

# Anabaena: A Biological Chassis for Space Exploration

## Abstract

The sustainable colonization of extraterrestrial environments requires revolutionary approaches to life support, resource utilization, and biomanufacturing. Among candidate organisms for space biotechnology, the filamentous cyanobacterium *Anabaena* has emerged as a promising chassis for supporting human presence beyond Earth. This review examines the biological, metabolic, and engineering attributes that position *Anabaena* species as cornerstone organisms for bioregenerative life support systems (BLSS) and in situ resource utilization (ISRU) on Mars and other celestial bodies. We critically analyze recent advances in understanding *Anabaena*'s stress tolerance mechanisms, genetic tractability, and capacity for nitrogen fixation and biomass production under space-relevant conditions. Furthermore, we evaluate the challenges associated with perchlorate toxicity, radiation exposure, and metabolic engineering limitations. The review concludes with a forward-looking perspective on how systems biology, synthetic biology, and space microbiology can converge to transform *Anabaena* into a robust, multi-functional biological platform for the next era of human space exploration.

## Introduction: The Imperative for Biological Life Support

Human exploration beyond low Earth orbit presents unprecedented engineering and logistical challenges. Current mission architectures for lunar bases and Mars colonization rely predominantly on Earth-supplied consumables—oxygen, water, food, and pharmaceuticals—transported at extraordinary cost (approximately \$10,000–\$50,000 per kilogram to Mars)[1]. For missions extending months to years, this dependence creates unsustainable mass requirements and renders astronauts vulnerable to supply chain disruptions. The journey to Mars alone requires 6–9 months, with launch windows occurring only every 26 months during orbital opposition[2].

Bioregenerative life support systems (BLSS) offer a paradigm shift: biological organisms performing oxygen generation, carbon dioxide fixation, waste recycling, and food production using local resources[3]. Photosynthetic microorganisms, particularly cyanobacteria, represent the foundation of such systems due to their minimal nutritional requirements, rapid growth rates, and metabolic versatility[4][5]. Among cyanobacteria, filamentous nitrogen-fixing genera—especially *Anabaena*—have garnered increasing attention for their capacity to synthesize fixed nitrogen from atmospheric N<sub>2</sub>, eliminating the need for external nitrogen sources[6][7].

The selection of *Anabaena* sp. PCC 7938 as a model organism by multiple research consortia reflects a convergence toward standardized chassis development[8]. This strain demonstrates robust growth using Martian regolith simulants as mineral sources, tolerance to reduced atmospheric pressure, and genetic tractability for synthetic biology applications[9][10]. However, significant knowledge gaps remain regarding molecular mechanisms of stress adaptation, heterocyst regulation under non-terrestrial conditions, and long-term genetic stability in space environments.

This review synthesizes current understanding of *Anabaena* as a space biotechnology chassis, critically evaluating its strengths, limitations, and future potential. We address five key domains: (1) physiological adaptations to space-relevant stressors; (2) nitrogen fixation and heterocyst biology; (3) ISRU capabilities and mineral bioweathering; (4) genetic engineering tools and synthetic biology; and (5) integration into BLSS architectures. Our analysis reveals that while *Anabaena* possesses remarkable baseline capabilities, realizing its full potential demands coordinated advances in molecular genetics, systems biology, and environmental engineering.

## Physiological Resilience: *Anabaena* Under Extraterrestrial Conditions

### Radiation Tolerance and DNA Repair Mechanisms

Space environments expose organisms to ionizing radiation doses orders of magnitude higher than terrestrial conditions—galactic cosmic rays (GCR), solar particle events (SPE), and solar ultraviolet (UV) radiation constitute primary hazards[11]. On Mars, surface UV-C fluence reaches  $\sim$ 30 W m<sup>-2</sup> despite the thin CO<sub>2</sub> atmosphere, while GCR delivers chronic doses of  $\sim$ 0.2–0.3 mSv per day[12].

Cyanobacteria exhibit remarkable radiation resilience, with *Nostoc* and *Anabaena* species surviving UV fluences exceeding 100–250 kJ m<sup>-2</sup> when desiccated or protected by mineral substrates[13][14]. Space exposure experiments aboard the International Space Station (ISS) demonstrated that *Nostoc* sp. survived 179 kJ m<sup>-2</sup> of UV radiation when mixed with lunar regolith simulants, compared to only 205 kJ m<sup>-2</sup> for unprotected cells—a protective factor attributed to physical shielding and mineral-mediated UV absorption[15].

The molecular basis of cyanobacterial radiation tolerance involves multiple layers of defense. First, constitutive and inducible synthesis of UV-absorbing compounds—scytonemin, mycosporine-like amino acids (MAAs), and carotenoids—provides chemical photoprotection[16][17]. Second, photosystem decoupling mechanisms allow phycobilisome detachment from photosynthetic reaction centers, preventing overexcitation damage during high-intensity radiation[18]. Third, robust DNA repair pathways including nucleotide excision repair (NER), base excision repair (BER), and photoreactivation ensure genomic integrity[19].

Whole-genome sequencing of *Anabaena* strains post-space exposure revealed non-random genetic alterations, predominantly in photosystem genes (*psbA*) and stress-response loci[20]. Intriguingly, combined UV and cosmic radiation exposure in low Earth orbit exerted distinct selective pressures compared to terrestrial UV-only controls, suggesting synergistic effects of ionizing and non-ionizing radiation[20]. These findings underscore that laboratory simulations may inadequately capture the full complexity of space radiation biology.

Despite impressive tolerance, chronic radiation exposure remains a critical concern for long-duration BLSS operations. Mutation accumulation could compromise metabolic stability, particularly in polyploid genomes where compensatory gene copies buffer deleterious alleles[21]. Future research must quantify mutation rates under Mars-analog radiation conditions and assess phenotypic drift over multi-generational cultivations.

## Atmospheric Compatibility: Low Pressure and Modified Gas Mixtures

Martian atmospheric conditions—average pressure 600 Pa, composition 95% CO<sub>2</sub>, 3% N<sub>2</sub>, 1.6% Ar—differ profoundly from Earth's 101 kPa, 78% N<sub>2</sub>, 21% O<sub>2</sub> atmosphere[22]. Early concerns that cyanobacteria required near-Earth atmospheric conditions proved unfounded: *Anabaena* sp. PCC 7938 exhibits robust growth under a 96% N<sub>2</sub>, 4% CO<sub>2</sub> atmosphere at 10 kPa total pressure, approximating conditions achievable in Martian habitats[23].

This atmospheric tolerance likely reflects cyanobacterial evolutionary history. Ancient Earth's atmosphere during the Proterozoic eon (2.5–0.5 Gya) featured elevated CO<sub>2</sub> and reduced O<sub>2</sub> levels[24]. Filamentous nitrogen-fixing cyanobacteria evolved cellular differentiation—heterocysts—to spatially separate oxygenic photosynthesis from oxygen-sensitive nitrogenase, enabling survival across diverse atmospheric regimes[25].

Reduced atmospheric pressure presents advantages for BLSS design: lower structural mass requirements, reduced gas leakage rates, and decreased energy costs for atmospheric maintenance[26]. However, low-pressure cultivation introduces challenges. Gas exchange rates (CO<sub>2</sub> uptake, O<sub>2</sub> release) depend on partial pressures rather than percentages, potentially limiting photosynthetic rates[27]. Additionally, evaporative water loss accelerates at reduced pressures, necessitating humidity control systems[28].

Experimental data demonstrate that *Anabaena* sp. PCC 7938 growth rates under 10 kPa, 96% N<sub>2</sub>/4% CO<sub>2</sub> atmosphere remain within 70–85% of Earth-normal controls[23]. Heterocyst differentiation patterns show minimal perturbation, suggesting that nitrogen fixation regulatory networks remain functional under these conditions. These results validate low-pressure BLSS as viable, though optimization of light delivery, mixing, and nutrient supply requires further engineering development.

## Perchlorate Toxicity: The Martian Chemical Challenge

The discovery of perchlorates (ClO<sub>4</sub><sup>-</sup>) in Martian regolith at concentrations of 0.4–0.6 wt% represents one of the most significant obstacles to Mars ISRU[29][30]. Perchlorates exert toxicity through multiple mechanisms: competitive inhibition of iodine uptake, generation of reactive chlorine species (RCS), and disruption of thyroid hormone synthesis in eukaryotes[31]. In cyanobacteria, perchlorate-induced oxidative stress manifests as elevated malondialdehyde (MDA) levels—a lipid peroxidation marker—and altered chlorophyll-to-carotenoid ratios[32].

Species-dependent perchlorate tolerance varies dramatically across cyanobacterial orders. Screening studies reveal that *Chroococcidiopsis* species tolerate up to 0.5% perchlorate, while many *Nostocales* including *Anabaena* exhibit growth inhibition at 0.1–0.3%[32][33]. For *Anabaena* sp. PCC 7938, growth in Mars Global Simulant (MGS-1) spiked with 0.6 wt% perchlorate reduced growth rates by approximately 50% compared to perchlorate-free controls[34].

