**S2 Table. Phylogenetic identification of 14 bioflocculant-producing isolates based on 16S rDNA sequences and EzBioCloud's database**

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| --- | --- | --- |
| Strain | Identification | Identity |
| GHF1 | *Pseudoalteromonas undina* | 100.00% |
| GHF2 | *Psychrobacter aquimaris* | 99.84% |
| GHF10 | *Psychrobacter cibarius* | 100.00% |
| GHF11 | *Halomonas taeanensis* | 98.83% |
| GHF12∗ | *[Kocuria assamensis](https://www.ezbiocloud.net/taxonomy?tn=Kocuria%20assamensis)*  *Kocuria palustris* | 100.00%  100.00% |
| GHF1031 | *Celeribacter baekdonensis* | 99.92% |
| GHF1032 | *Albirhodobacter marinus* | 99.61% |
| GHF1042 | *Halomonas taeanensis* | 98.83% |
| GHF1043 | *Psychrobacter cibarius* | 100.00% |
| GHS5∗ | *Pseudoalteromonas distincta*  *Pseudoalteromonas paragorgicola* | 100.00%  100.00% |
| GHS8-1 | *Bacillus aryabhattai* | 100.00% |
| GHS19∗ | *Pseudoalteromonas distincta*  *Pseudoalteromonas paragorgicola* | 100.00%  100.00% |
| GHS20∗ | *Pseudoalteromonas distincta*  *Pseudoalteromonas paragorgicola* | 99.92%  99.92% |
| GHS21 | *Pseudoalteromonas undina* | 100.00% |

∗ Isolates had two closely related type strains with the highest identity