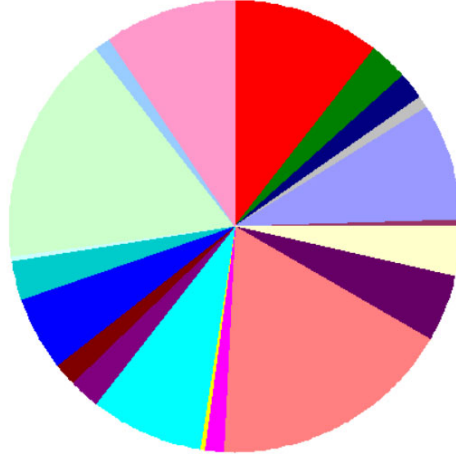
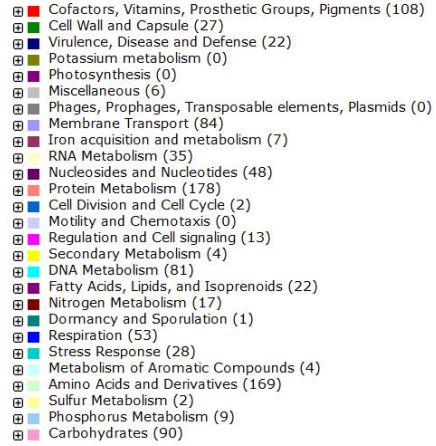
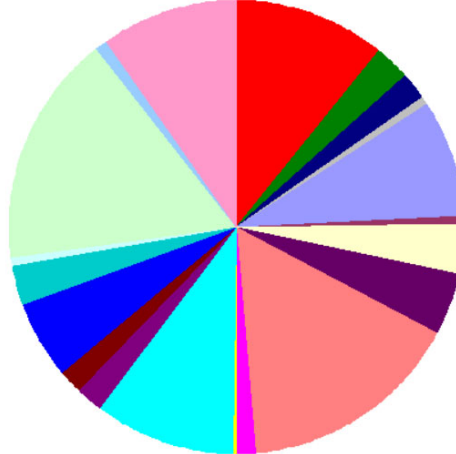
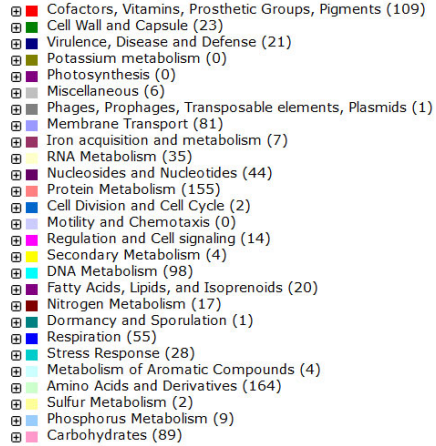
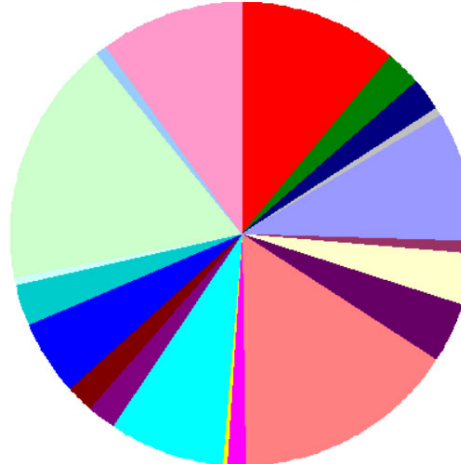
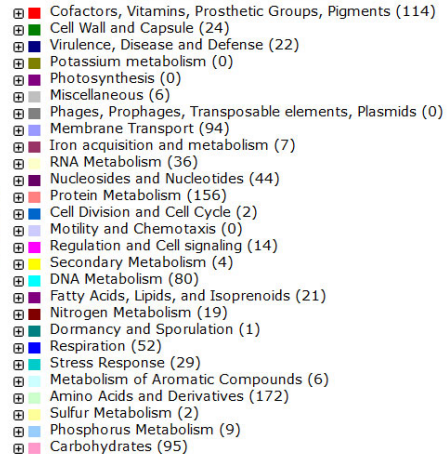
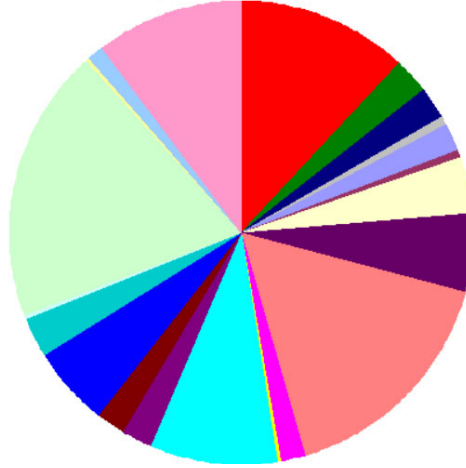
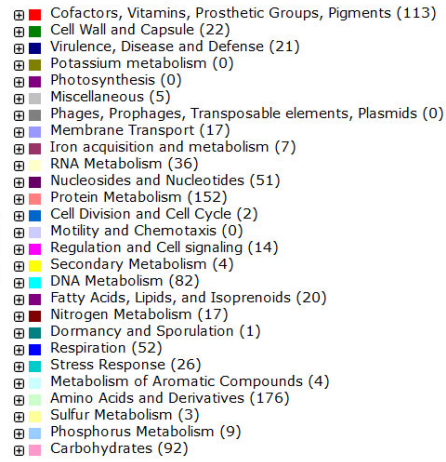
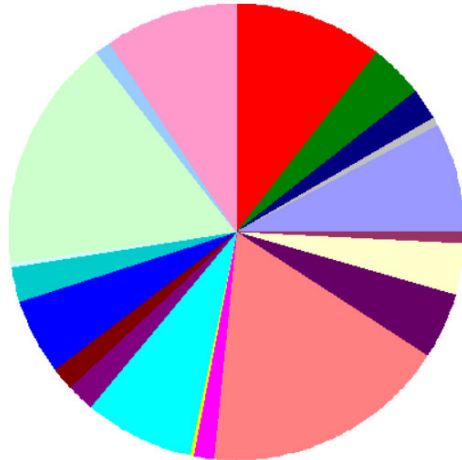
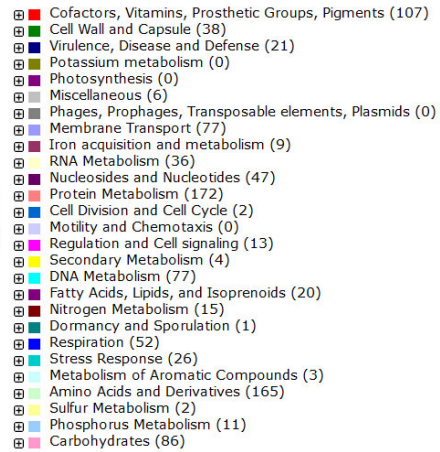