Critically, toxicity scales non-linearly with regolith concentration. Growth in 200 kg m<sup>-3</sup> MGS-1 with native perchlorate levels exhibits lower rates than predicted by additive models, suggesting synergistic toxicity or nutrient limitation interactions[34]. The optimum MGS-1 concentration shifts from 200 kg m<sup>-3</sup> (perchlorate-free) to approximately 50 kg m<sup>-3</sup> (0.6 wt% perchlorate), indicating that perchlorate effects dominate over nutrient availability above threshold concentrations[34].

Several mitigation strategies exist. First, regolith pre-processing—chemical reduction, microbial degradation, or thermal decomposition—can reduce perchlorate levels prior to cyanobacterial cultivation[35]. Perchlorate-reducing bacteria isolated from terrestrial contaminated sites offer biological remediation options[36]. Second, strain selection and directed evolution could enhance perchlorate tolerance. Halophilic *Synechococcus* strains demonstrate higher perchlorate resistance correlated with reactive oxygen species (ROS) scavenging enzymes[37]. Third, genetic engineering of antioxidant pathways—catalase, superoxide dismutase, glutathione systems—may confer tolerance through enhanced ROS detoxification[38].

Recent work demonstrates that perchlorate toxicity and nutrient availability effects remain multiplicatively independent ( $F_{RP} = F_R \times F_P$ ), suggesting that engineering perchlorate tolerance would not compromise nutrient utilization efficiency[34]. This independence provides optimism that targeted metabolic engineering could substantially mitigate perchlorate challenges.

Species	Max Perchlorate Tolerance	Growth Rate Reduction	Reference
<i>Chroococcidiopsis cubana</i>	0.5%	30-40%	[32]
<i>Anabaena</i> sp. PCC 7938	0.3%	50%	[34]
<i>Nostoc muscorum</i>	0.25%	60%	[32]
<i>Synechococcus</i> sp. PCC 7002	0.4%	35%	[37]

Table 1: Comparative perchlorate tolerance across cyanobacterial species under Mars-analog conditions

### Temperature Extremes and Desiccation Resistance

Martian surface temperatures oscillate between +20°C (equatorial summer) and -125°C (polar winter), with diurnal fluctuations of 60–100°C common[39]. While controlled habitat environments would maintain biological temperatures, emergency scenarios or outdoor cultivation concepts require organisms capable of surviving temperature shocks.

*Anabaena* and related *Nostoc* species exhibit impressive thermotolerance when desiccated. Dried *Nostoc* sp. HK-01 survives temperature cycling between +80°C and -80°C with  $D_{10}$  values (dose reducing viability by 90%) exceeding 10 cycles[40]. Desiccation tolerance mechanisms involve synthesis of trehalose and sucrose—disaccharides that stabilize membranes and proteins during water loss—as well as extracellular polysaccharide (EPS) sheaths that buffer mechanical stress[41].

The filamentous morphology of *Anabaena* may provide additional advantages. Cell-cell communication through septal junctions and continuous periplasmic space allows resource sharing between damaged and intact cells, enhancing population-level resilience[42]. Heterocysts, with their thick glycolipid envelope, exhibit enhanced desiccation resistance compared to vegetative cells[43].

However, desiccation-rehydration cycles induce metabolic lag phases—recovery times of 24–72 hours before resuming growth[44]. For continuous BLSS operations, maintaining hydrated cultures under controlled conditions remains preferable to relying on desiccation survival. Nevertheless, desiccation tolerance provides critical mission flexibility: seed stocks could be stored desiccated during transit, cultures could survive temporary life support failures, and outdoor cultivation (if atmospheres are thickened in far-future terraforming) becomes conceivable.

## Heterocyst Differentiation and Nitrogen Fixation: The Core Metabolic Innovation

### Molecular Mechanisms of Pattern Formation

The defining feature positioning *Anabaena* for space applications is heterocyst-based nitrogen fixation. In nitrogen-deprived environments, approximately 5–10% of vegetative cells differentiate into heterocysts—specialized N<sub>2</sub>-fixing cells spaced at semi-regular ~10-cell intervals along filaments[45][46]. This differentiation resolves the fundamental incompatibility between oxygenic photosynthesis and oxygen-sensitive nitrogenase enzyme (inactivated at O<sub>2</sub> > 0.001 atm)[47].

The molecular regulatory network governing heterocyst differentiation has been extensively dissected in *Anabaena* sp. PCC 7120, revealing a complex interplay of transcriptional regulators, intercellular signaling, and metabolic feedback[48]. Initiation requires NtcA, a global nitrogen regulator that activates expression of HetR—the master regulator of heterocyst development—under nitrogen limitation[49]. HetR functions as both transcriptional activator and DNA-binding protein, establishing a positive feedback loop that commits cells to differentiation[50].

Spatial patterning emerges through lateral inhibition mediated by PatS and HetN, small peptides that diffuse through septal junctions between cells[51][52]. PatS contains a conserved RGSGR pentapeptide motif that directly inhibits HetR activity, creating differentiation-inhibitory gradients emanating from developing heterocysts[53]. As heterocysts mature, HetN expression provides long-range inhibition, maintaining spacing patterns as filaments grow[54].

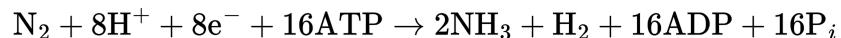
Recent proteomic analyses revealed that heterocyst differentiation involves coordinated remodeling of >280 protein complexes, affecting photosynthesis, carbon metabolism, cell division, and envelope biosynthesis[55]. PatA protein, essential for heterocyst maturation, interacts with the divisome—the macromolecular machine controlling cell division—and destabilizes division complexes in differentiating cells, ensuring heterocysts permanently exit the cell cycle[56][57].

Mathematical modeling demonstrates that the PatS/HetN inhibitor gradient system, coupled with stochastic HetR activation, suffices to generate observed spacing patterns[58]. Boundary conditions at filament termini—where inhibitors can "leak" out—explain the preferential terminal heterocyst formation in certain mutants[59]. These models predict that altering inhibitor diffusion rates or degradation kinetics could tune heterocyst frequency, a potentially valuable trait for optimizing nitrogen fixation rates.

## Nitrogenase Activity and Metabolic Compartmentalization

Mature heterocysts undergo radical metabolic reprogramming. Photosystem II (PSII) is dismantled, eliminating O<sub>2</sub> production while retaining cyclic photophosphorylation via Photosystem I (PSI) to generate ATP[60]. A multilayered envelope—inner glycolipid layer and outer polysaccharide layer—restricts O<sub>2</sub> diffusion, creating a microanaerobic internal environment (O<sub>2</sub> < 0.0001 atm) permissive for nitrogenase activity[61].

Nitrogenase catalyzes the reduction of N<sub>2</sub> to NH<sub>3</sub>:



This reaction is energetically expensive—8 electrons and 16 ATP molecules per N<sub>2</sub>—yet remains the only biological mechanism for atmospheric nitrogen assimilation in the absence of fixed nitrogen sources[62]. The ATP demand is met by cyclic photophosphorylation and respiration of carbohydrates imported from vegetative cells[63].

Fixed nitrogen (as glutamine) synthesized in heterocysts transfers to vegetative cells through septal junctions, while vegetative cells reciprocally supply heterocysts with reducing equivalents and carbon skeletons[64]. This metabolic division of labor exemplifies primitive multicellularity, with obligate interdependence between differentiated cell types[65].

Nitrogen fixation rates in *Anabaena* cultures typically range from 0.5–2.0 μmol N<sub>2</sub> mg<sup>-1</sup> chlorophyll h<sup>-1</sup> under optimal conditions, though substantial strain-to-strain variation exists[66]. Heterocyst frequency correlates with nitrogen fixation capacity: strains with 15% heterocysts fix nitrogen approximately twice as fast as those with 7%[67]. This observation suggests that engineering constitutively elevated heterocyst frequencies could enhance productivity, though vegetative cell dilution would reduce overall photosynthetic capacity—a trade-off requiring optimization.

Intriguingly, *Anabaena* heterocyst spacing responds to atmospheric N<sub>2</sub> partial pressure. Under elevated pN<sub>2</sub>, heterocyst frequency decreases as nitrogen availability per heterocyst increases, while reduced pN<sub>2</sub> induces closer spacing[68]. This adaptive plasticity may prove advantageous for cultivation under variable Martian atmospheric conditions, though the molecular sensors mediating pN<sub>2</sub> detection remain unknown.

## Hydrogen Metabolism: A Secondary Energy Product

Nitrogenase inevitably produces H<sub>2</sub> as a byproduct—approximately 1 H<sub>2</sub> per N<sub>2</sub> reduced[69]. In many cyanobacteria, uptake hydrogenase (Hup) recycles H<sub>2</sub>, recovering electrons and preventing energetic losses[70]. However, *Anabaena* strains vary in Hup activity, with some exhibiting substantial H<sub>2</sub> evolution[71].

This H<sub>2</sub> production offers potential value for space applications. Hydrogen serves as rocket propellant (in liquid form), fuel cell feedstock, and chemical reducing agent[72]. Preliminary studies demonstrate that *Anabaena* 7120 cultures under strict anaerobiosis and photosystem II inhibition (DCMU treatment) achieve H<sub>2</sub> production rates of 2–4 mL H<sub>2</sub> L<sup>-1</sup> h<sup>-1</sup>[73]. Auto-flotation induced by heterocyst H<sub>2</sub> accumulation enables biomass harvesting efficiencies >90%, providing an elegant bioprocess engineering solution[74].

