EzBioCloud database (formerly EzTaxon)

- Established in 2007
- Three layers of data
  - Nomenclature
  - 16S rRNA sequence
  - Genome sequence
- Maintained by ChunLab, Inc., mainly manual curation
- Cited >10K times
- > 40K registered users
- No MAG/SAGs were integrated but high-quality cultured genomes were included

The thoughts on the SeqCode

- Any new types of the nomenclatural type material should include the high-quality 16S rRNA gene sequence

- High-quality genome sequences from the cultured should be preferred over those from the MAG/SAG

- Adequate automation (against the lengthy manual review process) and data accessibility is the key to the success of the SeqCode

- Integration with the SeqCode data can be easily done with the cross-dictionary approach