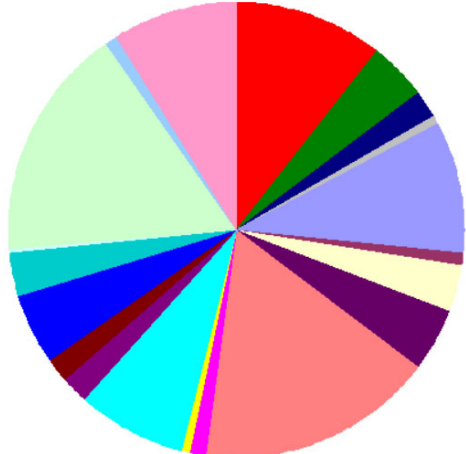
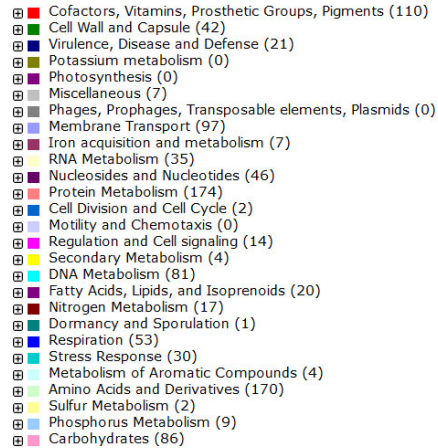
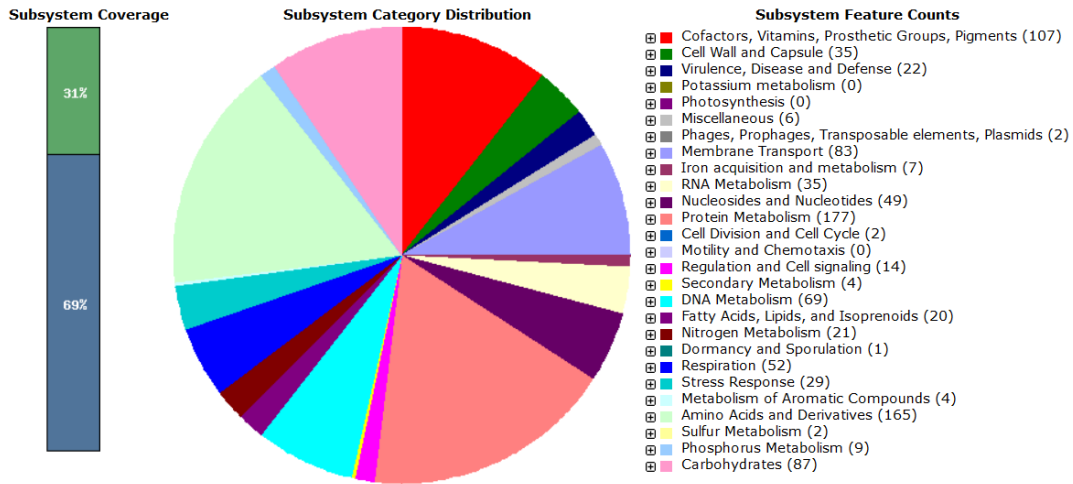
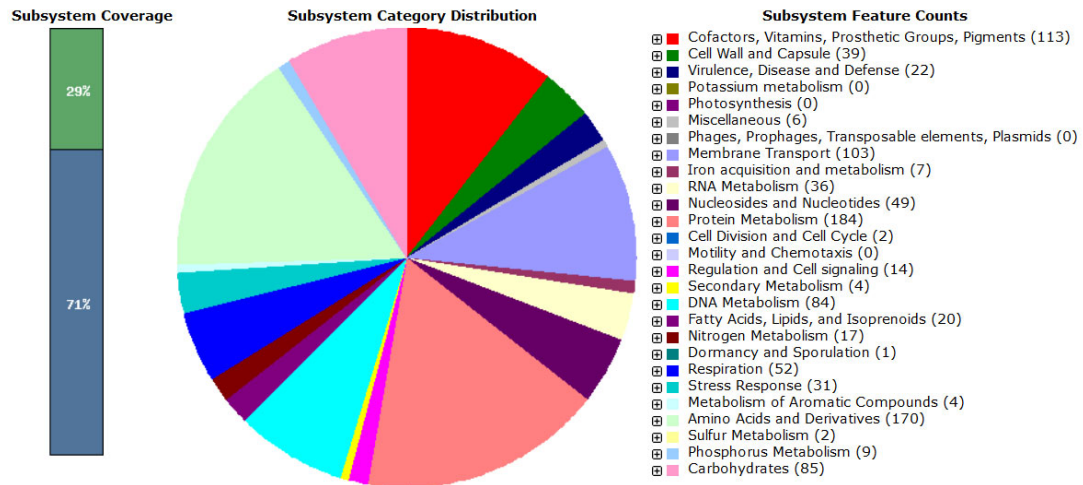
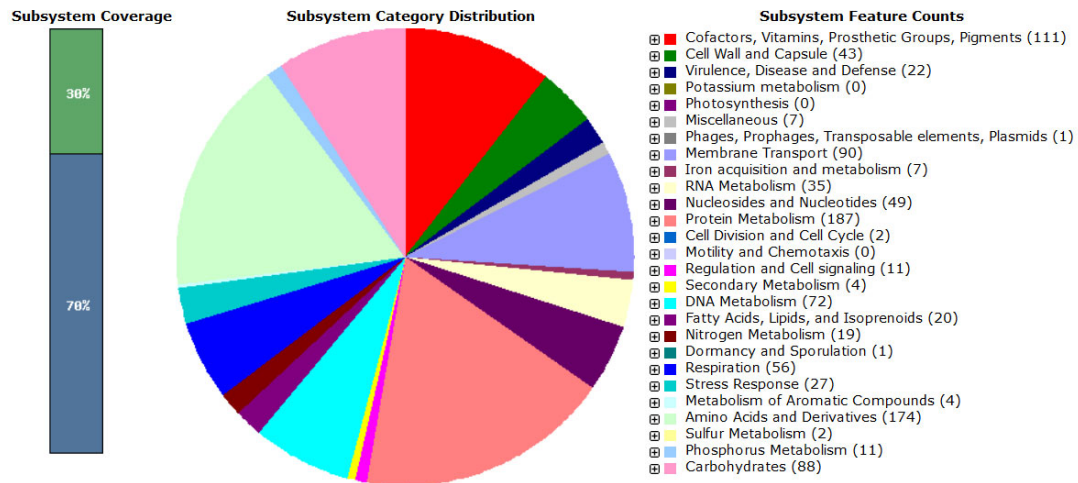
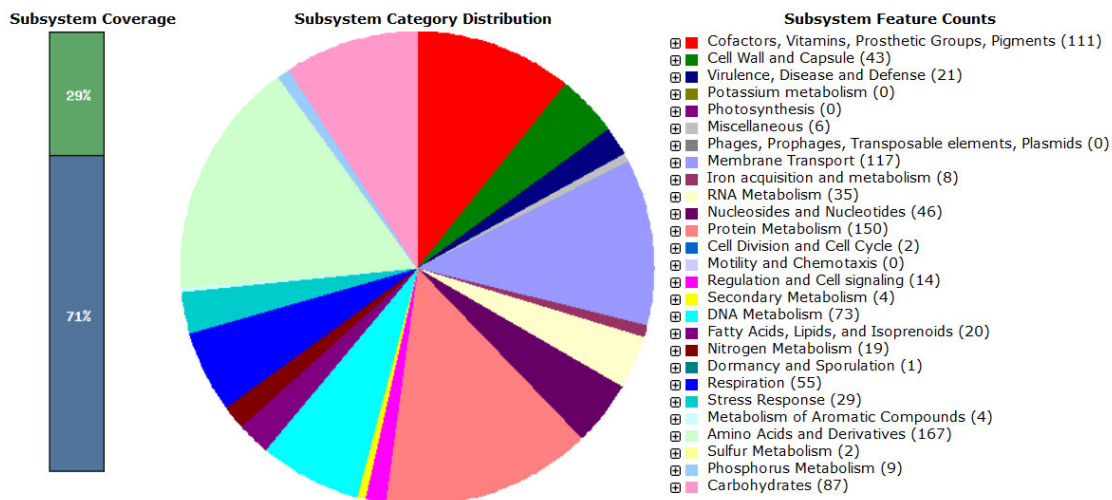


**A****Subsystem Coverage****Subsystem Category Distribution****Subsystem Feature Counts****B****Subsystem Coverage****Subsystem Category Distribution****Subsystem Feature Counts****C****Subsystem Coverage****Subsystem Category Distribution****Subsystem Feature Counts**

**D****Subsystem Coverage****Subsystem Category Distribution****Subsystem Feature Counts****E****Subsystem Coverage****Subsystem Category Distribution****Subsystem Feature Counts****F****Subsystem Coverage****Subsystem Category Distribution****Subsystem Feature Counts**

**G****H****I****J**



**Supplementary Figure S3.** Seed viewer obtained from RAST (Rapid Annotation using Subsystem Technology) (Overbeek et al., 2014) analysis of the whole genome sequence of *N. meningitidis* strains. (A) Isolate ID 119504; (B) Isolate ID 120132; (C) Isolate ID 120133; (D) Isolate ID 120134; (E) Isolate ID 120135; (F) Isolate ID 120136; (G) Isolate ID 120137; (H) Isolate ID 120138; (I) Isolate ID 120139; (J) Isolate ID 120140.