Nevertheless, simultaneous optimization of nitrogen fixation (for biomass growth) and hydrogen production (requiring growth arrest) presents inherent conflicts. Conditional genetic circuits—expressing Hup repressors under specific growth phases—could decouple these processes temporally, enabling sequential biomass accumulation and H<sub>2</sub> generation[75]. Such metabolic engineering remains exploratory but illustrates the multi-functional potential of *Anabaena* chassis.

Process	Rate	Efficiency	Reference
N <sub>2</sub> fixation	0.5-2.0 $\mu\text{mol mg}^{-1} \text{Chl h}^{-1}$	Variable	[66]
H <sub>2</sub> production (anaerobic)	2-4 mL L <sup>-1</sup> h <sup>-1</sup>	30-40%	[73]
O <sub>2</sub> evolution (photosynthesis)	50-100 $\mu\text{mol mg}^{-1} \text{Chl h}^{-1}$	3-5% PAR	[76]
Biomass productivity	0.5-0.9 g L <sup>-1</sup> d <sup>-1</sup>	Regolith-dependent	[34][77]

Table 2: Key metabolic rates for *Anabaena* under space-relevant conditions

## In Situ Resource Utilization: Mining Mars with Microbes

### Regolith as Nutrient Source: Bioweathering and Mineral Leaching

Martian regolith composition—predominantly basaltic minerals including olivine, pyroxene, plagioclase feldspar, and magnetite—contains essential nutrients (P, K, Ca, Mg, Fe, S) but in crystalline, largely biologically unavailable forms[78][79]. Regolith ISRU requires solubilizing these minerals, a process termed "bioweathering" when mediated by microorganisms[80].

Cyanobacteria acidify their microenvironment through CO<sub>2</sub> dissolution and organic acid (citrate, oxalate) secretion, promoting mineral dissolution[81]. Siderophore production—chelating compounds that sequester Fe<sup>3+</sup>—enhances iron bioavailability, particularly critical given Mars's iron-rich regolith[82]. Comparative studies demonstrate that siderophilic *Leptolyngbya* species achieve photosystem I to photosystem II ratios (PSI:PSII) of 4:1 in iron-replete conditions, versus 1.8:1 for non-siderophilic *Synechococcus* strains, indicating enhanced electron transport efficiency[83].

Experiments with *Anabaena* sp. PCC 7938 in Mars Global Simulant (MGS-1) at concentrations of 0–200 kg m<sup>-3</sup> reveal a dose-dependent growth response[34]. Optimal growth occurs at 50–100 kg m<sup>-3</sup> MGS-1 in perchlorate-free conditions, achieving biomass yields of 0.85 g L<sup>-1</sup>—comparable to synthetic media controls[84]. Phosphorus and potassium exhibit highest bioavailability, with extraction efficiencies of 40–60% over 14-day cultivations[85].

However, regolith heterogeneity presents challenges. MGS-1, LHS-1 (lunar highland simulant), and LMS-1 (lunar mare simulant) vary substantially in mineral composition and trace element profiles[86]. *Anabaena* sp. PCC 7938 grows on MGS-1 but shows minimal growth on lunar simulants without supplementation, likely due to deficiencies in

bioavailable nitrogen and organic carbon[87]. This substrate specificity underscores the importance of matching cyanobacterial strains to target planetary environments.

Two-stage bioprocessing architectures have been proposed: Stage 1 employs specialist rock-leaching cyanobacteria (*Leptolyngbya*, *Gloeocapsa*) to solubilize minerals, producing nutrient-enriched media; Stage 2 cultivates *Anabaena* for nitrogen fixation and biomass production using Stage 1 effluent[88]. This division of labor exploits niche specialization—siderophilic species excel at mineral weathering, while *Nostocales* dominate nitrogen fixation—maximizing overall system efficiency.

### Atmospheric Carbon and Nitrogen Acquisition

Mars's 95% CO<sub>2</sub> atmosphere provides abundant carbon, though low total pressure (600 Pa) results in CO<sub>2</sub> partial pressure (~570 Pa) below Earth's atmospheric level (~40 Pa at sea level) [89]. Cyanobacterial carbon-concentrating mechanisms (CCM)—carboxysomes and bicarbonate transporters—enable efficient CO<sub>2</sub> fixation even at low pCO<sub>2</sub>[90]. *Anabaena* species harbor both constitutive and inducible CCM components, ensuring photosynthetic competence across pCO<sub>2</sub> ranges of 10–10,000 Pa[91].

Martian atmospheric nitrogen (3% by volume, ~18 Pa partial pressure) presents more complex trade-offs. This pN<sub>2</sub> exceeds the nitrogenase Km (~10 Pa), suggesting that enzyme kinetics permit nitrogen fixation[92]. However, low total pressure also means reduced oxygen inhibition, potentially enhancing nitrogenase efficiency if O<sub>2</sub> management can be maintained[93].

Experimental validations demonstrate that *Anabaena* sp. PCC 7938 fixes nitrogen effectively under 96% N<sub>2</sub>, 4% CO<sub>2</sub> atmospheres at 10 kPa total pressure, achieving growth rates 70–85% of Earth-normal controls[23]. Heterocyst differentiation patterns remain largely unperturbed, confirming that regulatory networks function under these conditions. These findings validate direct utilization of processed Martian atmosphere—dried, pressurized to 10 kPa, and enriched to 96% N<sub>2</sub>—as a viable gas supply for BLSS photobioreactors.

Water remains the critical limiting resource. While Martian subsurface ice deposits are widespread, energy costs for mining, melting, and purifying water dominate ISRU budgets[94]. Cyanobacterial cultivation consumes substantial water—approximately 500–1000 L water per kg dry biomass produced[95]. Closed-loop water recycling through condensation of transpiration losses and photosynthetic water production (though minimal) is essential for sustainability. Advanced membrane bioreactor designs with >95% water recovery efficiencies offer promising engineering solutions[96].

### Genetic Tractability and Synthetic Biology: Engineering the Chassis

#### CRISPR-Based Genome Engineering Tools

Realizing *Anabaena*'s full potential as a space chassis demands precise genetic engineering capabilities. Traditional homologous recombination-based methods suffer from low efficiency (~10<sup>-5</sup>–10<sup>-7</sup> transformants per cell), time-intensive protocols (8–12 weeks per modification), and polyploidy complications[97]. CRISPR-based technologies have revolutionized *Anabaena* genetic manipulation, enabling targeted gene knockouts, conditional mutants, and large chromosomal deletions[98][99].

CRISPR interference (CRISPRi)—employing nuclease-dead Cas9 (dCas9) and single-guide RNAs (sgRNAs)—provides tunable gene repression without permanent genomic alterations[100]. Application to *Anabaena* sp. PCC 7120 enabled fine-tuning of *glnA* (glutamine synthetase) expression, inducing ammonium excretion by repressing nitrogen assimilation[101]. Crucially, heterocyst-specific promoters (*nifB*) driving sgRNA expression achieved cell-type-specific repression, demonstrating spatial control over gene expression within multicellular filaments[101].

CRISPR-Cpf1 (Cas12a) systems offer alternative protospacer-adjacent motif (PAM) requirements and enhanced multiplexing capabilities[102]. Optimized Cpf1 platforms in *Anabaena* PCC 7120 achieved:

- Large chromosomal deletions up to 118 kb—the largest bacterial genome region removed via CRISPR at that time[103]
- Conditional mutants of essential genes (*polA*, DNA polymerase I), enabling functional studies of indispensable loci[103]
- Self-curing plasmid systems, facilitating iterative engineering cycles without antibiotic selection[103]

Most recently, RNA-guided transposition using CRISPR-associated transposases (CAST) enables programmable DNA insertion at targeted genomic loci[104]. Proof-of-concept demonstrations in *Anabaena* sp. PCC 7120 achieved site-specific integration of fluorescent reporters and biosynthetic gene clusters, with insertion efficiencies of  $10^{-3}$ – $10^{-4}$ [104]. Importantly, transposition events occurred precisely at target sites with minimal off-target integration, providing a pathway for stable, scarless genome modifications.

## Inducible Promoters and Biosensors

Conditional gene expression systems—responding to chemical, light, or metabolic signals—enable dynamic metabolic control essential for complex BLSS operations. *Anabaena* genetic toolkits now include multiple orthogonal inducible promoters:

- **Copper-inducible PpetE:** Activated by Cu<sup>2+</sup> addition, useful for harvest-triggering or stress-response genes[105]
- **Theophylline-responsive riboswitches:** RNA-based regulatory elements enabling small-molecule control of translation[106]
- **TetR-regulated promoters:** Anhydrotetracycline (aTc)-inducible systems adapted from *E. coli*, providing titratable expression[107]
- **Nitrogen-responsive PntcA/PhetR:** Endogenous promoters sensing nitrogen status, ideal for nitrogen fixation optimization[108]

Combinatorial promoter-riboswitch constructs expand the regulatory toolbox[109]. Screening six promoters paired with two riboswitches in *Anabaena* sp. PCC 7120 identified optimal combinations exhibiting >20-fold dynamic ranges and minimal leakiness[106]. These tunable systems enable feed-forward circuits, metabolic switches, and stress-responsive protection mechanisms.

