



Arctic Microbial Resources: Treasure House for Bioprospecting

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Abstract: The Arctic region is one of the most extreme and rapidly transforming environments on Earth, characterized by low temperatures, extreme seasonal variations in light and accelerated warming that significantly influence fragile ecosystems. Microbial populations found in Arctic ecosystem play a crucial role in driving biogeochemical cycle. As such, polar microbes, serve as sensitive indicators of climate change and have the potential to be valuable resources for bioprospecting. Microorganisms that thrive in cold conditions, known as psychrophiles and psychrotolerants, have developed unique molecular adaptations, such as cold-active enzymes, antifreeze proteins, exopolysaccharides, pigments, and secondary metabolites, that provide significant biotechnological benefits across various industries, including pharmaceuticals, food production, bioremediation, and sustainable chemistry. This review delivers an in-depth synthesis of the diversity of Arctic microorganisms and their potential for bioprospecting. The coverage includes bacteria, archaea, cyanobacteria, microalgae, fungi, and viruses across terrestrial, cryospheric, and marine. The review also addresses challenges associated with climate-driven changes and ethical considerations related to polar resource exploration, while outlining future possibilities for sustainable biotechnological utilization.

Key words: Polar region, Arctic, microbial diversity, adaptation, bioprospecting, psychrophiles.

Microorganisms are widely distributed in nature and play a vital role in ecosystem functioning including in the extreme environments (Kasana and Singh, 2024). Among the extreme habitats, low temperature or cold climatic regions are the excellent natural and extreme resources for microbial research with reference to diversity, taxonomy, adaptation studies and biotechnological applications (Chauhan and Pandey, 2024). The Arctic represents one of the most extreme and swiftly changing polar environment located in the north pole of the planet. Since the year 2006, surface air temperatures in this region have increased at more than twice the global average rate. This rapid warming, driven by the loss of sea ice, thawing

permafrost, and changes in atmospheric circulation, is transforming ecosystems at unparalleled speeds and intensifying global climate feedback mechanisms through the release of greenhouse gases (Schuur *et al.*, 2022; Freitas *et al.*, 2025). Geographically, the Arctic comprises various coastal, marine, freshwater and terrestrial ecosystems across North America and northern Asia. It is categorized into three main biogeographic zones: High Arctic, Low Arctic, and Sub-Arctic, each characterized by unique climatic gradients and vegetation types. Significant landmasses include Greenland, the Canadian Arctic Archipelago (Nunavut), Russian islands such as Severnaya Zemlya, and the Svalbard archipelago. The Arctic Ocean, often referred to as an “Arctic Mediterranean,” is nearly landlocked (Coachman and Aagaard, 1974). Although it is the smallest of the world’s oceans, covering approximately 2.8% of the global ocean surface area (Malard and Pearce, 2018), it has the largest relative continental shelf area of any ocean basin. Despite its extreme eco-physiological conditions, microorganisms are highly flourished and widely distributed in nearly all Arctic habitats, including tundra, taiga, snow, glaciers, permafrost, air, sea ice, terrestrial soil and marine waters (Malard and Pearce, 2018). As like in other environments, the role of microbes in the Arctic are crucial for biogeochemical cycles and support entire polar food webs. Recent multi-omics studies have indicated that Arctic microbiomes possess polar-specific genetic adaptations for enduring cold, including genes associated with saccharide and lipid production, nitrate/sulfate reduction, secondary metabolite generation, and antibiotic resistance, with these adaptations often occurring at higher frequencies than in temperate or tropical ecosystems (Rizzo *et al.*, 2024).

In addition to their ecological importance, Arctic microbes offer a vast, largely unexploited reservoir for bioprospecting. Psychrophilic and psychrotolerant organisms have developed specific molecular adaptations, such as the production of cold-active enzymes, antifreeze and ice-binding proteins, cryoprotective exopolysaccharides, pigments, and bioactive secondary metabolites, that allow them to survive in sub-zero temperatures and hold considerable biotechnological promise in areas like pharmaceuticals, food processing,

bioremediation, and sustainable chemistry (de Pascale *et al.*, 2012; Rizzo *et al.*, 2024). The combination of intense selective pressures and limited prior exploration makes the Arctic an ideal setting for discovering new biomolecules with industrial and medical applications (Marcolefes *et al.*, 2019; Pylkkö *et al.*, 2024).

Arctic Bacterial Diversity

Microorganisms, particularly bacteria, are the most plentiful and functionally varied group found in the Arctic region where they play a significant role in biogeochemical cycling. Their exceptional adaptations to constant cold temperatures, limited nutrients, freeze-thaw cycles, and intense UV radiation have resulted in the development of cold-active enzymes, bioactive secondary metabolites, pathways for hydrocarbon degradation, and traits that confer metal resistance, all of which have significant industrial and pharmaceutical applications (de Pascale *et al.*, 2012; Marcolefes *et al.*, 2019; Rizzo *et al.*, 2024).

Soil in the Arctic tundra exhibit a pronounced depth-dependent bacterial structuring that supersedes seasonal fluctuations, forming distinct ecological niches that are highly relevant for bioprospecting cold-active enzymes and stress-tolerant metabolites. The surface layers (0-10 cm) are rich in copiotrophic taxa (e.g., Proteobacteria, Bacteroidetes) that efficiently decompose labile carbon, whereas the deeper active-layer and permafrost-transition zones host oligotrophic specialists (Acidobacteria, Verrucomicrobia) that are adapted for breaking down recalcitrant carbon and for surviving under ongoing cold and nutrient stress (Christiansen *et al.*, 2016). A multi-year investigation across the entire active-layer profile in low-Arctic tundra revealed that the composition of bacterial communities and their phylogenetic diversity change significantly more with soil depth than across different sampling seasons (late winter to autumn). The communities present at the surface are predominantly made up of fast-growing copiotrophs, while deeper layers close to the permafrost boundary display reduced diversity yet possess a greater potential for polymer degradation and stress responses (Christiansen *et al.*, 2016). In terrestrial regions, soil surveys conducted at 29 heath-tundra ridge locations across Canada, Alaska, and Europe revealed a consistent dominance of five main

phyla such as Actinobacteria, Bacteroidetes, Acidobacteria, Alphaproteobacteria, and Betaproteobacteria, with notable correlations in their relative abundance (Chu *et al.*, 2010). Tundra and undisturbed boreal forest soils in Canada primarily feature Proteobacteria, alongside substantial amounts of Actinobacteria, Acidobacteria, Firmicutes, Bacteroidetes, Verrucomicrobia, and Cyanobacteria (Neufeld and Mohn, 2005).

Surface and deep-water samples collected from five regions of the Arctic Ocean showed that surface communities were enriched in Alpha proteobacteria, Gamma proteobacteria, and Bacteroidetes, whereas deep waters were dominated by Alpha proteobacteria, Delta proteobacteria, and Gamma Proteobacteria across both abundant and rare fractions (Galand *et al.*, 2009). Samples of snow and freshwater from Station Nord in northeast Greenland indicated that snow layers were primarily dominated by Proteobacteria, Actinobacteria, and Bacteroidetes, while freshwater communities showed higher proportions of Planctomycetes (3%), Actinobacteria (23%), and unclassified bacteria (16%), with a lower percentage of Proteobacteria (9%). Marine air and surface samples collected from central Svalbard showed dominance by Proteobacteria, Firmicutes, and Actinobacteria, with frequently identified genera including *Pseudomonas*, *Acinetobacter*, *Corynebacterium*, *Staphylococcus*, *Delftia*, *Cloacibacterium*, *Arthrobacter*, *Sphingomonas*, *Alcanivorax*, *Comamonas*, *Streptomyces*, and *Brevibacterium* (Cuthbertson *et al.*, 2017).

