

# myBaits® Featured Publications

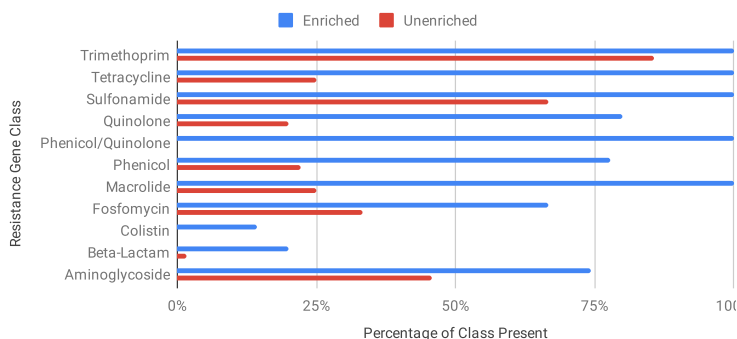
## Custom Community Panels for Antimicrobial Resistance Genes (ARGs)

Profiling genetic content of emerging resistant pathogenic bacteria is essential to improve surveillance and monitor trends in antimicrobial resistance (AMR). Research groups have turned to efficient myBaits® hybridization capture to provide targeted NGS that **reduces total sequencing costs while achieving the high sensitivity and specificity necessary for comprehensive ARG profiling**. Two published ARG enrichment panels are now available from Daicel Arbor Biosciences via our myBaits Custom Community Panels collection. Thank you to the study authors for allowing us to include them!

### BEAUDRY ET AL. (2021) - 'AMR-CAP'

*Escaping the Fate of Sisyphus: Assessing Resistome Hybridization Baits for Antimicrobial Resistance Gene Capture.* Beaudry, M.S., J.C. Thomas, R.P. Baptista, A.H. Sullivan, W. Norfolk, A. Devault, J. Enk, T.J. Kieran, ... T.C. Glenn. (2021). *Environmental Microbiology*, 23: 7523-7537

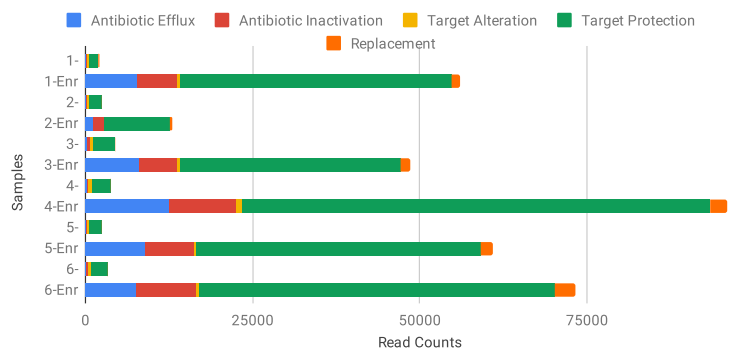
- Includes probes targeting >2,000 entries from CARD database, plus >1,200 entries from PAID database
- Demonstrated to be an effective discovery tool in mock and real complex samples, with >200-fold increase in the amount of target regions after myBaits enrichment and greater detection of many more members of most resistance gene classes, compared to shotgun whole-genome sequencing



### GUITOR ET AL. (2019) - 'RESISTOME'

*Capturing the Resistome: a Targeted Capture Method To Reveal Antibiotic Resistance Determinants in Metagenomes.* Guitor, A.K., A.R. Raphenya, J. Klunk, M. Kuch, B. Alcock, M.G. Surette, A.G. McArthur, H.N. Poinar, G.D. Wright. (2019). *Antimicrobial Agents and Chemotherapy* 64(1): e01324-19

- Includes probes targeting >2,000 entries from CARD database that are AMR-associated gene markers
- Shown to be an powerful discovery tool on both mock and real complex metagenomic community samples, with >90% reads on-target in mock community samples and >600-fold enrichment (Enr) vs. whole-genome sequencing (WGS) in six human gut microbiome samples



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