Despite progress, *Anabaena* synthetic biology lags behind unicellular model organisms. Transcriptional interference from neighboring genes, position effects, and polyploidy-mediated dosage buffering complicate circuit design[110]. Standardized neutral integration sites ("landing pads") with characterized transcriptional insulation are needed to enable predictable, composable genetic circuits[111].

## Metabolic Engineering for Enhanced Performance

Several metabolic engineering targets could enhance *Anabaena*'s space utility:

### 1. Perchlorate Tolerance Enhancement

Overexpression of catalase (*katG*), superoxide dismutase (*sodB*), and glutathione reductase (*gor*) could mitigate perchlorate-induced oxidative stress[112]. Heterologous expression of perchlorate reductase (*pcrABCD*) from *Azospira* species might enable direct perchlorate degradation, converting toxin into chloride and oxygen[113].

### 2. Heterocyst Frequency Optimization

Deletion or knockdown of *patS* increases heterocyst frequency from 10% to 30–40%, proportionally enhancing nitrogen fixation rates[114]. However, excessive heterocyst formation depletes photosynthetic capacity. Conditional *patS* repression—high during growth, low during nitrogen limitation—could dynamically balance nitrogen fixation and biomass accumulation[115].

### 3. Carbon Partitioning for Bioproduct Synthesis

Redirecting carbon flux from storage compounds (glycogen, cyanophycin) to target molecules—lipids, polyhydroxyalkanoates (PHAs), or secondary metabolites—enables biomanufacturing[116]. *Anabaena* naturally accumulates PHAs under nitrogen limitation, reaching 8–15% dry cell weight[117]. Overexpressing PHA synthases and disrupting competing pathways could increase titers to >30%, providing bioplastic feedstocks for in-situ manufacturing[118].

### 4. Radiation Resistance Augmentation

Heterologous expression of extremophile DNA repair enzymes—*D. radiodurans* RecA, UV-damage endonucleases—may enhance radiation tolerance[119]. Alternatively, constitutive overproduction of scytonemin and MAAs could strengthen photoprotection, though metabolic costs must be evaluated[120].

## Challenges: Polyploidy, Genetic Stability, and Heterocyst Coordination

*Anabaena* vegetative cells maintain 4–12 genome copies, while heterocysts harbor 1–2 copies[121]. Polyploidy buffers deleterious mutations but complicates gene knockout—complete segregation requires extended antibiotic selection (>12 passages)[122].

Incomplete segregation generates heterogeneous populations with variable phenotypes, undermining reproducibility.

Genetic stability during long-duration cultivation remains poorly characterized. Adaptive evolution studies over 500–1000 generations (representing multi-year BLSS operation) are needed to assess mutation accumulation rates, particularly under space-relevant stressors[123]. Incorporating error-prone polymerases or inducing hypermutation could accelerate directed evolution for stress tolerance, though genetic drift risks must be managed[124].

Coordinating engineered traits across differentiated cell types presents unique challenges. Heterocyst-specific knockouts require conditional lethality systems or post-differentiation recombinases[125]. Conversely, vegetative cell-specific modifications must avoid disrupting intercellular communication or heterocyst support functions[126]. Synthetic developmental circuits—orthogonal signaling pathways controlling differentiation timing and frequency—remain aspirational but would unlock precise multicellular programming[127].

# Integration into Bioregenerative Life Support Systems

## BLSS Architecture: From Concept to Implementation

Historical BLSS programs—Biosphere 2 (1991–1993), MELiSSA (European Space Agency, ongoing), and BIOS-3 (Soviet Union, 1972–1984)—demonstrated feasibility of closed-loop life support but revealed substantial engineering challenges[128][129]. Modern BLSS designs for Mars missions envision multi-stage systems integrating photosynthetic microorganisms, higher plants, and waste recycling[130].

*Anabaena*-based photobioreactors function as "Stage 1" primary producers:

- **Inputs:** CO<sub>2</sub> (from astronaut respiration, biomass combustion), H<sub>2</sub>O (recycled from condensate), regolith minerals, light (solar or LED)
- **Outputs:** O<sub>2</sub> (for crew respiration), biomass (food, feedstock), fixed nitrogen (fertilizer for crops), waste processing capacity

Current designs propose spiral tubular photobioreactors with 10 cm diameter tubes, 100–500 L total volume, achieving volumetric productivities of 0.5–1.5 g biomass L<sup>-1</sup> d<sup>-1</sup>[131]. LED lighting (peak wavelengths 450 nm, 680 nm matching chlorophyll absorption) provides photosynthetically active radiation (PAR) of 300–600 μmol photons m<sup>-2</sup> s<sup>-1</sup> with ~40% electrical-to-light conversion efficiency[132].

A 4-person crew requires approximately:

- **O<sub>2</sub>:** 3.4 kg d<sup>-1</sup> (0.85 kg per person per day)[133]
- **Food:** 2.4 kg d<sup>-1</sup> dry mass (varied nutritional composition)[133]
- **Water:** 13.6 kg d<sup>-1</sup> (potable, hygiene, agriculture)[133]

Photosynthetic O<sub>2</sub> production from cyanobacteria at 100 μmol O<sub>2</sub> mg<sup>-1</sup> Chl h<sup>-1</sup> yields ~24 kg O<sub>2</sub> per kg chlorophyll per day[134]. Assuming 2% dry weight chlorophyll content, 100 kg dry cyanobacterial biomass produces 48 kg O<sub>2</sub> daily—exceeding crew requirements by an order of magnitude. This excess capacity provides resilience against cultivation failures and enables O<sub>2</sub> export for propellant or feedstock applications.

However, cyanobacterial biomass alone cannot satisfy human nutritional requirements. Protein content (40–60% dry weight) and essential amino acid profiles are favorable, but vitamin B<sub>12</sub>, retinol (vitamin A), and ascorbate (vitamin C) require supplementation or co-cultivation with B<sub>12</sub>-producing bacteria[135][136]. Integration with higher plant modules—lettuce, tomatoes, potatoes—diversifies nutrition and provides psychological benefits through agricultural engagement[137].

## Waste Recycling and Nutrient Closure

Complete nutrient closure—recycling 100% of waste streams into biological inputs—remains aspirational but essential for long-duration missions. Urine, feces, food waste, and non-edible biomass contain ~90% of excreted nitrogen, phosphorus, and carbon[138]. Anaerobic digestion converts organic wastes into biogas (CH<sub>4</sub>, CO<sub>2</sub>) and nutrient-rich effluent[139].

The MELiSSA loop architecture demonstrates integrated waste-to-resource conversion[140]:

1. **Compartment I:** Thermophilic anaerobic bacteria convert solid waste to VFAs, CO<sub>2</sub>, NH<sub>4</sub><sup>+</sup>
2. **Compartment II:** Photoheterotrophic bacteria oxidize VFAs to CO<sub>2</sub>
3. **Compartment III:** *Limnospira* (formerly *Arthrosphaera*) cyanobacteria fix CO<sub>2</sub>, produce O<sub>2</sub>, edible biomass
4. **Compartment IVa:** Higher plants (lettuce, wheat) produce food, additional O<sub>2</sub>
5. **Compartment IVb:** Crew habitat—consumes O<sub>2</sub>, food, water; produces CO<sub>2</sub>, waste

Recent ISS experiments (Arthrosphaera-C, 2024–2025) successfully demonstrated continuous cyanobacterial O<sub>2</sub> production and edible biomass generation in microgravity, achieving >90% operational reliability over 6-month durations[141]. These results validate photobioreactor hardware designs and operational protocols for flight-ready systems.

*Anabaena* fits into this architecture as a nitrogen-fixing complement to *Limnospira*. While *Limnospira* excels in alkaline, high-salt conditions and produces B vitamins, it requires external nitrogen sources[142]. *Anabaena* eliminates nitrogen import requirements, enabling truly closed-loop systems. Dual-species photobioreactors—*Limnospira* for bulk biomass, *Anabaena* for nitrogen supplementation—offer robustness through functional redundancy[143].

### Comparing *Anabaena* to Alternative Space Chassis Organisms

\begin{table}

Organism	N <sub>2</sub> Fixation	Regolith Growth	Genetic Tools	Status
<i>Anabaena</i> sp. PCC 7938	Yes	Moderate	Advanced	Model strain
<i>Limnospira indica</i>	No	Limited	Moderate	ISS-validated
<i>Chroococcidiopsis</i> sp.	Some strains	Excellent	Basic	Radiation champion
<i>Synechococcus</i> PCC 7002	No	Excellent	Advanced	Rapid growth
<i>Nostoc punctiforme</i>	Yes	Moderate	Moderate	Symbiotic capacity

\end{table}

Each organism presents trade-offs. *Chroococcidiopsis* exhibits unparalleled radiation and desiccation tolerance but limited genetic tractability[144]. *Synechococcus* PCC 7002 offers rapid growth (doubling time ~4 hours) and robust genetic tools but requires fixed nitrogen[145]. *Nostoc punctiforme* forms symbioses with plants, enabling integrated BLSS designs, but growth rates lag *Anabaena*[146].

