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| **Databases** | **NCBI 16S RefSeq1** | **RDP**2 | **SILVA Ref3** |
| Number of entries | 21,314 | 3,356,809 | 2,090,668 |
| Description | Manually curated 16S ribosomal rRNA sequences | Aligned and annotated 16S ribosomal rRNA sequences (and 28S rRNA fungi sequences) | Manually curated 16S small and large subunit rRNAs (16S prokaryotes and 18S eukaryotes) |
| Domains/Type materials | Bacteria, archaea | Bacteria, archaea, eukarya | Bacteria, archaea and eukarya |
| Sequence validation steps | Trimming of long sequences, removal of low quality sequences, vector screening, removal of terminal Ns, chimera check, corrected or added intron annotation | Chimera detection | Alignment quality score above 50, sequence length above 1,200 bases for Bacteria and Eukarya, and above 900 for bases for Archaea |