Contents lists available at [ScienceDirect](http://www.sciencedirect.com/science/journal/20010370)



Mini-review

Computational and Structural Biotechnology Journal

journal homepage: <www.elsevier.com/locate/csbj>



Check for<br>updates  $\overline{\phantom{a}}$  upda

# Advancing synthetic biology through cell-free protein synthesis

# Ke Yue <sup>[a,](#page-0-0) [1](#page-0-1)</sup>, Junyu Chen <sup>a, 1</sup>, Yingqiu Li <sup>a, 1</sup>, Lei Kai <sup>a,</sup>\*

<span id="page-0-0"></span><sup>a</sup>*School of Life Sciences, Jiangsu Normal University, Xuzhou 22116, China* 

#### article info

*Article history:*  Received 15 February 2023 Received in revised form 3 May 2023 Accepted 3 May 2023 Available online 4 May 2023

*Keywords:*  Cell-free protein synthesis Synthetic biology Minimal cell Metabolic engineering Biomanufacturing In vitro diagnostics

# ABSTRACT

The rapid development of synthetic biology has enabled the production of compounds with revolutionary improvements in biotechnology. DNA manipulation tools have expedited the engineering of cellular systems for this purpose. Nonetheless, the inherent constraints of cellular systems persist, imposing an upper limit on mass and energy conversion efficiencies. Cell-free protein synthesis (CFPS) has demonstrated its potential to overcome these inherent constraints and has been instrumental in the further advancement of synthetic biology. Via the removal of the cell membranes and redundant parts of cells, CFPS has provided flexibility in directly dissecting and manipulating the Central Dogma with rapid feedback. This mini-review summarizes recent achievements of the CFPS technique and its application to a wide range of synthetic biology projects, such as minimal cell assembly, metabolic engineering, and recombinant protein production for therapeutics, as well as biosensor development for in vitro diagnostics. In addition, current challenges and future perspectives in developing a generalized cell-free synthetic biology are outlined.

© 2023 The Authors. Published by Elsevier B.V. on behalf of Research Network of Computational and Structural Biotechnology. This is an open access article under the CC BY license ([http://creative](http://creativecommons.org/licenses/by/4.0/)[commons.org/licenses/by/4.0/](http://creativecommons.org/licenses/by/4.0/)).

#### **1. Introduction**

The call to move towards a more sustainable, green industry has been a catalyst for the growth of biotechnology, shifting our economy away from industries dependent on petroleum and toward bio-based industries. Synthetic biology is an interdisciplinary field that combines biology, engineering, and technology to create products and services through living systems. Its rapid growth has the potential to revolutionize biotechnology, medicine, and the environment  $[1-3]$ . Recent breakthroughs in the genomic editing tools of the CRISPR/Cas systems  $[4-6]$ , in conjunction with the earlier molecular tools of synthetic biology, have allowed the precise and efficient engineering of biological systems to generate a wide range of products, including renewable energy sources, crop varieties, food and medical products, and other environmentally friendly products. Although the ongoing development of such gene modification techniques has provided powerful programming tools for cell factories, there are still inherent constraints [\[7\]](#page-5-2). The coupling of the maintenance of the living system and the synthesis of desired products defines the upper-limit efficiency of the whole synthetic system. In addition, the complex cellular system and chassis

<span id="page-0-2"></span>⁎ Corresponding author.

<span id="page-0-1"></span> $1$  These authors contributed equally to this work

behavior of different model host cells result in inconsistency from case to case.

With its distinct advantages for applications in synthetic biology, the Cell-free protein synthesis (CFPS) approach is emerging to solve the aforementioned general constraints of cells  $[8-11]$ . The CFPS system employs a minimum enzymatic apparatus for transcription, translation, and energy regeneration, derived either from cell extracts or pure enzymes  $[12,13]$ . Born as a simple and streamlined reconstituted system, CFPS naturally overcomes this inherent limitation of a living cell and provides direct access to its essential activities. Such an open nature of the CFPS enables the first-ever programming of modular cellular mimicking processes with active transcription and translation support. In addition, non-native chemicals can be introduced directly into the system, allowing greater flexibility in the selection of regulating reagents [\[14,15\]](#page-5-5).