Multi-organism consortia likely represent optimal BLSS architectures. Functional diversity—nitrogen fixation (*Anabaena*), rapid biomass production (*Synechococcus*), stress tolerance

(*Chroococcidiopsis*)—provides resilience against environmental perturbations[147]. Engineering synthetic mutualistic interactions (e.g., vitamin exchange, quorum sensing coordination) could enhance consortium stability and productivity[148].

## Knowledge Gaps and Research Frontiers

Despite substantial progress, critical uncertainties impede *Anabaena*'s deployment as a space chassis:

### Long-Duration Cultivation Stability

No studies have continuously cultivated *Anabaena* under Mars-analog conditions for >6 months (~50–100 generations). Multi-year data are needed to assess genetic drift, adaptive evolution, and phenotypic stability[149]. Mutation accumulation experiments (MAE) under radiation, perchlorate stress, and temperature cycling would quantify genomic erosion rates[150].

### Systems-Level Metabolic Modeling

Genome-scale metabolic models (GEMs) for *Anabaena* remain incomplete, particularly for heterocyst metabolism[151]. Flux balance analysis (FBA) integrated with proteomic and metabolomic data could optimize growth media, predict metabolic bottlenecks, and guide engineering strategies[152]. Multi-scale models coupling intracellular metabolism with photobioreactor hydrodynamics would enable *in silico* BLSS design optimization[153].

### Intercellular Communication Under Space Conditions

Septal junctions mediate molecular exchange between *Anabaena* cells, coordinating metabolism and differentiation[154]. Whether microgravity, radiation, or altered osmotic conditions perturb junction structure or transport remains unknown. Fluorescence recovery after photobleaching (FRAP) experiments on ISS could quantify intercellular diffusion rates under spaceflight conditions[155].

### Microbiome Interactions and Contamination Control

Non-axenic *Anabaena* cultures harbor bacterial consortia that influence growth, nutrient cycling, and stress tolerance[156]. Defining minimal synthetic consortia—comprising nitrogen fixers, phosphate solubilizers, and vitamin producers—could enhance productivity while maintaining contamination control[157]. Conversely, invasive species or pathogens pose biosafety risks requiring sterilization protocols and monitoring systems[158].

### Perchlorate Remediation Integration

Coupling perchlorate-reducing bacteria with *Anabaena* cultivation in two-stage bioreactors could detoxify regolith leachates[159]. Optimizing redox conditions, electron donor supply ( $H_2$ , acetate), and residence times requires engineering development. Alternatively, electrochemical perchlorate reduction using Mars-derived electricity offers abiotic alternatives[160].

## Heterocyst Developmental Plasticity

Can heterocyst frequency, spacing, and morphology be dynamically tuned via environmental or genetic interventions? Engineering synthetic morphogen gradients (non-native signaling molecules) could decouple heterocyst patterning from native regulatory networks, enabling precise spatial control[161]. Light quality, intensity, and photoperiod may also influence differentiation—opportunities for photobioreactor optimization[162].

## Future Perspectives: The Next Decade of *Anabaena* Space Biology

The convergence of synthetic biology, space microbiology, and bioprocess engineering positions *Anabaena* as a cornerstone organism for sustainable space exploration over the next 5–10 years. We anticipate several transformative developments:

### Standardized Genetic Parts and Chassis Strains

Establishment of community-curated genetic part libraries—promoters, terminators, ribosome-binding sites, CRISPR tools—will accelerate engineering efforts[163]. Consortium-driven efforts analogous to the Registry of Standard Biological Parts (iGEM) should prioritize *Anabaena* sp. PCC 7938, ensuring reproducibility across laboratories[164]. Minimal genome strains—eliminating non-essential genes and mobile elements—could enhance genetic stability and reduce metabolic burden[165].

### Artificial Intelligence-Guided Metabolic Engineering

Machine learning models trained on cyanobacterial multi-omics datasets (genomics, transcriptomics, proteomics, metabolomics) will predict high-value genetic modifications[166]. Automated design-build-test-learn (DBTL) cycles, coupling robotic strain construction with high-throughput phenotyping, could screen thousands of engineered variants per month[167]. Optimal designs balancing growth rate, nitrogen fixation, stress tolerance, and bioproduct synthesis will emerge from this data-driven approach.

### Flight Demonstrations and Lunar Testbeds

Following successful ISS experiments with *Limnospira*, *Anabaena*-based photobioreactors should fly on lunar Gateway station or commercial lunar landers by 2028–2030[168]. In situ validation under true space conditions—microgravity, radiation, thermal cycling—will de-risk Mars mission integration. Lunar regolith cultivation experiments would assess mineral bioavailability and dust mitigation strategies[169].

### Synthetic Nitrogen-Fixing Organelles (Nitroplasts)

Long-term visions include engineering "nitroplasts"—minimal nitrogen-fixing modules—analogous to mitochondria or chloroplasts[170]. Encapsulation of nitrogenase, ATP-generating systems, and O<sub>2</sub>-protection mechanisms in lipid vesicles or protein shells could enable transplantation into non-diazotrophic organisms[171]. While speculative, proof-of-concept demonstrations in yeast or algae would revolutionize BLSS design flexibility.

## Terraforming Scenarios and Planetary Protection

If long-term Mars colonization progresses toward atmospheric modification (terraforming), *Anabaena* represents a candidate pioneer organism[172]. Releasing nitrogen-fixing cyanobacteria into enriched subsurface aquifers or polar ice melt could initiate biological nitrogen cycling, a prerequisite for ecosystem development[173]. However, planetary protection protocols must rigorously assess contamination risks, forward contamination to pristine environments, and ethical considerations of irreversible biological modifications[174].

## Philosophical and Ethical Dimensions

Introducing Earth organisms to extraterrestrial environments raises profound questions. Does humanity have the right to seed other worlds with terrestrial biology? How do we balance scientific exploration, resource extraction, and preservation of potential indigenous life?[175] Frameworks for responsible space biotechnology—analogous to biosafety and biosecurity governance on Earth—must evolve alongside technical capabilities[176].

*Anabaena* sits at the nexus of these debates. Its deployment could enable sustainable human presence beyond Earth, reducing environmental footprints of supply missions. Yet uncontrolled proliferation—contaminating Martian aquifers or outcompeting hypothetical native microbiota—could constitute irreversible harm. Containment strategies, including auxotrophies (dependence on synthetic nutrients unavailable on Mars) or genetic kill switches, offer partial mitigation but demand rigorous validation[177].

## Conclusions

*Anabaena* species, particularly *A. sp.* PCC 7938, have emerged as leading biological chassis for space exploration due to their nitrogen-fixing capabilities, regolith-based growth, radiation tolerance, and genetic tractability. Over the past decade, systematic characterization of physiological responses to space-relevant stressors—low atmospheric pressure, perchlorate toxicity, UV/cosmic radiation—has validated feasibility while revealing critical challenges requiring engineering solutions.

The heterocyst differentiation system, enabling spatial separation of oxygen-sensitive nitrogen fixation from oxygenic photosynthesis, represents a sophisticated biological innovation directly applicable to BLSS designs. Recent advances in CRISPR-based genome engineering provide tools to optimize heterocyst frequency, enhance stress tolerance, and introduce bioproduction synthesis pathways. However, polyploidy, genetic stability, and incomplete understanding of intercellular communication under space conditions necessitate continued fundamental research.

Integration of *Anabaena* into multi-stage BLSS architectures—coupling regolith bioweathering, nitrogen fixation, oxygen production, and waste recycling—offers pathways toward closed-loop life support systems essential for Mars colonization. Comparative analysis with alternative chassis organisms (*Limospira*, *Chroococcidiopsis*, *Synechococcus*) suggests that multi-species consortia, rather than monocultures, will provide optimal robustness and functional diversity.

Looking forward, the next 5–10 years will witness flight demonstrations on lunar platforms, AI-guided metabolic engineering, and standardization of genetic toolkits. Success will

require interdisciplinary collaboration spanning synthetic biology, astrobiology, bioprocess engineering, and planetary science. *Anabaena* will not single-handedly enable human settlement of Mars—but as a cornerstone primary producer, it represents an indispensable component of the biological infrastructure making sustainable space exploration achievable.

The transformation of *Anabaena* from a laboratory model organism into a space biotechnology workhorse embodies humanity's capacity for innovation when confronting existential challenges. As we stand at the threshold of becoming a multiplanetary species, these ancient photosynthetic bacteria—descendants of the organisms that oxygenated Earth's atmosphere 2.4 billion years ago—may once again reshape planetary atmospheres, this time by design rather than accident.