Permafrost and its overlying active layer constitute one of the most dynamic yet extreme habitats found in the Arctic, where seasonal thawing produces steep gradients in redox potential, temperature, and carbon that significantly influence bacterial communities and reveal substantial bioprospecting opportunities. These environments host diverse microbial lineages that are adapted to endure prolonged sub-zero temperatures, nutrient scarcity, and freeze-thaw cycles, rendering them valuable sources of cold-active enzymes, hydrocarbon-degrading pathways, and stress-resistant metabolites (Dziurzynski *et al.*, 2023; Singh *et al.*, 2021). Within the active layer of Spitsbergen permafrost, *Candidatus udaeobacter* predominates in most samples, although recoverability is low (~6% of bacterial genera

obtained through conventional methods). The strategic application of R2A and Marine Broth media recovered 93.6% of cultivable diversity and resulted in 14 psychrotolerant, multi-metal-resistant strains, including noteworthy *Rhodococcus* spp., which exhibit strong capabilities for degrading petroleum hydrocarbons, emphasizing their potential for bioremediation in cold regions (Dziurzynski *et al.*, 2023). The marine water column beneath sea ice and the ice itself form an interconnected system where bacterial communities display significant seasonal variation, depth-related structuring, and substantial responses to the availability of substrates, characteristics that increase their potential for discovering cold-active enzymes and bioactive compounds. In sea-ice brines and surface waters, psychrophilic taxa are concentrated, possessing the ability to produce exopolysaccharides, antifreeze proteins, and secondary metabolites that protect cells in hypersaline, sub-zero conditions (Wietz *et al.*, 2024; Rego *et al.*, 2021). Bacteria associated with sea ice often create cryoprotective exopolysaccharides and pigments that help maintain membrane fluidity and provide protection from UV radiation, qualities that have straightforward applications in cosmetics, food preservation, and bioremediation. Studies that rely on culturing continue to isolate strains exhibiting strong hydrolytic enzyme activity at temperatures between 0 and 5°C, including lipases, esterases, and proteases that are well-suited for industrial processes at low temperatures (Rizzo *et al.*, 2024; Jaarsma *et al.*, 2023). The close relationship between sea-ice and pelagic communities promotes the horizontal transfer of genes related to cold adaptation and biosynthesis, further enhancing their biotechnological prospects. As the extent of sea ice declines due to climate change, these communities are undergoing rapid shifts, highlighting the need to document their diversity before unique genetic resources are lost.

Metagenomic studies of plankton in the Arctic Ocean uncover an exceptionally diverse range of biosynthetic gene clusters (BGCs), especially for non-ribosomal peptide synthases and polyketide synthases, many of which are specific to polar ecosystems and have the potential to produce antimicrobial or anticancer agents (Rego *et al.*, 2021).

Archaea in Arctic ecosystems: Archaea constitute a significant but often overlooked component of Arctic microbial communities, particularly in anaerobic permafrost, sediments, and cryopeg brines. Metagenome-assembled genomes (MAGs) from permafrost aged between 20,000 and 1,000,000 years have identified eight unique archaeal lineages, including groups from *Asgardarchaeota*, *Crenarchaeota*, and *Euryarchaeota*, that possess advanced adaptations for prolonged survival: superior DNA repair mechanisms, pathways for osmoprotectant synthesis, cold-shock proteins, and efficient energy conservation strategies (Sipes *et al.*, 2021; Liang *et al.*, 2021). Studies in 25-meter-deep boreholes in ancient northeastern Siberian permafrost revealed a significant reduction in overall microbial diversity with increasing depth and age; however, archaea, especially uncultured groups within *Asgardarchaeota* and *Crenarchaeota*, continued to be prevalent in the oldest strata (>900,000 yr), facilitating anaerobic carbon mineralization and engaging in syntrophic interactions with bacterial species (Liang *et al.*, 2021).

Recent studies highlight archaeal enrichment in thawing permafrost, where they mediate anaerobic carbon mineralization and interact closely with bacterial partners (Jaarsma *et al.*, 2023). These findings underscore archaea's role in greenhouse gas production and their potential for novel cold-adapted enzymes. In contrast to bacteria, various Arctic archaea flourish under continuous energy scarcity and severe anoxia, positioning them as prime candidates for discovering extremozymes and secondary metabolites useful in biotechnology, bioremediation, and synthetic biology. In the sediments of Arctic lakes, methanogenic archaea (*Euryarchaeota*) play a crucial role in methane emissions that are sensitive to temperature changes, with community composition accounting for up to 60% of the spatial variation in methane output (Emerson *et al.*, 2021). Specialized archaeal communities that can perform methanogenesis and ammonia oxidation under the extreme conditions of hypersaline, sub-zero habitats exist within cryopeg brines and sub-permafrost aquifers. *Thaumarchaeota* ammonia oxidizers are commonly found in both marine and terrestrial Arctic environments, significantly contributing to nitrogen cycling in low-oxygen areas and

generating nitrous oxide as a byproduct, thus directly connecting archaeal activity to the production of climate-relevant greenhouse gases (Qin *et al.*, 2023).

Archaea sourced from Arctic permafrost produce cold-active DNA polymerases, proteases, and lipases that maintain activity between -10°C and 10°C , making them ideal for molecular biology tools and low-temperature industrial applications (Sipes *et al.*, 2021). Methanogenic archaea derived from cryopegs provide pathways for biogas production in colder climates, while lineages from *Asgardarchaeota* yield novel biosynthetic gene clusters related to secondary metabolites with antimicrobial and anticancer effects (Dziurzynski *et al.*, 2023). As permafrost continues to thaw due to climate change, these ancient archaeal lineages are becoming more exposed, presenting both ecological threats (increased CH_4 emissions) and biotechnological prospects for enzyme discovery before valuable genetic resources are lost.

Cyanobacteria and microalgae: Cyanobacteria and microalgae constitute the essential primary producers in Arctic food webs, inhabiting cryoconite holes, biological soil crusts (biocrusts), sea ice, and meltwater ponds. Adaptation of these organisms to extreme light conditions, sub-zero temperatures, and low nutrient availability result in the production of pigments, exopolysaccharides (EPS), and enzymes with significant biotechnological potential (Dory *et al.*, 2025). These photoautotrophs not only support polar ecosystems but are also abundant sources of UV-protective compounds, cryoprotectants, and precursors for biofuels, which directly relates to the review's emphasis on Arctic microbial bioprospecting.

In Canadian Arctic cyanobacterial mats, the diversity of prokaryotic and eukaryotic organisms diminishes sharply as latitude increases, a trend that reflects heightened selective pressures due to shorter growing seasons and harsher winter conditions (Hooper *et al.*, 2024). Cryoconite communities on polar ice sheets show remarkable morphological and phylogenetic diversity, primarily consisting of pigmented species like *Gloeocapsopsis*, *Sanguina*, and *Chroococciopsis*, which decrease ice albedo through their dark pigmentation.