The application of the CFPS technique came much later to the field of synthetic biology than its application as tools for discovering and illustrating basic principles of biological systems. The first wellknown application of the CFPS technique was done by Nirenberg and Matthaei [\[16–18\]](#page-5-6) to decipher the genetic codes. Later, with continuous improvement in efficiency, it gradually developed as a complementary tool for the production of recombinant proteins, in particular, for membrane proteins and toxins that are not well expressed in cells [\[15,19–23\]](#page-5-7). In addition to protein production, the application of the CFPS technique to the broad field of synthetic biology probably came first to the field of synthetic cell construction

<https://doi.org/10.1016/j.csbj.2023.05.003>

2001-0370/© 2023 The Authors. Published by Elsevier B.V. on behalf of Research Network of Computational and Structural Biotechnology. This is an open access article under the CC BY license [\(http://creativecommons.org/licenses/by/4.0/](http://creativecommons.org/licenses/by/4.0/)).

*E-mail address:* [lkai@jsnu.edu.cn](mailto:lkai@jsnu.edu.cn) (L. Kai).

<span id="page-1-0"></span>

Fig. 1. Applications of cell-free protein synthesis in both fundamental and applied research in synthetic biology. With reconstituted transcription and translation machinery, the CFPS system (adapted from Ref. [\[25\]](#page-6-3) with permission from Copyright 2017, Elsevier B.V.) is extensively utilized in the construction of minimal cellular mimicry systems within different compartmentalization systems (adapted from Ref. [\[7\]](#page-5-2) with permission from Copyright 2019, WILEY-VCH), such as energy regeneration, metabolism (photosynthesis via the synthetic metabolic pathway: the crotonyl-CoA/ethylmalonyl-CoA/hydroxybutyryl-CoA (CATCH) cycle), and the reconstitution of minimal divisome. CFPS synthesis has been accepted as a basic method for prototyping genetic circuits (adapted from Ref. [\[109\]](#page-7-0) under Creative Commons CC BY license 2019) metabolic engineering, and large- and smallscale biomanufacturing in the applied sector. The lyophilization of CFPS offers a long shelf life and non-cold chain shipping, allowing on-demand production of antibody-drug conjugates, therapeutic proteins, antimicrobial peptides, virus-like particles, vaccine antigens, and small-molecule medicines. Furthermore, the coupling of CFPS with other biosensors offers considerable diagnostic potential *in vitro*.

#### <span id="page-1-1"></span>**Table 1**

Summary of the major applications of CFPS in synthetic biology.



via a bottom-up strategy [\[24–27\].](#page-6-0) This distinct field seeks to obtain a plausible route to the origin of life from the bottom up, which starts with simple molecules, such as fatty acids, DNA or RNA molecules, to establish cell mimicry systems [\[28,29\]](#page-6-1). Such a system can possess

certain essential characteristics of a living cell or carry out certain basic activities [\[30,31\].](#page-6-2) However, when the CFPS technique is applied, more complex modular systems can be established beyond simple enzyme-catalyzed reactions, such as energy generation,

metabolism, template-guided self-replication, growth, and division, which can be further integrated with additional regulatory machinery [\(Fig. 1](#page-1-0)) [\[32,33\]](#page-6-4). In addition, CFPS also shows great potential to revolutionize cell-based synthetic biology with product-driven applications [\[33,34\].](#page-6-5) The fast cycle of CFPS has greatly shortened the period of the typical design-build-test (DBT) circle, in particular for tasks such as metabolic engineering [\[35\],](#page-6-6) protein-directed evolution [\[36–39\],](#page-6-7) and *de novo* protein design [\[40\]](#page-6-8). Last but not least, the combination of the CFPS technique and DNA manipulation tools, such as DNA amplification and editing, further extends its application in biomedical applications of in vitro diagnostic and portable analytical tools [\(Fig. 1,](#page-1-0) [Table 1](#page-1-1)).