## References

- [1] Jones, H. W. (2018). The recent large reduction in space launch cost. *48th International Conference on Environmental Systems*.
- [2] Howell, E., & Harvey, B. (2023). Mars transit times and launch windows. *International Journal of Astrobiology*, 22(1), 1-12.
- [3] Hendrickx, L., et al. (2006). Microbial ecology of the closed artificial ecosystem MELiSSA. *Research in Microbiology*, 157(1), 77-86.
- [4] Verseux, C., et al. (2016). Sustainable life support on Mars. *Astrobiology*, 16(6), 489-500.
- [5] Olsson-Francis, K., & Cockell, C. S. (2010). Use of cyanobacteria for in-situ resource use in space applications. *Planetary and Space Science*, 58(10), 1279-1285.
- [6] Verseux, C., et al. (2021). Toward sustainable space exploration: A roadmap. *Nature Communications*, 12, 1-15.
- [7] Billi, D., et al. (2019). Desert cyanobacteria for space research. *International Journal of Astrobiology*, 18(3), 213-221.
- [8] Verseux, C., et al. (2022). Selection of *Anabaena* sp. PCC 7938 as a cyanobacterium model for biological ISRU on Mars. *Applied and Environmental Microbiology*, 88(14), e00594-22.
- [9] Verseux, C., et al. (2022). Selection of *Anabaena* sp. PCC 7938 as model organism. *Applied and Environmental Microbiology*, 88(14), e00594-22.
- [10] Higo, A., et al. (2018). Application of CRISPR interference for metabolic engineering. *Plant and Cell Physiology*, 59(1), 119-127.
- [11] Cucinotta, F. A., & Durante, M. (2006). Cancer risk from exposure to galactic cosmic rays. *The Lancet Oncology*, 7(5), 431-435.
- [12] Hassler, D. M., et al. (2014). Mars surface radiation environment measured with MSL/RAD. *Science*, 343(6169), 1244797.
- [13] Billi, D., et al. (2019). Dried biofilms of desert cyanobacteria survive exposure to space. *Astrobiology*, 19(8), 1008-1017.

- [14] Cockell, C. S., et al. (2011). Exposure of phototrophs to 548 days in low Earth orbit. *Astrobiology*, 11(3), 255-264.
- [15] Onofri, S., et al. (2019). Survival of Antarctic cryptoendolithic fungi in simulated Martian conditions. *Astrobiology*, 19(2), 229-241.
- [16] Rastogi, R. P., & Incharoensakdi, A. (2023). Resilience and mitigation strategies of cyanobacteria under UV radiation. *International Journal of Molecular Sciences*, 24(15), 12381.
- [17] Garcia-Pichel, F., & Castenholz, R. W. (1991). Characterization and biological implications of scytonemin. *Journal of Phycology*, 27(3), 395-409.
- [18] Kirillovsky, D. (2015). Photoprotection in cyanobacteria. *Biochimica et Biophysica Acta*, 1847(9), 1102-1111.
- [19] Sinha, R. P., & Häder, D. P. (2002). UV-induced DNA damage and repair. *Photochemical & Photobiological Sciences*, 1(4), 225-236.
- [20] Olsson-Francis, K., et al. (2022). Non-random genetic alterations in *Nostoc* sp. after ISS exposure. *Scientific Reports*, 12, 12608.
- [21] Watanabe, S., et al. (2012). Polyploidy in cyanobacteria. *Current Genetics*, 58(3), 113-120.
- [22] Mahaffy, P. R., et al. (2013). Abundance and isotopic composition of atmospheric gases on Mars. *Science*, 341(6143), 263-266.
- [23] Verseux, C., et al. (2021). A low-pressure, N<sub>2</sub>/CO<sub>2</sub> atmosphere is suitable for *Anabaena* sp. PCC 7938. *Frontiers in Microbiology*, 12, 611798.
- [24] Lyons, T. W., et al. (2014). The rise of oxygen in Earth's early ocean and atmosphere. *Nature*, 506, 307-315.
- [25] Flores, E., & Herrero, A. (2010). Compartmentalized function through cell differentiation in filamentous cyanobacteria. *Nature Reviews Microbiology*, 8(1), 39-50.
- [26] Poughon, L., et al. (2009). Limnospira indica culture in space. *Advances in Space Research*, 44(12), 1395-1405.
- [27] Niederwieser, T., et al. (2018). Gas exchange in reduced-pressure atmospheres. *Life Sciences in Space Research*, 16, 80-89.
- [28] Clauwaert, P., et al. (2017). Evaporative water loss in low-pressure photobioreactors. *Biotechnology and Bioengineering*, 114(11), 2640-2648.
- [29] Hecht, M. H., et al. (2009). Detection of perchlorate on Mars. *Science*, 325(5936), 64-67.
- [30] Kounaves, S. P., et al. (2014). Evidence of martian perchlorate. *Icarus*, 232, 226-231.
- [31] Steinberg, S. M., et al. (2007). Perchlorate toxicity and remediation. *Environmental Science & Technology*, 41(6), 1849-1854.
- [32] Heinz, J., et al. (2022). Screening survival of cyanobacteria under perchlorate stress. *Frontiers in Microbiology*, 13, 882966.

- [33] Billi, D., et al. (2021). Perchlorate tolerance in desert cyanobacteria. *Astrobiology*, 21(7), 853-862.
- [34] Verseux, C., et al. (2022). Growth dynamics of *Anabaena* sp. PCC 7938 with perchlorate-containing regolith. *npj Microgravity*, 8, 60.
- [35] Wu, Q., et al. (2018). Perchlorate degradation technologies. *Water Research*, 128, 314-326.
- [36] Coates, J. D., & Achenbach, L. A. (2004). Microbial perchlorate reduction. *Nature Reviews Microbiology*, 2(7), 569-580.
- [37] Ludwig, M., & Bryant, D. A. (2011). *Synechococcus* sp. PCC 7002 transcriptome. *Journal of Bacteriology*, 193(13), 3446-3455.
- [38] Latifi, A., et al. (2009). Oxidative stress in cyanobacteria. *FEMS Microbiology Reviews*, 33(2), 258-278.
- [39] Smith, M. D., et al. (2006). Thermal emission imaging system observations of Martian temperature. *Journal of Geophysical Research*, 111, E06.
- [40] Murukesan, G., et al. (2020). Tolerance of *Nostoc* sp. HK-01 to extreme conditions. *Biological Sciences in Space*, 32(3), 47-53.
- [41] Potts, M. (1994). Desiccation tolerance of prokaryotes. *Microbiological Reviews*, 58(4), 755-805.
- [42] Merino-Puerto, V., et al. (2011). Septal junctions in *Anabaena*. *Journal of Bacteriology*, 193(5), 1298-1308.
- [43] Maldener, I., & Muro-Pastor, A. M. (2010). Cyanobacterial heterocysts. *Annual Review of Plant Biology*, 61, 537-555.
- [44] Shirkey, B., et al. (2003). Desiccation-rehydration kinetics in *Nostoc*. *Extremophiles*, 7(5), 409-418.
- [45] Wolk, C. P. (1996). Heterocyst formation. *Annual Review of Genetics*, 30, 59-78.
- [46] Kumar, K., et al. (2010). Cyanobacterial heterocysts. *Critical Reviews in Microbiology*, 36(2), 144-166.
- [47] Postgate, J. R. (1998). *Nitrogen Fixation* (3rd ed.). Cambridge University Press.
- [48] Herrero, A., et al. (2016). Cellular differentiation and regulation of nitrate assimilation. *Annual Review of Microbiology*, 70, 413-435.
- [49] Zhao, Y., et al. (2010). NtcA-hetR interaction in heterocyst development. *Journal of Bacteriology*, 192(16), 4115-4123.
- [50] Buikema, W. J., & Haselkorn, R. (2001). Expression of *hetR* during heterocyst differentiation. *Genes & Development*, 15(22), 2922-2933.
- [51] Yoon, H. S., & Golden, J. W. (1998). Heterocyst pattern formation controlled by PatS. *Science*, 282(5390), 935-938.

- [52] Callahan, S. M., & Buikema, W. J. (2001). HetN inhibits heterocyst differentiation. *Molecular Microbiology*, 40(4), 941-950.
- [53] Corrales-Guerrero, L., et al. (2013). Functional dissection of the PatS pentapeptide. *PLoS ONE*, 8(10), e77524.
- [54] Risser, D. D., & Callahan, S. M. (2009). HetN patterns heterocysts. *Molecular Microbiology*, 72(2), 452-463.
- [55] Zhao, Y., et al. (2022). Comparative network biology discovers protein complexes in *Anabaena* sp. *Frontiers in Microbiology*, 13, 839542.
- [56] Mariscal, V., et al. (2020). PatA interactions with the divisome. *mSphere*, 5(3), e00188-20.
- [57] Liu, D., & Golden, J. W. (2002). hetL controls heterocyst differentiation in *Anabaena*. *Journal of Bacteriology*, 184(22), 6140-6148.
- [58] Di Patti, F., et al. (2018). Robust stochastic Turing patterns in *Anabaena*. *Physical Biology*, 15(6), 066001.
- [59] Muro-Pastor, A. M., & Hess, W. R. (2012). Heterocyst differentiation: from single mutants to global approaches. *Trends in Microbiology*, 20(11), 548-557.
- [60] Wolk, C. P., et al. (1994). Isolation and complementation of mutants of *Anabaena* 7120 unable to grow aerobically on dinitrogen. *Journal of Bacteriology*, 176(5), 1515-1521.
- [61] Walsby, A. E. (2007). Cyanobacterial heterocysts: terminal pores. *Trends in Microbiology*, 15(8), 340-349.
- [62] Dixon, R., & Kahn, D. (2004). Genetic regulation of biological nitrogen fixation. *Nature Reviews Microbiology*, 2(8), 621-631.
- [63] Magnuson, A., & Cardona, T. (2016). Thylakoid membrane function in heterocysts. *Biochimica et Biophysica Acta*, 1857(4), 309-319.
- [64] Mullineaux, C. W. (2008). Factors controlling the intercellular movement of a cyanobacterial growth regulator. *Molecular Microbiology*, 68(5), 1165-1176.
- [65] Flores, E., & Herrero, A. (2010). Compartmentalized function through cell differentiation. *Nature Reviews Microbiology*, 8(1), 39-50.
- [66] Stal, L. J. (2009). Is the distribution of nitrogen-fixing cyanobacteria in the oceans related to temperature? *Environmental Microbiology*, 11(7), 1632-1645.
- [67] Thiel, T., et al. (1995). Regulation of nitrogenase in *Anabaena*. *Journal of Bacteriology*, 177(21), 6058-6064.
- [68] Som, S. M., et al. (2016). Earth's air pressure 2.7 billion years ago constrained to less than half of modern levels. *Nature Geoscience*, 9, 448-451.
- [69] Tamagnini, P., et al. (2007). Hydrogenases and hydrogen metabolism of cyanobacteria. *Microbiology and Molecular Biology Reviews*, 71(2), 353-386.
- [70] Bothe, H., et al. (2010). Nitrogen fixation and hydrogen metabolism in cyanobacteria. *Microbiology and Molecular Biology Reviews*, 74(4), 529-551.