These organisms modify their surroundings by producing large amounts of EPS, creating protective structures that hold moisture and nutrients while safeguarding cells against desiccation, freeze-thaw cycles, and intense UV radiation. Notable adaptations include the creation of scytonemin (a pigment found in cyanobacterial sheaths) and mycosporine-like amino acids (MAAs), which efficiently absorb UV-A and UV-B radiation. Recent research on cryoconite in Svalbard and biocrusts in Alaska has measured scytonemin production at levels of 1-2% of dry biomass, establishing Arctic cyanobacteria as sustainable sources for UV-blocking agents used in cosmetics, sunscreens, and protective coatings (Qin *et al.*, 2023; Pushkareva *et al.*, 2024). Climate change is moving cyanobacterial and microalgal populations into recently deglaciated regions, boosting primary production but also exacerbating albedo feedback and possible toxin release, highlighting the urgent need to catalogue their genetic resources

Fungi: Fungi play a crucial but often overlooked role in Arctic microbial ecosystems, acting as primary decomposers, symbiotic partners, and prolific sources of cold-active enzymes, cryoprotectants, exopolysaccharides (EPS), pigments, and secondary metabolites with significant bioprospecting potential (Hagestad *et al.*, 2020; Zhang *et al.*, 2023; Rumenapp *et al.*, 2025). Recent studies that do not rely on culture methods have significantly enhanced our knowledge of fungal diversity in the Arctic and its potential applications in biotechnology. Shotgun metagenomic analysis of seawater from Kongsfjorden has uncovered a highly varied mycobiome predominantly consisting of Ascomycota and Basidiomycota, along with a considerable number of unclassified taxa and an abundance of biosynthetic gene clusters that could produce antimicrobial and anticancer substances (Zhang *et al.*, 2023). Fungal communities found in Arctic biocrusts exhibit strong responses to variations in elevation and spatial gradients, with functional traits associated with carbon and nitrogen cycling shifting, including increased production of ligninolytic and cellulolytic enzymes under warming conditions (Rumenapp *et al.*, 2025; Pushkareva *et al.*, 2024).

Fungal communities in Arctic habitats are mainly composed of *Ascomycota* and

Basidiomycota, the key terrestrial decomposers, although *Zygomycota*, *Chytridiomycota*, and several unclassified groups are also present (Zhang *et al.*, 2016). The soil microbial communities near Denali National Park in Alaska are abundant in *Agaricomycetes*, *Sordariomycetes*, *Lecanoromycetes*, and *Glomeromycetes*, with notable dominance of *Agaricales*, *Pleosporales*, and *Sordariales*, and *Moniliophthora* is among the most frequently identified genera). In the Ny-Ålesund region of Svalbard, lichen thalli host highly diverse mycobiomes, with *Ascomycota* comprising 23 orders (with *Helotiales* being the most abundant and diverse), followed by *Capnodiales* and *Chaetothyriales*; notable genera include *Atradiidymella*, *Cladosporium*, *Geltingia*, *Gorgomyces*, *Hyphodiscus*, *Pichia*, *Polyblastia*, *Rachicladosporium*, and *Rhizoscyphus*, along with *Basidiomycota* represented by *Cryptococcus* and *Sebacina* (Zhang *et al.*, 2016). Collectively, Arctic soils contain at least 78 fungal genera including *Acremonium*, *Alternaria*, *Arrhenia*, *Arthrinium*, *Aspergillus*, *Cladosporium*, *Exophiala*, *Herpotrichia*, *Mortierella*, *Phialocephala*, *Oidiodendron*, and *Preussia*. Fungal genera which are commonly found on mosses are *Cladosporium*, *Fusarium*, and *Mortierella* whereas *Cladosporium*, *Mortierella*, and *Alternaria* are found on the leaves. Plant roots are commonly inhabited by *Alatospora*, *Cadophora*, *Cenococcum*, *Cladophialophora*, *Cryptococcus*, *Fusarium*, *Herpotrichia*, *Hymenoscyphus*, *Mrakia*, *Monodictys*, *Mortierella*, *Phaeosphaeria*, *Rhodotorula*, *Russula*, *Sebacina*, and *Tomentella*. *Rachicladosporium* species, which are specialized black fungi that inhabit rocks, display remarkable physiological adaptations for extreme environments and are commonly found in lichen and soil habitats (Tsuji *et al.*, 2019; Rumenapp *et al.*, 2025).

In marine sediments and driftwood from Svalbard, cultivable fungi mainly *Lulworthiales* and *Eurotiales* display significant antibacterial properties against Gram-positive pathogens, emphasizing the potential for bioprospecting directly from Arctic marine mycobiomes (Hagestad *et al.*, 2020). In the active-layer soils of permafrost in Spitsbergen, *Dothideomycetes* are the dominant group, and culture-dependent methods have isolated strains that are suitable for producing cold-active hydrolases and metabolites that can withstand multiple stresses (Dziurzynski *et al.*, 2023). These adaptations make Arctic fungi a valuable source

for industrial enzymes such as cold-active cellulases, lipases, and proteases for detergents and food processing, bioactive secondary metabolites including antibacterial, antifungal, and anticancer compounds, cryoprotective extracellular polysaccharides (EPS), and pigments that provide UV protection.

Lichen-associated and endophytic fungi are among the most diverse and biotechnologically significant groups in the Arctic, forming close symbiotic relationships that improve stress tolerance, nutrient uptake, and the production of secondary metabolites, while also serving as abundant sources of novel cold-active enzymes, antimicrobial substances, and bioactive compounds. These fungi frequently display high specificity to their hosts and flourish in nutrient-deficient, high-UV, and freeze-thaw conditions, generating melanin-rich cell walls, cryoprotective exopolysaccharides (EPS), and extracellular hydrolases that facilitate survival at sub-zero temperatures and provide direct industrial applications in pharmaceuticals, cosmetics, and bioremediation (Rizzo *et al.*, 2022).

In the Russian Subarctic, culture-independent metabarcoding of six lichen species uncovered a highly diverse mycobiome enriched with *Ascomycota* (*Helotiales*, *Capnodiales*) and *Basidiomycota*, including numerous unclassified lineages and endolichenic fungi that produce bioactive polyketides and non-ribosomal peptides with significant antimicrobial and antioxidant properties. In Svalbard, lichen thalli support intricate intrathalline fungal communities that vary significantly between endemic and cosmopolitan lichens, with endemic species supporting a greater variety of rare and potentially novel taxa. Endophytic fungi isolated from Arctic vascular plants and mosses often produce cold-active cellulases, lipases, and proteases, as well as phytohormone-like compounds that enhance the host's cold tolerance and serve as candidates for agricultural biostimulants. Lichen-associated and endophytic fungi highlight the Arctic's dual role as both an ecological indicator and a biotechnological reservoir, where symbiotic adaptations directly translate into cold-active enzymes and bioactive metabolites with significant commercial potential. Biocrusts and cryptoendolithic habitats in the Arctic contain uniquely adapted fungal communities

that are essential for stabilizing soil, retaining moisture, cycling carbon and nitrogen, and providing protection against extreme desiccation, radiation, and freeze-thaw cycles, while also offering significant bioprospecting opportunities for melanin-based pigments, cold-active hydrolases, and metabolites that resist stress (Pushkareva *et al.*, 2024; Rügenapp *et al.*, 2025; Canini *et al.*, 2023). These fungi typically dominate the interfaces of rock and soil in high-Arctic and polar desert areas, creating resilient networks that shape microhabitats and generate compounds useful in bioremediation, cosmetics, and sustainable materials.

Viral diversity: Viruses play a significant role in regulating Arctic microbial communities by exerting top-down control over bacterial and archaeal populations, facilitating nutrient cycling through cell lysis, and promoting the horizontal transfer of genes associated with cold adaptation. Their auxiliary metabolic genes (AMGs) and the enzymes they encode can provide new opportunities for bioprospecting cold-active biocatalysts and phage-based antimicrobials (Trubl *et al.*, 2021; Zhong *et al.*, 2020). In these extreme environments, viruses remain active at sub-zero temperatures, influencing greenhouse gas dynamics and supporting host survival under various stress conditions, characteristics that have direct applications in biotechnology and medicine.