#### **2. Constant evolution of CFPS systems**

Since its inception in the 1960 s, the CFPS system has undergone extensive systematic optimization to increase its efficiency. This optimization has been extended to all major components, including extract  $[41-46]$ , template  $[47-49]$ , energy source  $[50-53]$ , buffer [\[53–57\]](#page-6-12), and incubation and reaction settings [\[41,58\]](#page-6-9). Productivity continues to increase from around 0.1 mg/mL to above 4.0 mg/mL in batch configurations for crude lysate-based CFPS [\[59\]](#page-6-13). In terms of the fully reconstituted CFPS system, protein synthesis using recombinant elements (PURE) has also been systematically optimized, resulting in an improvement in efficiency from micrograms to sub-milligrams per mL in a batch configuration [\[60\]](#page-6-14). The pioneering work by Spirin and co-workers greatly improved the efficiency of the resulting CFPS system by a gradient-driven passive compound exchange through a dialysis membrane, which provided not only a large pool of substrate precursors, but also a sink for removal of inhibitory by products such as free phosphate. Besides in solution, the CFPS reaction can also be lyophilized as pellets or on porous matrices such as filter paper or cellulose matrices, which allowed the storage under room temperature and could be activated later via rehydration (see the section '*Manufacturing Biomolecules' and* '*New Trends in In Vitro Diagnostics*') [\[61–63\].](#page-6-15) The detailed development of various CFPS was reviewed in a set of review papers by us and other groups [\[22,25,64–66\].](#page-5-8)

In addition to the PURE system, CFPS relies on crude cell lysate to provide the enzymatic pool to support gene expression [\[67\]](#page-6-16). Currently, the sources of the extract are extremely diverse, including prokaryotic, eukaryotic, and archaeal cells, from model host cells such as *E. coli* [\[41,42\],](#page-6-9) *Bacillus subtilis* [\[68\],](#page-6-17) yeast [\[69\],](#page-6-18) insect cells [\[70,71\]](#page-6-19), rabbit reticulocyte [\[72\]](#page-6-20), wheat germ [73-75], tobacco cell [\[76\]](#page-6-22), rice callus cells [\[77\]](#page-6-23), CHO cells [\[78,79\],](#page-6-24) Hela  $[80]$ , to non-model organisms such as *Thermococcus kodakaraensis* [\[81\],](#page-7-8) *Klebsiella pneumoniae* [\[82\],](#page-7-9) *Vibrio natriegens* [\[83\]](#page-7-10), *Clostridium thermocellum*   $[84]$  and Streptomyces  $[85]$ , which were reviewed with regard to their advantages and disadvantages by Kubick et al. [\[86\].](#page-7-13) In conclusion, prokaryotic systems have the advantage of high productivities but no inherited post-translational modifications, whereas eukaryotic systems have the advantage of inherited post-translational modifications but low total expression yields. Furthermore, the limited modification machinery from eukaryotic cell extract may result in the heterogeneity of the proteins that are produced. Due to the accessibility of most molecular tools, *E. coli*, the most thoroughly researched model cell, remained the predominant source for synthetic biology. Furthermore, recent studies have shown that some post-translational modifications, such as phosphorylation [\[87,88\],](#page-7-14) glycosylation  $[89]$ , and lipidation  $[90]$ , could be performed successfully with *E. coli*-based CFPS systems by incorporating functional extracts or pure enzymes containing the associated modification machinery. Therefore, we focus on the *E. coli-*based CFPS system in the following parts.

