Supplementary Table S5. References, title and DOI of the studies included in the present systematic review.

	Reference	Title of articles	DOI
1	Shestakova et al. (2011) [15]	Characterization of the Aerobic Hydrocarbon Oxidizing Enrichments from a High Temperature Petroleum Reservoir by Comparative Analysis of DNA and RNA Derived Clone Libraries	10.1134/s0026261711010140
2	Zapata-Penãsco et al. (2016) [4]	Bisulfite reductase gene expression of thermophilic sulphate-reducing bacteria from saline connate water of oil reservoirs with high temperature	10.1016/j.ibiod.2015.05.029
3	Nazina et al. (2017) [3]	Diversity of Metabolically Active Bacteria in Water-Flooded High-Temperature Heavy Oil Reservoir	10.3389/fmicb.2017.00707
4	Li et al. (2017) [17]	Diversity and Composition of Sulfate-Reducing Microbial Communities Based on Genomic DNA and RNA Transcription in Production Water of High Temperature and Corrosive Oil Reservoir	10.3389/fmicb.2017.01011
5	Liu et al. (2018) [16]	Metabolic capability and in situ activity of microorganisms in an oil reservoir	10.1186/s40168-017-0392-1
6	Salgar-Chaparro and Machuca (2019) [1]	Complementary DNA/RNA-based profiling: characterisation of corrosive microbial communities and their functional profiles in an oil production facility	10.3389/fmicb.2019.02587
7	Zheng et al (2019) [19]	Effect of Reservoir Salinity between Bioacid and Carbonate Rock Based on Biometabolic Analysis	10.1021/acs.energyfuels.9b01522
8	Liu et al. (2020) [35]	Anaerobic Degradation of Paraffins by Thermophilic Actinobacteria under Methanogenic Conditions	10.1021/acs.est.0c02071
9	Liu et al. (2020) [48]	Dominance of Pseudomonas in bacterial community and inhibition of fumarate addition pathway by injection of nutrients in oil reservoir revealed by functional gene and their transcript analyses	10.1016/j.ibiod.2020.105039
10	Liu et al. (2020) [47]	Genomic and transcriptomic evidence supports methane metabolism in Archaeoglobi	10.1128/msystems.00651-19

11	Zhou et al. (2020) [22]	Microbial community composition and diversity in production water of a high-temperature offshore oil reservoir assessed by DNA- and RNA-based analyses	10.1016/j.ibiod.2020.104970
12	Liu et al. (2020) [49]	Simultaneous detection of transcribed functional assA gene and thecorresponding metabolites of linear alkanes (C4, C5, and C7) in production water of a low-temperature oil reservoir	10.1016/j.scitotenv.2020.141290
13	Salgar-Chaparro et al. (2020) [43]	Microbiologically influenced corrosion as a function of environmental conditions: A laboratory study using oilfield multispecies biofilms	10.1016/j.corsci.2020.108595
14	Salgar-Chaparro et al. (2020) [44]	Nutrient Level Determines Biofilm Characteristics and Subsequent Impact on Microbial Corrosion and Biocide Effectiveness	10.1128/aem.02885-19
15	Alhefeiti et al. (2021) [13]	Bioremediation of various aromatic and emerging pollutants by Bacillus cereus sp. isolated from petroleum sludge	10.2166/wst.2021.065
16	Zhou et al. (2021) [45]	Dominant and Active Methanogens in the Production Waters From a High-Temperature Petroleum Reservoir by DNA- and RNA-Based Analysis	10.1080/01490451.2020.1822958
17	Albahri et al (2021) [18]	Investigating the mechanism of microbiologically influenced corrosion of carbon steel using X-ray micro-computed tomography	10.1007/s10853-021-06112-9
18	Su et al. (2022) [20]	Genetic and Comparative Genome Analysis of Exiguobacterium aurantiacum SW-20, a Petroleum-Degrading Bacteria with Salt Tolerance and Heavy Metal-Tolerance Isolated from Produced Water of Changqing Oilfield, China	10.3390/microorganisms10010066
19	Zhou et al. (2022) [14]	Non-syntrophic methanogenic hydrocarbon degradation by an archaeal species	10.1038/s41586-021-04235-2
20	Prajapat et al. (2023) [46]	Control of reservoir souring by incomplete nitrate reduction in Indian oil fields	10.1016/j.biteb.2022.101302