In the surface waters of the Arctic Ocean, viral communities exhibit significant seasonal variation and bipolar distribution patterns, strongly linking with dominant bacterial species such as *Polaribacter* and *Colwellia*. Network analyses have identified six ecological modules associated with specific environmental conditions, many of which encode AMGs that produce fatty acid desaturases to enhance host membrane fluidity under cold and saline conditions (Zhong *et al.*, 2020; Trubl *et al.*, 2021). Cryopeg brines and sea ice possess exceptionally unique viral populations (with 476 viral operational taxonomic units recovered), showing high viral abundance in cryopeg brines ($1.2 \times 10^8 \text{ mL}^{-1}$) (Zhong *et al.*, 2020). Active interactions between viruses and hosts continue in Arctic peat soils at sub-freezing temperatures, where viruses affect carbon cycling through lysis and metabolic reprogramming, contributing to greenhouse gas emissions and nutrient turnover (Trubl *et al.*, 2021).

Giant viruses (*Nucleocytoviricota*) are particularly varied in permafrost, making up to 12% of sequence coverage in some deep samples and encoding complex metabolic genes that might enhance host fitness in ancient frozen habitats (Rigou *et al.*, 2022). Viral-encoded cold-active DNA polymerases, proteases, and lipases from Arctic viromes are under investigation for use in molecular biology kits and low-temperature industrial applications. As the loss of sea ice and thawing of permafrost accelerate, viral communities are experiencing rapid changes, which may heighten carbon feedback while revealing unique viral genetic resources. Hence, systematic viral bioprospecting is crucial to capture this diversity before it undergoes alteration or loss, emphasizing the importance of viruses as critical yet often overlooked contributors to Arctic microbial biotechnology.

Methodological Advances in Arctic Microbial Research

Recent advancements in methodology have transformed our capacity to investigate microbial diversity in the Arctic, revealing its bioprospecting potential and addressing long-standing issues such as low biomass, harsh conditions, and cultivation bias that previously hindered access to the immense “microbial dark matter” found in polar regions (Berdy *et al.*, 2025). Conventional culture-dependent methods only captured a small portion of Arctic microbes, but the combination of high-throughput culturomics, *in situ* cultivation devices, long-read sequencing, single-cell genomics, and multi-omics technologies now facilitates the systematic retrieval of previously unculturable lineages and connects taxonomy to active metabolic functions, expediting the discovery of cold-active enzymes, bioactive secondary metabolites, and stress-resistant biomolecules with potential industrial and pharmaceutical applications (Rizzo *et al.*, 2024).

Various cultivation strategies have proven particularly effective in the sediments of High Arctic lakes and permafrost, where low nutrient availability and freezing temperatures impede growth. *in situ* incubation devices used in Svalbard lakes, alongside customized media formulations for example R2A, Marine Broth, and oligotrophic media that mimic permafrost, have retrieved taxa that metagenomics alone overlooked, increasing cultivable diversity

by as much as 10-fold and generating new psychrotolerant strains with promising biosynthetic gene clusters (Berdy *et al.*, 2025). Culturomics-based metagenomics, large-scale parallel isolation followed by shotgun sequencing, has successfully isolated high-quality metagenome-assembled genomes (MAGs) and identified novel biosynthetic gene clusters (BGCs) that produce cold-active enzymes and antimicrobial compounds from Arctic permafrost and marine sediments (Dziurzynski *et al.*, 2023).

Long-read sequencing (PacBio, Oxford Nanopore) and hybrid assemblies now clarify complex repetitive regions in low-biomass Arctic samples, allowing for near-complete genomes of rare and novel taxa that short-read metagenomics couldn't reconstruct. Single-cell genomics and multi-omics approaches (metatranscriptomics + metaproteomics) connect taxonomy to expressed functions in real-time, uncovering active cold-adaptation mechanisms and secondary metabolite production even in low-biomass cryoconite and sea-ice communities. These tools have been especially groundbreaking in Arctic permafrost, where they have revealed ancient archaeal and bacterial lineages with distinct cold-active DNA repair systems and biosynthetic capabilities (Sipes *et al.*, 2021; Liang *et al.*, 2021).

Adaptation Strategies of Arctic Microorganisms

Adaptation to permanent cold requires coordinated optimization of three fundamental cellular processes: enzyme catalysis, nutrient transport, and membrane fluidity (Kuddus, 2024). Protein-profiling studies of the cold-adapted archaeon *Methanococcus burtonii* revealed reduced hydrogen-bond networks, increased surface hydrophobicity, and flexible active sites that maintain high catalytic efficiency at low temperatures while preserving structural integrity (Sipes *et al.*, 2021). These structural modifications are widespread across Arctic bacteria, archaea, fungi, and microalgae, enabling the production of cold-active enzymes (proteases, lipases, glycosidases, amylases) that function optimally at 0-20°C and are rapidly inactivated by mild heat, ideal for energy-efficient industrial processes in food, detergents, and bioremediation (Hamid *et al.*, 2022; Kumari *et al.*, 2021).

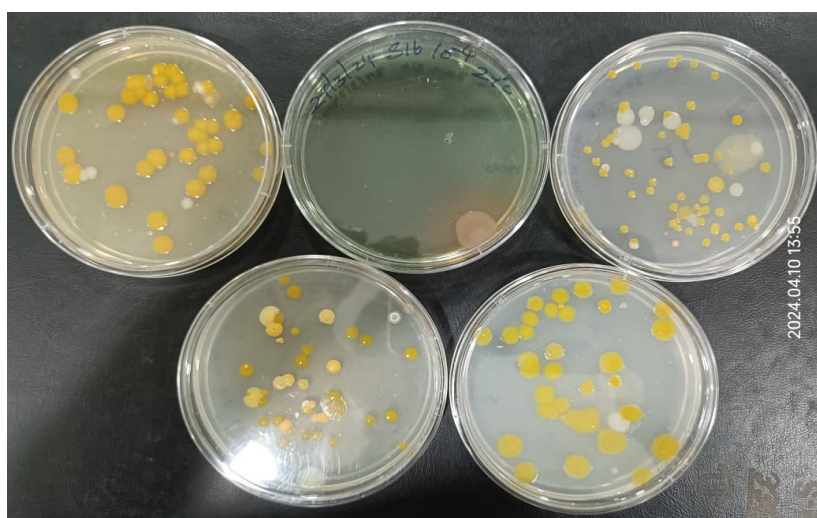


Fig. 1. Culturable bacterial colonies isolated from rhizosphere soil collected from Ny-Ålesund, High Arctic region.

Bioprospecting Potential of Arctic Microorganisms

Extremophiles from stressful habitats such as the Arctic remain prime candidates because they have evolved unique molecular strategies to maintain cellular function at sub-

zero temperatures, low nutrient availability, high UV radiation, and repeated freeze-thaw cycles, adaptations that translate directly into biotechnologically valuable traits (Yusof *et al.*, 2021). The Arctic's extreme selective pressures have also enriched genomes with biosynthetic

Table 1. Bioactive compounds derived from Arctic microorganisms and their reported biological activities