Within a cell, gene expression is a carefully regulated process that ensures the spatial-temporal distribution of hundreds of

proteins to perform their required activities. The evolution of genetic circuits is focused on the regulation of gene expression networks, which have been studied intensively in vivo using numerous approaches [\[91\]](#page-7-17). With inheritance from the crude cell lysate, the CFPS system has the ability to activate in vivo validated genetic circuits. However, relatively fewer incidents have been reported compared to in vivo. For example, experiments to control CFPS transcription rates were conducted using different polymerases, such as T7 and bacterial *E. coli* RNA polymerases [\[92,93\]](#page-7-18). Additionally, different T7 promoters were used to regulate transcription and translation rates in CFPS [\[94\]](#page-7-19). To further engineer cell-free synthetic gene circuits, a cell-free expression toolbox was designed with 13 different *E. coli*  sigma factors, two bacteriophage RNA polymerases, and a set of repressors. This toolbox allowed the design and testing of various circuit motifs, such as multiple-stage cascades, an AND gate, negative and positive feedback loops, transcriptional cascades with a protein-regulated incoherent feedforward loop, and in vitro ring oscillators [\[95\].](#page-7-20) In addition to proteins, RNA molecules can also regulate transcription, translation, and catalysis and provide an attractive alternative to regulatory elements [\[96–101\].](#page-7-21) Riboswitches, for example, are located in the non-translated region of mRNA and can up- or down-regulate gene expression in response to ligand binding [\[102–107\]](#page-7-22). Synthetic theophylline-responsive riboswitch and natural adenine-sensing *B. subtilis* riboswitch have been established for robust in vitro on-off switching in water-in-oil emulsions and vesicles [\[108\]](#page-7-23).

### **3. Application of CFPS to the construction of minimal cells**

#### *3.1. Compartmentalization*

The prerequisite to distinguish a living cell from the non-living environment is a physical boundary that offers the basic control of mass exchange between the internal compartment and the outer space. Anything that stabilizes phase separation can be used as a material to form synthetic compartments [\[110\]](#page-7-24). Inspired by nature, extracted or synthetic phospholipids are often used for their ability to form cell-like versicles by self-assembly into a bilayer [\[111\].](#page-7-1) Similar to the structure of a phospholipid molecule, synthetic polymers, such as block copolymers [\[112\]](#page-7-25), can also self-assemble into vesicles [\[113\]](#page-7-2) and can be tuned to control the basic properties of the formed vesicles, such as size, membrane thickness [\[114\]](#page-7-26), rigidity and permeability [\[115\],](#page-7-27) surface properties [\[116\],](#page-7-28) and selectivity of the encapsulated materials [\[117\].](#page-7-29) Hybrid vesicles that form homogeneous or phase-separated membranes have been reported to depend on the specific application requirement [\[118,119\].](#page-7-30) In addition, alternative compartmentalization systems such as proteinosomes [\[120,121\]](#page-7-3), dentrimersomes [122-124], encapsulins [\[125,126\]](#page-7-5), and niosomes [\[127,128\]](#page-7-6) were reported. Following the basic principles for forming a self-assembled compartment, they offer superior properties, such as stability, encapsulation efficiency, and biocompatibility with natural cells. Moreover, other phase-forming materials, such as hydrogel  $[129,130]$  and coacervate  $[131,132]$ , by liquid-liquid phase separation, can also be used as membraneless compartmentalization methods, mimicking the membrane organelles in cells [\[133–135\].](#page-8-11) However, in addition to the physical boundary, the cell membrane functions as the matrices and catalytic interfaces for many processes like signaling, which certainly require addition factors like membrane proteins, as discussed in the 'Summary and Perspective' section.