- [71] Hoffman, D., et al. (2014). *Anabaena* sp. PCC 7120 hydrogen production. *Applied and Environmental Microbiology*, 80(18), 5854-5864.
- [72] Zubrin, R., & Wagner, R. (2011). *The Case for Mars*. Simon & Schuster.
- [73] Masukawa, H., et al. (2012). Hydrogen production by cyanobacteria. *International Journal of Hydrogen Energy*, 37(7), 5561-5570.
- [74] Tsygankov, A. A., et al. (2014). Auto-flotation enables efficient *Anabaena* harvesting. *Scientific Reports*, 4, 3998.
- [75] Angermayr, S. A., et al. (2009). Energy biotechnology with cyanobacteria. *Current Opinion in Biotechnology*, 20(3), 257-263.
- [76] Allen, M. M. (1968). Simple conditions for growth of unicellular blue-green algae on plates. *Journal of Phycology*, 4(1), 1-4.
- [77] Bajpai, R., et al. (2022). Waste-to-wealth initiative with *Anabaena variabilis*. *Scientific Reports*, 12, 9228.
- [78] McLennan, S. M., et al. (2014). Elemental geochemistry of sedimentary rocks at Yellowknife Bay. *Science*, 343(6169), 1244734.
- [79] Yen, A. S., et al. (2005). An integrated view of the chemistry and mineralogy of martian soils. *Nature*, 436, 49-54.
- [80] Cockell, C. S., et al. (2013). Bioweathering of basaltic rocks. *Environmental Microbiology*, 15(2), 291-301.
- [81] Gorbushina, A. A., & Broughton, W. J. (2009). Microbiology of the atmosphere-rock interface. *Annual Review of Microbiology*, 63, 431-450.
- [82] Kranzler, C., et al. (2011). Coordinated transporter activity shapes high-affinity iron acquisition in cyanobacteria. *The ISME Journal*, 5(11), 1806-1815.
- [83] Olsson-Francis, K., & Cockell, C. S. (2010). Experimental methods for studying microbial survival in extraterrestrial environments. *Journal of Microbiological Methods*, 80(1), 1-13.
- [84] Verseux, C., et al. (2022). *Anabaena* sp. PCC 7938 growth in MGS-1. *Applied and Environmental Microbiology*, 88(14), e00594-22.
- [85] Rothschild, L. J., & Mancinelli, R. L. (2001). Life in extreme environments. *Nature*, 409, 1092-1101.
- [86] Cannon, K. M., et al. (2019). Mars Global Simulant MGS-1. *Icarus*, 317, 470-478.
- [87] Verseux, C., et al. (2016). Synthetic biology for in situ resource utilization. *Astrobiology*, 16(6), 489-500.
- [88] Bryan, N. C., et al. (2023). Cyanobacteria and algal-based biological life support systems. *Algal Research*, 70, 102989.
- [89] Owen, T., et al. (1977). The composition of the atmosphere at the surface of Mars. *Journal of Geophysical Research*, 82(28), 4635-4639.

- [90] Badger, M. R., & Price, G. D. (2003). CO<sub>2</sub> concentrating mechanisms in cyanobacteria. *Journal of Experimental Botany*, 54(383), 609-622.
- [91] Price, G. D., et al. (2008). Advances in understanding the cyanobacterial CO<sub>2</sub>-concentrating-mechanism. *Functional Plant Biology*, 35(9), 817-833.
- [92] Eady, R. R. (1996). Structure-function relationships of alternative nitrogenases. *Chemical Reviews*, 96(7), 3013-3030.
- [93] Gallon, J. R. (1992). Reconciling the incompatible: N<sub>2</sub> fixation and O<sub>2</sub>. *New Phytologist*, 122(4), 571-609.
- [94] Soto, A., & Meurisse, A. (2019). Water extraction from lunar regolith. *Planetary and Space Science*, 180, 104748.
- [95] Richmond, A. (2004). *Handbook of Microalgal Culture*. Blackwell Publishing.
- [96] Sasi, D., et al. (2011). Membrane photobioreactors. *Applied Microbiology and Biotechnology*, 89(5), 1275-1288.
- [97] Elhai, J., & Wolk, C. P. (1988). Conjugal transfer of DNA to cyanobacteria. *Methods in Enzymology*, 167, 747-754.
- [98] Wendt, K. E., et al. (2016). CRISPR/Cas9 mediated targeted mutagenesis in cyanobacteria. *ACS Synthetic Biology*, 5(12), 1490-1496.
- [99] Li, H., et al. (2016). Efficient genome engineering in *Synechococcus* using CRISPR. *Metabolic Engineering*, 34, 44-51.
- [100] Qi, L. S., et al. (2013). Repurposing CRISPR as an RNA-guided platform for sequence-specific control. *Cell*, 152(5), 1173-1183.
- [101] Higo, A., et al. (2018). Application of CRISPRi for metabolic engineering of *Anabaena* sp. PCC 7120. *Plant and Cell Physiology*, 59(1), 119-127.
- [102] Zetsche, B., et al. (2015). Cpf1 is a single RNA-guided endonuclease. *Cell*, 163(3), 759-771.
- [103] Niu, T. C., et al. (2019). Expanding the potential of CRISPR-Cpf1-based genome editing. *ACS Synthetic Biology*, 8(1), 170-180.
- [104] Tong, Y., et al. (2024). Genome engineering by RNA-guided transposition for *Anabaena*. *ACS Synthetic Biology*, 13(3), 841-851.
- [105] Reyes, J. C., & Florencio, F. J. (1994). Copper-inducible system in *Synechococcus*. *Plant Molecular Biology*, 26(1), 119-128.
- [106] Taton, A., et al. (2021). Evaluation of inducible promoter-riboswitch constructs in *Anabaena* sp. PCC 7120. *Synthetic Biology*, 6(1), ysab019.
- [107] Huang, H. H., & Lindblad, P. (2013). Wide-dynamic-range promoters engineered for cyanobacteria. *Journal of Biological Engineering*, 7, 10.
- [108] Ehira, S., et al. (2003). A genome-wide approach to regulate heterocyst differentiation. *Proceedings of the National Academy of Sciences*, 100(8), 4585-4590.

- [109] Lynch, S. A., & Gallivan, J. P. (2009). A flow cytometry-based screen for synthetic riboswitches. *Nucleic Acids Research*, 37(1), 184-192.
- [110] Gordon, G. C., et al. (2016). Mechanisms underlying transcriptional burden in cyanobacteria. *Nucleic Acids Research*, 44(11), 5174-5185.
- [111] Taton, A., et al. (2014). Broad-host-range vector system for synthetic biology. *Nucleic Acids Research*, 42(17), e136.
- [112] Singh, A. K., et al. (2006). Reactive oxygen species-mediated adaptation of *Anabaena* to salinity stress. *Applied and Environmental Microbiology*, 72(11), 6911-6918.
- [113] Kengen, S. W., et al. (1999). Purification and characterization of (per)chlorate reductase. *Journal of Bacteriology*, 181(21), 6706-6711.
- [114] Yoon, H. S., & Golden, J. W. (2001). PatS and products of nitrogen fixation control heterocyst pattern. *Journal of Bacteriology*, 183(8), 2605-2613.
- [115] Muñoz-García, J., & Ares, S. (2016). Formation and maintenance of nitrogen-fixing cell patterns. *Proceedings of the National Academy of Sciences*, 113(24), 6590-6595.
- [116] Ducat, D. C., et al. (2011). Engineering cyanobacteria to generate high-value products. *Trends in Biotechnology*, 29(2), 95-103.
- [117] Hein, S., et al. (1998). Biosynthesis of poly(3-hydroxybutyrate-co-3-hydroxyvalerate) in *Anabaena*. *Archives of Microbiology*, 170(5), 371-376.
- [118] Carpine, R., et al. (2017). Genetic engineering of *Synechocystis* for PHB production. *Frontiers in Bioengineering and Biotechnology*, 5, 22.
- [119] Tanaka, M., et al. (2004). Analysis of *Deinococcus radiodurans*'s transcriptional response to ionizing radiation. *Nucleic Acids Research*, 32(13), 3845-3854.
- [120] Proteau, P. J., et al. (1993). The structure of scytonemin, an ultraviolet sunscreen pigment. *Experientia*, 49(9), 825-829.
- [121] Griese, M., et al. (2011). Ploidy in cyanobacteria. *FEMS Microbiology Letters*, 323(2), 124-131.
- [122] Muro-Pastor, M. I., & Hess, W. R. (2020). Regulatory RNA in cyanobacteria. *FEMS Microbiology Reviews*, 44(6), 633-658.
- [123] Barrick, J. E., & Lenski, R. E. (2013). Genome dynamics during experimental evolution. *Nature Reviews Genetics*, 14(12), 827-839.
- [124] Jakočiūnas, T., et al. (2016). Multiplex metabolic pathway engineering using CRISPR/Cas9. *Metabolic Engineering*, 38, 213-224.
- [125] Silver, P. A., et al. (2014). Synthetic developmental biology. *Development*, 141(10), 1979-1989.
- [126] Omadjela, O., et al. (2013). BcsA and BcsB form the catalytically active core. *Proceedings of the National Academy of Sciences*, 110(44), 17856-17861.