Bioactive compound	Organism	Sample / habitat	Origin	Application	Reference
Mixirins A, B, C	<i>Bacillus sp.</i>	Sea Mud	Arctic Pole	Cytotoxicity	Zhang <i>et al.</i> , 2016
Aromatic nitro compounds	<i>Salegentibacter sp.</i>	Sea Ice floe	Arctic Ocean	Antimicrobial and cytotoxicity	Al-Zereini <i>et al.</i> , 2007
Pseudofactin I and II	<i>Pseudomonas fluorescens</i>	Freshwater	Arctic Archipelago of Svalbard	Biosurfactants	Janek <i>et al.</i> , 2010
Glyciapoyrroles A, B and C	<i>Streptomyces sp.</i>	Sediment	Alaska (Arctic)	-	Macherla <i>et al.</i> , 2005
Cyclo (L-Pro-L-Met)	<i>Nocardiopsis sp.</i>	Seaweed associated	Arctic Ocean	Anti-angiogenesis	Shin <i>et al.</i> , 2010
N-(2-hydroxyphenyl)-2-Phenazinamine	<i>Nocardia dassonvillei</i>	Sediment	Arctic Ocean	Antifungal and cytotoxic	Gao <i>et al.</i> , 2012
Psychrophilin D	<i>Penicillium algidum</i>	Soil	Greenland	Anticancer	Dalsgaard <i>et al.</i> , 2005
Cytochalasins Z24, Z25, Z26	<i>Eutypella sp.</i>	Soil	London Island, Kongsfjorden, Ny-Alesund, Arctic	Cytotoxicity, Antibacterial, Immunosuppression	Liu <i>et al.</i> , 2014; Lu <i>et al.</i> , 2014; Zhang <i>et al.</i> , 2016
Antibacterial compounds (e.g., against ESKAPE pathogens)	<i>Paenibacillus sp.</i> , <i>Pseudomonas sp.</i>	Saline spring sediments, Permafrost soil	Canadian High Arctic (Axel Heiberg Island)	Antibacterial (MRSA, Listeria, Salmonella, E. coli)	Marcolefes <i>et al.</i> , 2019
Secondary metabolites (polyketides, non-ribosomal peptides)	<i>Endolichenic fungi</i> , <i>Marine actinobacteria</i>	Lichens, Invertebrates	Svalbard, Greenland	Antimicrobial, Anticancer	Hagestad <i>et al.</i> , 2020; Zhang <i>et al.</i> , 2023; Pylkkö <i>et al.</i> , 2024



Fig. 2. Kongsfjorden at the Ny Alesund, the High Arctic region during summer season.



Fig. 3. Sampling site at Kongsfjorden, Arctic region at Ny Alesund Norway during winter season.

gene clusters for secondary metabolites (polyketides, non-ribosomal peptides, alkaloids) that exhibit potent antimicrobial, anticancer, and anti-inflammatory activities at low temperatures (Siro *et al.*, 2025; Zhang *et al.*, 2023). As climate warming accelerates permafrost thaw and sea-ice loss, these unique genetic resources are becoming more accessible but are also at risk of being lost before systematic exploration, making urgent, responsible bioprospecting essential (Schuur *et al.*, 2022). Culture-dependent bioprospecting campaigns from Canadian High Arctic permafrost, saline springs, and lake sediments recovered 70 antibacterial strains ($\approx 2\text{-}5\%$ hit rate) active against ESKAPE pathogens at 5°C . Notably, *Paenibacillus* and *Pseudomonas* spp. harbouring 23 novel biosynthetic gene clusters suitable for cold-active antibiotics and biopreservatives (Marcoletas *et al.*, 2019). Actinobacteria isolated

from Arctic invertebrates produce antivirulence phospholipids and antimicrobial peptides that inhibit pathogenic *E. coli* without affecting growth, offering resistance-bypassing strategies (Pylkkö *et al.*, 2024).

Cold-Active Enzymes and Industrial Biocatalysis

Enzymes derived from the Arctic psychrophilic microorganisms exhibit remarkably high catalytic efficiency at both low and moderate temperatures which allowing significant energy savings in industrial processes by negating the necessity for heating while providing quick, selective inactivation through mild heat, essential benefits for sustainable biocatalysis in sectors such as food, detergents, leather, and bioremediation (Hamid *et al.*, 2022; Kuddus, 2024). These enzymes usually display flexible active sites, a reduction

Table 2. Cold-active enzymes produced by Arctic microorganisms and their industrial applications

Enzyme	Organism	Sample / Habitat	Origin	Application	Reference
β -galactosidase	<i>Enterobacter ludwigii</i>	Sediment	Kongsfjorden, Arctic	Lactose removal from dairy products at low temperatures	Alikkunju <i>et al.</i> , 2016
β -galactosidase	<i>Alkalilactibacillus ikkense</i>	Ikka columns	South-West Greenland	Lactose removal from dairy products at low temperatures	Schmidt and Stougaard <i>et al.</i> , 2010
α -Amylase	<i>Bacterial strains</i>	Sediment	Midtre Lovenbreen Arctic glacier	Additives in processed food, detergents, wastewater treatment	Srinivas <i>et al.</i> , 2012
Aminopeptidase	<i>Colwellia psychrerythraea</i>	Sediment	Greenland	Low-temperature food processing, textile, leather, detergents	Huston <i>et al.</i> , 2004; 2008
Lipase	<i>Bacillus pumilus</i>	Seawater	Arctic (Chukchi Sea)	Biocatalysts	Wi <i>et al.</i> , 2014
Esterase	<i>Pseudoalteromonas arctica</i>	Sea-ice	Spitsbergen, Norway	Detergents and biocatalysts	Al Khudary <i>et al.</i> , 2010
Pullulanase	<i>Shewanella arctica</i>	Seawater	Spitsbergen, Norway	Food and biofuel industries	Elleuche <i>et al.</i> , 2015
Cold-active hydrolases (lipases, esterases, proteases)	<i>Pseudomonas</i> , <i>Rhodococcus spp.</i>	Permafrost active layer	Spitsbergen (Svalbard)	Bioremediation, detergents, food processing	Dziurzyński <i>et al.</i> , 2023; Kuddus, 2024

in hydrogen bonding, and increased surface hydrophobicity that sustain their activity at 0–20°C, which makes them particularly suitable for applications in cold regions and with heat-sensitive substrates (Bruno *et al.*, 2019). Comparative genomic analysis of *Nesterenkonia* sp. PF2B19, which was isolated from Arctic permafrost, identified a comprehensive set of cold-adaptation genes including cold-shock proteins, osmoprotectants, and DNA repair mechanisms alongside biosynthetic clusters for cold-active enzymes such as α -amylases, proteases, lipases/esterases, β -glucosidases, and β -galactosidases, as well as alkaline phosphatases. These enzymes demonstrate high catalytic efficiency at low temperatures, providing direct applications in industrial sectors like detergents, food processing, and molecular biology, while underscoring permafrost as a rich source of novel biocatalysts (Singh *et al.*, 2021). Soils in the Euro-Arctic tundra (Rybachy Peninsula) demonstrate significant enzymatic activity (β -glucosidase, urease) even in the presence of human disturbances, with bacterial communities primarily composed of Proteobacteria and Actinobacteria, phyla that

have been consistently shown to yield cold-active hydrolases and secondary metabolites (Korneykova *et al.*, 2025). These functional characteristics render tundra bacteria promising candidates for bioprospecting enzymes utilized in detergents, food processing, and the bioremediation of cold-contaminated sites. Some notable cold active enzymes produced from Arctic microorganisms are given in Table 2.

Antifreeze and Ice-Binding Proteins

Antifreeze and ice-binding proteins (AFPs/IBPs) generated by Arctic microorganisms exemplify a remarkable adaptation to enduring cold, facilitating survival by preventing the growth and recrystallization of ice (Table 3). These proteins firmly attach to specific planes of ice, producing thermal hysteresis and inhibiting ice recrystallization (IRI), which helps avoid cellular damage during freeze-thaw cycle features that can be directly utilized to prolong the shelf-life of frozen goods and enhance cell/tissue cryopreservation.