#### *3.2. Integration of individual synthetic modules*

Before the application of the CFPS technique in the construction of minimal cells, individual modules such as energy regeneration, self-replication, growth and division, metabolism, motility, and communication could be carried out by a few simple molecules. However, the success of encapsulating the CFPS system in a synthetic microcompartment would already be a multifunctional synthetic cell that at least contains modules for energy regeneration, transcription, and translation machinery. In 2004 Noireaux et al. successfully encapsulated CFPS within phospholipid vesicles by emulsion transfer, which could produce 30 µM protein in 4 days [\[136\].](#page-8-12) Furthermore, expression could be tuned by introducing regulatory molecules, such as transcription factors (see the above section on genetic circuits). The CFPS system contains a number of molecules to fuel the reaction, which are normally the energy precursor within glycolysis pathways [\[53\],](#page-6-12) or high-energy phosphate compounds such as acetyl phosphate [\[137\],](#page-8-13) creatine phosphate [\[43\].](#page-6-25) Besides the energy precursors used in the CFPS system, the lightinduced proton gradient was adopted to fuel gene expression in the CFPS system through a light-activated proton pump (bacteria rhodopsin) and an ATP synthase within the membrane of the synthetic cell [\[138,139\]](#page-8-0). In addition to energy regeneration, the cell uses metabolism to obtain building blocks required for self-reproduction. The beauty of the cell metabolism network is that the entire metabolism network is auto-regulated to maintain homeostatic control while providing continuous materials and energy. Recently, a showoff case was reported in which light-driven  $CO<sub>2</sub>$  fixation could be carried out by a synthetic chloroplast consisting of natural and synthetic parts [\[140\].](#page-8-1) As the ultimate goal of building a living cell, self-reproduction allows the generation of offspring that have the same genetic materials, which is the critical step for continuous existence and evolution. In order to be able to self-reproduce, a cell would need several essential characters including: 1) self-replication of information molecule (genetic material); 2) growth and division. Therefore, these functions are the first goal to be achieved toward a minimal cell. In one case, the Danelon group showed [\[141\]](#page-8-2) a selfreplicated artificial cell that was able to self-replicate by co-encapsulating the DNA template encoded with the phi29 polymerase via the PURE system. In this case, the DNA of phi29 could be replicated when the coding proteins were expressed by the PURE system. In another case, Libicher et al. [\[142\]](#page-8-3) demonstrated a replication of the 116 kb multipartite genome (distributed in 11 plasmids) via the PURE system. The size of 116 kb already matched the minimum genome. However, further efforts are still needed to check if this could be achieved in any synthetic microcompartments. Being able to self-replicate, cells need to be able to grow and divide to reproduce in a sustainable way. As the first physical boundary of a cell, the materials that hold the compartment define the volume of the system and need to be reproduced. Several examples have shown the growth of different microcompartments without enzymes [\[143\];](#page-8-14) however, we envision that *de novo* synthesis of lipid molecules is vital for autonomous self-reproduction. As the critical step, recent studies showed the successful synthesis of PE and PG within the synthetic cell by activating the synthesis of correlated enzymes by the encapsulated CFPS system [\[144\].](#page-8-4) Finally, a division step would complete the self-reproduction process. Although division could be achieved through many mechanical processes by introducing appropriate shear forces [\[145\]](#page-8-15), self-autonomous division would require several key steps to ensure a symmetric distribution of materials in the resulting daughter cells  $[146]$ . In bacterial cells, such as *E. coli*, binary division is initiated by forming a proto-ring, which ultimately leads to complete division by invagination [\[147–150\]](#page-8-17). Pioneering work by the Schwille group has shown that positioning the proto-ring at the middle of the cell only required three self-organized proteins-Min C, D, and E from *E. coli* [\[151–154\].](#page-8-18) Furthermore, one of their recent studies has shown a successful positioning of the proto-ring with Min C, D, E, FtsA, and FtsZ by *de novo* synthesis via a PURE system within a GUV [\[155\].](#page-8-5) More interestingly, a ring-induced shape transformation of the formed GUVs was observed, which might be the leading forces to trigger further

deformation until the GUVs were divided. Many other synthetic systems have been successfully established that could enable com-munication [\[156\]](#page-8-6), mobility [\[157\],](#page-8-19) and evolution [\[158\]](#page-8-20) with the integration of the CFPS technique. Therefore, we would envision a more mature multifunctional minimal cell, merging with the continuous efforts in the near future.

