probeBase.net
an online resource for
rRNA-targeted oligonucleotide probes

## Coverage of group-specific probes

Coverage of the main prokaryotic lines of descent by group-specific, rRNA-targeted oligonucleotide probes. Sensitivity and specificity of the probes were determined by using the Arb "probe match" module on current Arb databases of almost complete 16S and 23S rRNA sequences.

This table was modified from:
**Loy, A., Daims, H., and Wagner, M.** 2002. Activated Sludge: Molecular techniques for determining community composition. pp. 26-43 in The Encyclopedia of Environmental Microbiology, (G. Bitton, ed.). Wiley, New York.

| Probe | Sensitivity[a] (%) | Specificity[b] | Total coverage[c] (%) | Target group |
|---|---|---|---|---|
| **ALF1b** | 37.6 | 1,105 | 84.7 | *Alphaproteobacteria* |
| **ALF968** | 76.6 | 132 | | |
| **BET42a** | 92.6 | 22 [d] | 92.6 | *Betaproteobacteria* |
| **GAM42a** | 90.8 | 45 [d] | 90.8 | *Gammaproteobacteria* |
| **LGC354A** | 41.1 | 9 | 52.1 | *Firmicutes* (Low G+C gram-positive bacteria) |
| **LGC354B** | 29.1 | 7 | | |
| **LGC354C** | 10.9 | 0 | | |
| **CYA762** | 53.7 | 38 | 92.2 | *Cyanobacteria* |
| **CYA664** | 35.3 | 0 | | |
| **CYA361** | 86.9 | 8 | | |
| **CIV/V1342** | 6.2 | 5 | | |
| **DHP1006** | 100 | 0 | 100 | *Synergistes* |
| **TM7905** | 100 | 2 | 100 | TM7 |
| **GSB532** | 75 | 0 | 75 | *Chlorobi* |
| **CFB286** | 49.3 | 0 | 90.5 | *Cytophagales* |
| **CFB563** | 27.2 | 0 | | |
| **CFB719** | 31.1 | 4 | | |
| **CFB972** | 27.2 | 96 | | |
| **CFB1082** | 39.2 | 2 | | |
| **CF319** | 41.9 | 28 | | |
| **BAC303** | 33.1 | 0 | | |
| **Fibro** | 100 | 0 | 100 | *Fibrobacter* |
| **Pla46** | 92.6 | 6 | 95.1 | *Planctomycetes* |
| **Pla886** | 82.7 | 2,561 [d] | | |
| **EUB338 II** | 75.3 | 1 [d,e] | | |
| **EUB338 III** | 70 | 31 [d,e] | 70 | *Verrucomicrobiales* |
| **Ntspa712** | 85 | 0 [d] | 85 | *Nitrospira* |
| **IRog1** | 38.4 | 1 | 44.2 | *Acidobacteria* |
| **IRog2** | 44.2 | 0 | | |

| | | | | |
|---|---|---|---|---|
| **HGC69A** | 82.5 | 10 | 82.5 | *Actinobacteria* (High G+C gram-positive bacteria) |
| **EUB338** | 90.4 | 0 | 91.8 | domain *Bacteria* |
| **EUB338 II** | 0.8 | 0 | | |
| **EUB338 III** | 0.6 | 0 | | |
| **CREN499** | 30.6 | 0 | 30.6 | *Crenarchaeota* |
| **EURY498** | 50 | 2 | 50 | *Euryarchaeota* |
| **Arch915** | 88.3 | 0 | 88.3 | *Archaea* |

[a] The fraction of the sequences within the target group which have not more than 0.4 weighted mismatches to the probe sequence.
[b] The number of non-target sequences which have up to 0.4 weighted mismatches to the probe sequence.
[c] Total coverage of the target group by a combination of all listed probes which are specific for this group.
[d] The probe specificity is improved by a competitor oligonucleotide as detailed in the publication cited.
[e] The probe targets parts of the specified group and additional bacteria, because it belongs to the Bacteria-specific probe set.