Table 3. Antifreeze and ice-binding proteins from Arctic microorganisms and their biotechnological applications

Protein	Organism	Sample / Habitat	Origin	Application	Reference
LeIBP (glycosylated AFP)	<i>Glaciozyma sp.</i>	Freshwater pond	Ny-Ålesund, Svalbard	Cryoprotectants, food preservation, cryopreservation	Lee <i>et al.</i> , 2010; Majewska <i>et al.</i> , 2025
TisAFP isoforms	<i>Typhula ishikariensis</i>	Soil	Northern Norway, Svalbard, Greenland	Cryoprotection	Hoshino <i>et al.</i> , 2003; Gharib <i>et al.</i> , 2022
AFPs / IBPs	<i>Cryobacterium psychrophilum</i> , <i>Pseudomonas ficuserectae</i>	Cryoconite sediment	Glaciers in Svalbard	Cryoprotection, food industry	Singh <i>et al.</i> , 2014

In addition, these proteins provide transformative uses in food preservation, cryopreservation, biomedicine, and nanotechnology. The glycosylated ice-binding protein LeIBP (25 kDa) sourced from the Arctic yeast *Glaciozyma sp.* demonstrates significant thermal hysteresis and IRI functionality. The production of this protein recombinantly in *E. coli* and *Pichia pastoris* on a pilot scale (700 L) produces yields of up to 300 mg/L. Snowmold such as *Typhula ishikariensis* and *Coprinus psychromorbidus* release various isoforms of AFPs (TisAFPs), including highly active versions

Actinobacteria from the permafrost of Svalbard and Greenland generate new cryoprotective proteins that possess emulsification and membrane-stabilizing abilities, improving freeze-thaw survival rates for both the producing organisms and foreign cells, making them well-suited for applications in food science, vaccine stabilization, and regenerative medicine. Recombinant Arctic AFPs enhance the survival rates of mammalian cells, sperm, and oocytes post-thaw and offer protection to organs during cryopreservation. The thawing of permafrost due to climate change reveals ancient lineages of AFP producers, which pose both threats (altered carbon cycling) and opportunities for the discovery of enzymes and proteins before this unique genetic diversity is lost.

Exopolysaccharides and Cryoprotectants

Several bacterial cultures from the Arctic region were found to produce exopolysaccharides. These high-molecular-weight polymers (frequently exceeding 1 MDa) with intricate repeating units of glucose, galactose, fucose, and uronic acids create

hydrated microenvironments that mitigate ice crystal damage and preserve membrane integrity at sub-zero temperatures. EPS from Arctic microbes are not only safeguard indigenous microbes under harsh conditions but also present sustainable, biodegradable alternatives to synthetic cryoprotectants and emulsifiers in sectors like food, cosmetics, pharmaceuticals, and environmental technologies – advancing the bioprospecting objectives of this review while emphasizing the importance of cataloguing these resources before habitat loss induced by climate change.

A noteworthy example is the complex α -mannan EPS produced by the sea-ice bacterium *Pseudoalteromonas sp.* SM20310, which significantly enhances freeze-thaw tolerance for both itself and *E. coli* by generating a thick protective barrier (Liu *et al.*, 2013). *Polaribacter sp.* SM1127, isolated from Arctic brown algae, produces high amounts (2.11 g/L) of EPS characterized by significant cryoprotective and antioxidant properties, making it suitable for applications in food and cosmetics (Sun *et al.*, 2015). *Colwellia psychrerythraea* 34H, a typical Arctic psychrophile, produces EPS and CPS that serve as cryoprotectants and facilitate the overcoming of dissolved-organic-carbon limitations in frigid marine environments, with proven applications in cell cryopreservation (Marx *et al.*, 2009; Carillo *et al.*, 2015). Metagenomic analyses of Arctic sea ice and permafrost reveal numerous novel EPS biosynthetic gene clusters with unique sugar compositions and branching structures that provide enhanced freeze-thaw resistance and rheological properties for use as industrial thickeners and stabilizers (Ribeiro *et al.*, 2023; Finore *et al.*, 2020). A newly identified EPS (EPS0-1, Mw 4.35 MDa) from the Arctic marine sediment derived *Pseudoalteromonas sp.* LP6-

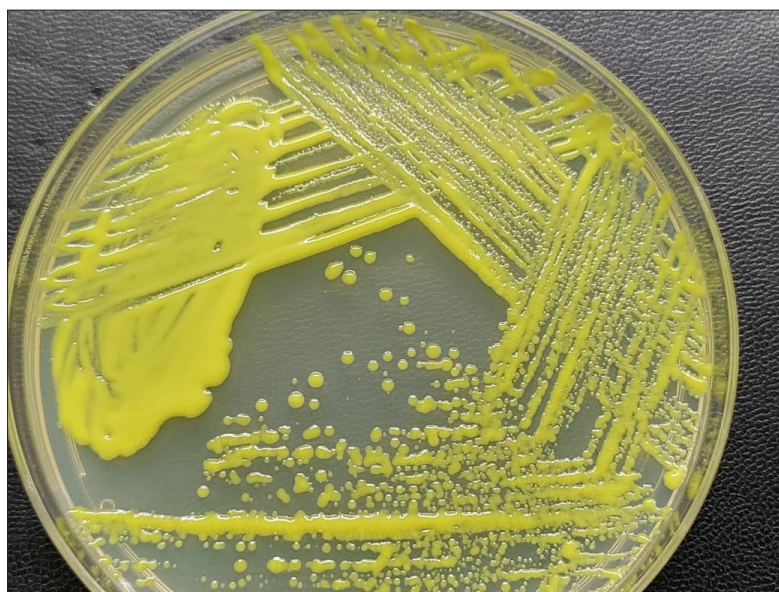


Fig. 4. Yellow pigmented bacterial cultures isolated from Ny Alesund, high arctic region.

12-2, exhibits extraordinary cryoprotective properties and emulsifying capabilities, exceeding those of commercial agents for the preservation of frozen foods and probiotics (Kong *et al.*, 2024). *Pseudoalteromonas* strains sourced from Svalbard sediments produce EPS with the capacity to chelate heavy metals and function as emulsifiers, making them suitable for bioremediation of cold-contaminated sites (Rizzo *et al.*, 2022).

Pigments and Photoprotective Molecules

Polar organisms experience intense irradiance, prolonged darkness, low temperatures, and frequent freeze-thaw cycles, driving the evolution of carotenoid, scytonemin, and mycosporine-like amino acid (MAA) pigments that maintain membrane fluidity, provide photoprotection, act as antioxidants, and serve as cryoprotectants, traits with direct applications in cosmetics, sunscreens, food colourants, and nutraceuticals (Table 4) (Singh *et al.*, 2017; Ručová *et al.*, 2023; Rümenapp *et al.*, 2025; Zhang *et al.*, 2023). These pigments absorb harmful UV radiation while quenching reactive oxygen species and stabilising membranes under cold stress, offering sustainable, biodegradable alternatives to synthetic UV filters.

Pigmented Arctic microbes from Kongsfjorden (Svalbard) accumulate zeaxanthin-like carotenoids that rigidify membranes during freeze-thaw cycles and reduce photodamage, with demonstrated

cryoprotectant activity in heterologous systems (Singh *et al.*, 2017). Arctic cyanobacteria in biocrusts and cryoconite produce high levels of scytonemin and MAAs that absorb the entire UV-A/UV-B spectrum; recent quantification in Svalbard and Greenland samples shows yields suitable for industrial extraction as natural sunscreen ingredients with estimated SPF values >30. Melanin-rich fungi in biocrusts and cryptoendolithic habitats produce dark pigments that confer dual UV and desiccation protection, with antioxidant and photoprotective properties superior to many commercial additives (Rümenapp *et al.*, 2025; Canini *et al.*, 2023).