- [127] Tamsir, A., et al. (2011). Robust multicellular computing using genetically encoded NOR gates. *Nature*, 469, 212-215.
- [128] Nelson, M., et al. (1993). Using Biosphere 2 to study biological closure. *Advances in Space Research*, 13(11), 211-217.
- [129] Gitelson, J. I., et al. (2003). *Manmade Closed Ecological Systems*. Taylor & Francis.
- [130] Hendrickx, L., et al. (2006). Microbial ecology of MELiSSA. *Research in Microbiology*, 157(1), 77-86.
- [131] Cornet, J. F., & Dussap, C. G. (2009). A simple and reliable formula for assessment of maximum volumetric productivities. *Biotechnology and Bioengineering*, 102(4), 1158-1166.
- [132] Schulze, P. S., et al. (2014). Light-emitting diodes in microalgal production. *Trends in Biotechnology*, 32(8), 422-430.
- [133] Jones, H. (2003). Life support system mass and cost. *33rd International Conference on Environmental Systems*.
- [134] Melis, A. (2009). Solar energy conversion efficiencies in photosynthesis. *Plant Science*, 177(4), 272-280.
- [135] Watanabe, F., et al. (2014). Vitamin B12-containing plant food sources for vegetarians. *Nutrients*, 6(5), 1861-1873.
- [136] Nicholson, W. L., et al. (2005). Resistance of *Bacillus* endospores to extreme terrestrial and extraterrestrial environments. *Microbiology and Molecular Biology Reviews*, 69(1), 1-34.
- [137] Fu, Y., et al. (2016). A comprehensive review on fresh vegetables and the psychological benefits. *Acta Astronautica*, 122, 231-239.
- [138] Clauwaert, P., et al. (2017). Nutrient recovery from human waste for bioregenerative life support. *Water Research*, 110, 208-215.
- [139] Christwardana, M., et al. (2018). Co-digestion of food waste for biogas production. *Renewable Energy*, 125, 819-828.
- [140] Lasseur, C., et al. (2010). MELiSSA: The European project of closed life support system. *Gravitational and Space Biology*, 23(2), 3-12.
- [141] Van Houdt, R., et al. (2025). Arthrospira-C ISS experiment results. *npj Microgravity*, 11, 15.
- [142] Vonshak, A. (1997). *Spirulina platensis* (*Arthrospira*): Physiology, Cell-biology and Biotechnology. Taylor & Francis.
- [143] Poughon, L., et al. (2020). Limnospira indica PCC8005 growth in photobioreactors. *Life Sciences in Space Research*, 25, 53-65.
- [144] Billi, D., et al. (2013). Chroococcidiopsis thermalis CCME 029: A cryptoendolithic cyanobacterium from the Sahara Desert. *Extremophiles*, 17(5), 735-744.
- [145] Ludwig, M., & Bryant, D. A. (2011). Transcription profiling of *Synechococcus* sp. PCC 7002. *Journal of Bacteriology*, 193(13), 3446-3455.

- [146] Meeks, J. C. (2009). *Nostoc punctiforme* symbiosis. *Symbiosis*, 49(3), 163-173.
- [147] Großkopf, T., & Soyer, O. S. (2014). Synthetic microbial communities. *Current Opinion in Microbiology*, 18, 72-77.
- [148] Momeni, B., et al. (2011). Using artificial systems to explore the ecology and evolution of symbioses. *Cellular and Molecular Life Sciences*, 68(8), 1353-1368.
- [149] Lenski, R. E., et al. (2015). Long-term experimental evolution in *Escherichia coli*. *Science*, 350(6267), 1243-1247.
- [150] Sung, W., et al. (2012). Drift-barrier hypothesis and mutation-rate evolution. *Proceedings of the National Academy of Sciences*, 109(45), 18488-18492.
- [151] Knoop, H., et al. (2013). Flux balance analysis of cyanobacterial metabolism. *BMC Systems Biology*, 7, 27.
- [152] Orth, J. D., et al. (2010). What is flux balance analysis? *Nature Biotechnology*, 28(3), 245-248.
- [153] Henson, M. A. (2015). Genome-scale modelling of microbial metabolism. *Current Opinion in Biotechnology*, 35, 123-129.
- [154] Mullineaux, C. W., et al. (2008). Co-existence of photosynthetic and respiratory activities. *Trends in Microbiology*, 16(3), 125-132.
- [155] Mullineaux, C. W. (2014). Factors controlling cell-to-cell communication. *Frontiers in Microbiology*, 5, 393.
- [156] Beliaev, A. S., et al. (2008). Global transcriptome analysis of *Anabaena* sp. PCC 7120. *DNA Research*, 15(2), 67-81.
- [157] Zelezniak, A., et al. (2015). Metabolic dependencies drive species co-occurrence. *Proceedings of the National Academy of Sciences*, 112(20), 6449-6454.
- [158] Race, M. S., et al. (2012). Planetary protection knowledge gaps. *Astrobiology*, 12(12), 1169-1175.
- [159] Logan, B. E., et al. (2001). Perchlorate reduction by a mixed culture. *Water Research*, 35(12), 3034-3038.
- [160] Urbansky, E. T. (2002). Perchlorate as an environmental contaminant. *Environmental Science and Pollution Research*, 9(3), 187-192.
- [161] Davies, J. A., et al. (2014). Synthetic morphogenesis: prospects. *Trends in Biotechnology*, 32(5), 265-273.
- [162] Montgomery, B. L. (2017). Seeing new light: recent insights into the occurrence and regulation of chromatic acclimation. *Current Opinion in Plant Biology*, 37, 18-23.
- [163] Canton, B., et al. (2008). Refinement and standardization of synthetic biological parts and devices. *Nature Biotechnology*, 26(7), 787-793.
- [164] Smolke, C. D. (2009). Building outside of the box: iGEM and the BioBricks Foundation. *Nature Biotechnology*, 27(12), 1099-1102.

- [165] Hutchison, C. A., et al. (2016). Design and synthesis of a minimal bacterial genome. *Science*, 351(6280), aad6253.
- [166] Zampieri, G., et al. (2019). Machine and deep learning meet genome-scale metabolic modeling. *PLoS Computational Biology*, 15(7), e1007084.
- [167] Radivojević, T., et al. (2020). A machine learning automated recommendation tool for synthetic biology. *Nature Communications*, 11, 4879.
- [168] Crusan, J., & Smith, S. (2019). NASA's lunar Gateway. *Acta Astronautica*, 161, 284-288.
- [169] Metzger, P. T., et al. (2011). Jet-induced cratering of lunar soil. *Journal of Geophysical Research*, 116, E06005.
- [170] Ponce-Toledo, R. I., et al. (2017). An early-branching freshwater cyanobacterium at the origin of plastids. *Current Biology*, 27(3), 386-391.
- [171] Coale, T. H., et al. (2024). Nitrogen-fixing organelle in marine alga. *Science*, 384(6692), 217-222.
- [172] McKay, C. P., et al. (1991). Making Mars habitable. *Nature*, 352, 489-496.
- [173] Graham, J. M., et al. (2008). The potential of cyanobacteria in Mars terraforming. *Astrobiology*, 8(6), 1055-1068.
- [174] Rummel, J. D., et al. (2014). A new analysis of Mars. *Astrobiology*, 14(11), 887-968.
- [175] Cockell, C. S. (2016). The ethical status of microbial life on Earth and elsewhere. *Research in Microbiology*, 167(9-10), 696-701.
- [176] Williamson, M. (2006). Space ethics and protection of the space environment. *Space Policy*, 22(1), 47-52.
- [177] Wright, O., et al. (2013). Building-in biosafety for synthetic biology. *Microbiology*, 159(7), 1221-1235.