Metagenomic and culture studies confirm that carotenoid and melanin biosynthetic pathways are enriched in Arctic seawater and biocrust communities under intensified UV and oxidative stress caused by climate-driven ice loss (Zhang *et al.*, 2023). These pigments also exhibit cryoprotectant synergies with EPS and AFPs, enabling applications in frozen food preservation and cell cryopreservation (Majewska *et al.*, 2025). As Arctic warming intensifies UV exposure in newly ice-free areas, pigment-producing microbes are expanding, creating both ecological shifts and expanded opportunities for sustainable bioprospecting of natural photoprotectants. Arctic microbial pigments thus exemplify the seamless integration of ecological adaptation and biotechnological innovation, providing safe, effective, and eco-friendly solutions for UV

Table 4. Pigments and photoprotective compounds from Arctic microorganisms and their applications

Pigment	Organism	Source	Origin	Application	References
Yellow pigments	<i>Leeuwenhoekiella aequorea</i> , <i>Pseudomonas pelagia</i> , <i>Halomonas boliviensis</i> , <i>Rhodococcus yunnanensis</i>	Glacial fjord	Kongsfjorden	Photoprotection, antioxidants	Singh <i>et al.</i> , 2017
Red pigment	<i>Algoriphagus ratkowskyi</i>	Glacial fjord	Kongsfjorden	Photoprotection	Singh <i>et al.</i> , 2017
Dark red-brown to black	<i>Janthinobacterium svalbardensis</i>	Glacier ice	Spitsbergen	UV protection	Ambrozic <i>et al.</i> , 2013
Scytonemin and MAAs	<i>Nostoc sp.</i> , <i>Oscillatoria sp.</i> , etc.	Pond and lake samples	Canadian High Arctic	UV-blocking in cosmetics, sunscreens	Quesada <i>et al.</i> , 1999; Ručová <i>et al.</i> , 2023

protection and oxidative stress management in a changing climate.

Bioactive Secondary Metabolites from Arctic Microbes

Microbes from the Arctic region are reported to produce diverse secondary metabolites that exhibit strong antibacterial, antitumor, antiviral, antifungal, anti-virulence, and antioxidant properties (Table 5). Many of these compounds remain effective at lower temperatures and present promising frameworks for the development of next-generation pharmaceuticals and biopreservatives (Selim *et al.*, 2021; Liu *et al.*, 2023; Schneider *et al.*, 2022). The interplay of cold stress, limited nutrients, and intense UV radiation drives the development of distinctive biosynthetic gene clusters (BGCs) responsible for producing polyketides, non-ribosomal peptides, alkaloids, and terpenoids that are frequently found lacking in temperate microbes.

Bioremediation and Hydrocarbon Degradation in Cold Environments

Microbes that thrive in cold environments, such as Arctic permafrost, sea ice, and sediments, exhibit remarkable abilities for hydrocarbon degradation at low temperatures, making them suitable candidates for sustainable bioremediation of oil spills and contaminated areas in polar regions where mesophilic microorganisms are ineffective (Dziurzynski *et al.*, 2023; Lirette *et al.*, 2024; Caro *et al.*, 2025). These organisms possess cold-active enzymes such as alkane monooxygenases, catechol dioxygenases, and pathways for biosurfactant production that operate effectively at temperatures between 0 and 10°C, facilitating the breakdown of alkanes, aromatics, and

polycyclic aromatic hydrocarbons without the need for external heating.

In the active-layer soils of Spitsbergen permafrost, focused culturing efforts yielded 14 psychrotolerant strains resistant to multiple metals (including *Rhodococcus* spp.) that demonstrated strong capability for degrading petroleum hydrocarbons, even when subjected to heavy-metal stress, providing direct solutions for bioremediation in cold regions (Dziurzynski *et al.*, 2023). Beach sediments in the Northwest Passage contain various hydrocarbon-degrading microbial communities primarily composed of *Pseudomonas*, *Rhodococcus*, and *Shewanella*, which mineralize model hydrocarbons at temperatures of 4 to 10°C, with biosurfactant production increasing their availability (Lirette *et al.*, 2024). Microbes found in deep permafrost exhibit slow yet detectable recovery and growth after thawing, with hydrocarbon-degrading species becoming active within a few months, contributing to both natural attenuation processes and greenhouse gas dynamics (Caro *et al.*, 2025).

Microbial communities in Arctic sea ice and under the ice degrade hydrocarbons during microcosm experiments conducted at near-freezing temperatures, with Proteobacteria and Actinobacteria being the predominant. Metagenomic analyses have identified an abundance of cold-active degradation genes in thawing permafrost, indicating a genetic reservoir that could be utilized for engineering improved bioremediation consortia (Svarovskaya *et al.*, 2019)

These cold-adapted degraders not only help alleviate environmental harm caused by oil exploration and shipping in the Arctic but also produce biosurfactants and cold-

Table 5. Secondary metabolites from Arctic microorganisms and their biological activities

Microbial Group	Organism / Genus	Source / Habitat	Key Secondary Metabolites	Biological Activities / Applications	Reference
Actinobacteria	<i>Kocuria</i> spp.	Arctic marine invertebrates (sponges, bryozoans, molluscs)	Antivirulence phospholipids	Disrupt actin polymerization of enteropathogenic <i>E. coli</i> (EPEC) without inhibiting growth; antivirulence strategy against pathogens	Pylkkö <i>et al.</i> , 2024
Actinobacteria	<i>Rhodococcus</i> spp.	Arctic marine invertebrates	Antimicrobial peptides	Direct growth inhibition of pathogenic bacteria; potential against ESKAPE pathogens	Pylkkö <i>et al.</i> , 2024
Actinobacteria	<i>Streptomyces</i> spp.	Arctic marine sediments, invertebrates	Glaciapyrroles, phenazine derivatives	Antiviral, antifungal, cytotoxic activities active at 4-10°C	Schneider <i>et al.</i> , 2022; Selim <i>et al.</i> , 2021
Actinobacteria	<i>Nocardiosis</i> spp.	Arctic marine sediments	Nitrosporeusins and related compounds	Broad antimicrobial, antifungal, and cytotoxic properties	Schneider <i>et al.</i> , 2022; Liu <i>et al.</i> , 2023
Actinobacteria	<i>Micromonospora</i> spp.	Deep-sea Arctic sediments	Polyketides, non-ribosomal peptides	Anti-inflammatory activity in macrophage models; novel BGCs	Ribeiro <i>et al.</i> , 2023
Actinobacteria (Ancient strains)	Various polar Actinobacteria	Sub-Arctic and Antarctic sediments	Cold-active polyketides and peptides (via genome mining)	Potential antibiotics and anticancer compounds	Millán-Aguíñaga <i>et al.</i> , 2019
Fungi	<i>Penicillium algidum</i>	Greenland soil	Psychrophilin D, Cycloaspeptides A and D	Anticancer (leukemia, breast cancer) and antiplasmodial activity	Dalsgaard <i>et al.</i> , 2005; Liu <i>et al.</i> , 2023; Phi <i>et al.</i> , 2026
Marine fungi	Driftwood-associated fungi	Svalbard Arctic marine environment	Polyketides and alkaloids	Antibacterial activity against Gram-positive bacteria; active at 4-10°C	Hagestad <i>et al.</i> , 2020
Endolichenic fungi	Arctic lichen-associated fungi	Svalbard and Greenland	Cytochalasins, polyketides	Cytotoxic and antifungal activity; stability during freeze-thaw cycles	Rümenapp <i>et al.</i> , 2025
Biocrust fungi	Arctic soil biocrust fungi	Polar soils	Diketopiperazines, polyketides	Anticancer and antimicrobial properties	Zhang <i>et al.</i> , 2023
Yeasts	<i>Glaciozyma</i> spp.	Glacier-front soils, sea ice	Antifreeze proteins (AFPs), antioxidant metabolites	Cryoprotection, cryopreservation, food preservation	Majewska <i>et al.</i> , 2025
Yeasts	<i>Vishniacozyma</i> spp.	Arctic sea ice and glacier soils	Cryoprotective metabolites, terpenoids	Antioxidant and cryoprotective properties	Feng <i>et al.</i> , 2025
Marine invertebrate-associated microbes	<i>Streptomyces</i> , <i>Micromonospora</i> , <i>Nocardiosis</i> , <i>Rhodococcus</i>	Arctic sponges, corals, tunicates, bryozoans	Polyketides, non-ribosomal peptides, halogenated compounds	Antimicrobial, cytotoxic, anti-inflammatory activities	Masaki <i>et al.</i> , 2025; Schneider <i>et al.</i> , 2022
Permafrost / sea-ice microbiomes	Mixed microbial communities	Arctic permafrost, sediments, sea ice	Halogenated and thioester-containing compounds (via BGCs)	Potential antibiotics, antivirals, and anticancer compounds	Schneider <i>et al.</i> , 2022

active enzymes that hold additional industrial significance, underscoring the Arctic's vital role in microbial biotechnology within a warming climate.

Challenges, Ethical Considerations, and Sustainable Bioprospecting

Despite the enormous biotechnological potential of Arctic microorganisms, most discoveries remain at the laboratory or early experimental stage, with only a limited number progressing toward pilot-scale or commercial applications. Recent advances in genomics, cultivation technologies, metagenomics, culturomics, and process engineering have significantly accelerated the identification of novel cold-adapted enzymes, antifreeze proteins, exopolysaccharides, pigments, and secondary metabolites from Arctic microbes (Rizzo *et al.*, 2024; Berdy *et al.*, 2025). In addition, genome mining, recombinant expression systems, and synthetic biology approaches are increasingly improving the feasibility of producing psychrophilic biomolecules at industrial scales. However, compared with microbial resources from temperate environments, the commercial translation of Arctic microbial products remains relatively limited due to technical and economic constraints (Kuddus, 2024).

Among Arctic microbial products, cold-active enzymes currently represent the most commercially promising biomolecules because of their high catalytic efficiency at low and moderate temperatures, which significantly reduces industrial energy consumption. These enzymes have important applications in food processing, detergents, leather industries, molecular biology, wastewater treatment, and environmental bioremediation (Hamid *et al.*, 2022). Antifreeze and ice-binding proteins also demonstrate considerable market potential in cryopreservation, frozen-food preservation, regenerative medicine, and vaccine stabilization (Lee *et al.*, 2010; Majewska *et al.*, 2025). Similarly, Arctic microbial pigments such as carotenoids, scytonemin, melanin, and mycosporine-like amino acids are increasingly being explored as sustainable alternatives to synthetic antioxidants and UV-protective compounds in cosmetic and nutraceutical industries (Ručová *et al.*, 2023; Rūmenapp *et al.*, 2025). Exopolysaccharides and biosurfactants produced by Arctic bacteria and fungi further provide promising applications

as emulsifiers, stabilizers, cryoprotectants, and heavy-metal chelators in pharmaceutical, environmental, and food sectors (Finore *et al.*, 2020; Kong *et al.*, 2024).

Future commercialization of Arctic microbial products will likely depend on the integration of genomics, artificial intelligence-assisted genome mining, synthetic biology, metabolic engineering, and advanced bioprocess optimization. Heterologous expression systems, enzyme stabilization strategies, and scalable fermentation technologies may help overcome current production limitations associated with psychrophilic biomolecules. Furthermore, international collaborations, open-access genomic databases, and ethical frameworks promoting fair benefit-sharing will be essential for ensuring sustainable and equitable utilization of Arctic microbial resources. As climate change rapidly transforms Arctic ecosystems, there is an urgent need to document, preserve, and responsibly utilize these unique microbial genetic resources before they are irreversibly lost (Schuur *et al.*, 2022; Rizzo *et al.*, 2024).

Future Perspectives and Research gaps

Future studies on microbial diversity and bioprospecting in the Arctic should focus on integrative methodologies to address rapid climate-driven changes and to unlock emerging biotechnological opportunities. Multi-omics approaches, including metagenomics, metatranscriptomics, metaproteomics, and metabolomics, provide powerful tools for understanding microbial community structure, function, and responses to environmental stress. Integration of these datasets with artificial intelligence and machine-learning approaches can improve predictive modeling of microbial dynamics under changing environmental conditions, including warming temperatures, permafrost thaw, and altered nutrient cycling (Edwards *et al.*, 2020; Rizzo *et al.*, 2024).

Long-term monitoring of Arctic ecosystems remains essential for understanding seasonal and interannual shifts in microbial communities inhabiting sea ice, glacier forefields, and permafrost environments (Edwards *et al.*, 2020). Expanding culturomics approaches together with genome-resolved metagenomics will help overcome cultivation bias and facilitate the discovery of novel microbial taxa, biosynthetic gene clusters, cold-active

enzymes, and bioactive metabolites (Rizzo *et al.*, 2024). Advances in synthetic biology and genome-mining technologies further provide opportunities to optimize psychrophilic biocatalysts and accelerate the development of Arctic-derived biotechnological applications.

Significant knowledge gaps remain regarding the ecological roles of Arctic archaea and viruses. Archaea contribute substantially to biogeochemical processes such as methane cycling in thawing permafrost, yet their diversity and ecological interactions remain poorly understood. Similarly, viruses influence microbial population dynamics and nutrient turnover in Arctic ecosystems, but the ecological significance of viral communities in deep permafrost and other extreme habitats requires further investigation. Bridging microbial processes with ecosystem-scale responses will require the integration of single-cell genomics, metagenome-assembled genomes (MAGs), and biogeochemical modelling approaches (Edwards *et al.*, 2020; Rizzo *et al.*, 2024).

Underexplored habitats such as cryopegs and subglacial lakes harbor unique psychrophilic communities with considerable potential for the discovery of novel extremozymes and bioactive metabolites, although logistical challenges continue to limit sampling and functional characterization (Rapp *et al.*, 2021). Collaborative research frameworks that incorporate Indigenous knowledge systems and follow ethical bioprospecting guidelines can promote sustainable exploration of Arctic microbial resources while ensuring equitable benefit sharing and environmental stewardship (Eritja, 2017).

Conclusions

Microorganisms found in the Arctic act as critical indicators of environmental changes and hold significant potential for biotechnological applications, such as cold-active enzymes, antibiotics, and agents for bioremediation. The rapid rise in temperatures enhances microbial feedback loops, resulting in the release of greenhouse gases and changes in diversity, while also revealing new genetic resources. By combining traditional microbiology with advanced multi-omics, AI-enhanced analytics, synthetic biology, and ethical bioprospecting, researchers can fully leverage this potential

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Competing Interests

The authors declare no competing interests.

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About the Authors

Radhakrishnan Manikkam is a microbiologist specializing in microbial bioprospecting, specifically focusing on actinobacteria from understudied habitats in India and polar regions to support sustainable development in health, environment, and agriculture. Notably, he participated in the first-ever Indian Arctic Winter Expedition in 2024, where he studied actinobacterial and general bacterial diversity in the High-Arctic region of Ny-Ålesund to understand their adaptation strategies during the polar nights. His research involves isolating psychrophilic microbes from these regions to explore their biotechnological potential, including the production of cold-active enzymes, pigments, and exopolysaccharides, as well as their role in plant growth promotion.

Sai Mahesh Kumar is a marine biotechnologist focusing on bacterial collections from the Arctic and Antarctic Oceans for various biotechnological applications. His doctoral research centers on Arctic microbes, specifically their anti-infective properties, cold-active enzymes, and potential for plant growth promotion.

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