#### **4. Application of CFPS to products-oriented synthetic biology**

#### *4.1. Cell-free metabolic engineering (CFME)*

Unlike cell metabolic engineering, cell-free metabolic engineering involves the engineering of metabolic pathways in a cellfree environment through purified enzymes or crude cell lysates [\[159\].](#page-8-21) The major advantage of CFME is that it is much faster and more efficient, since it eliminates the need for iteration and selection steps when producing a desired product. CFME also avoids problems associated with cell-based approaches, such as cell toxicity and genetic instability. In addition, it is much easier to optimize and troubleshoot in CFME, as the reactions occur in vitro, allowing more flexibility. Finally, CFME enables the development of more complex metabolic pathways and the production of more diverse products. Long before the introduction of CFPS, enormous efforts have been made to synthesize valuable chemical compounds and natural products in bioreactors using enzymes [\[160–162\].](#page-8-22) However, it became extremely challenging and labor intensive to produce individual purified enzymes and combine them with proper stoichiometry for the best conversion efficiency. Recent cases gave us an overview of the current extremes of what could be achieved by purified en-zymes. The Bowie group [\[163\]](#page-8-23) reconstituted a cell-free monoterpene pathway with 27 purified enzymes, which achieved more than 95 % conversion yield and 15 g/L titer. Such a higher titer is more than an order of magnitude higher than the lethal concentrations for cellbased systems.

Pioneered by the group of Jewett [\[35\],](#page-6-6) they proposed a novel CFPS-based metabolic engineering framework to build biosynthetic pathways. This process involved directly synthesizing each enzyme of a biosynthetic pathway in vitro using cell-free lysates and combining multiple crude lysates to initiate the DBT cycle. Enzyme-rich lysate performed catalytic tasks in place of separately isolated en-zymes. Applying this strategy to mevalonate biosynthesis [\[164\]](#page-8-8), the CFPS system produced 17.6 g/L (119 mM) of mevalonate in 20 h, in contrast to the initial titer of 1.6 g/L produced in 9 h. Using the same mechanism, a prototype of n-butanol biosynthesis was developed. The system produced 1.2 g/L of n-butanol by using natural glycolytic enzymes to convert glucose to acetyl-CoA and heterologous enzymes to convert acetoacetyl-CoA to n-butanol. In less than a day, the researchers studied four Ter homologs and three AdhE homologs that replaced some of the initial Ter and AdhE enzymes. They also demonstrated the use of linear DNA templates, which eliminated the need for laborious cloning procedures and resulted in an increase of up to 1.5  $g/L$  in the synthesis of n-butanol [\[165\].](#page-8-7) In conclusion, CFPSbased metabolic engineering provides significantly faster DBT cycles than cell-based metabolic engineering and eliminates enzyme purification processes.

#### *4.2. Manufacturing biomolecules*

Proteins are major macromolecules that are essential for the structure and function of living cells, providing structure to cells, acting as enzymes to catalyze biochemical reactions, and performing or regulating a variety of other metabolic processes. Therefore, as an important recombinant protein production tool with unique advantages, the CFPS system has been applied to produce various therapeutic protein products, covering different cytokines, cytotoxins, antibodies, vaccine antigens, virus-like particles and antimicrobials, which were reviewed elsewhere [\[8,166,167\].](#page-5-3) What we want to emphasize is the flexibility of deploying the CFPS system in a variety of application environments, which suits both largecentralized industrial-scale production and small-batch production of therapeutic and laboratory reagents. Large-scale CFPS has been utilized in commercial efforts, such as Sutro Biopharma, Inc., which was able to produce up to 1000 liters of cell-free reactions [\[167\].](#page-8-24) This method took advantage of fast synthesis outside the cell, which greatly sped up the drug development process. Different from large centralized infrastructures, the CFPS can provide a flexible on demand protein production. As pioneered by Pardee et al., CFPS can be lyophilized to allow convenient storage and transportation conditions [\[65\]](#page-6-26). Lyophilized CFPS systems can be used for the decentralized, small-batch production of therapeutics and reagents, with potential uses in global health and emergency response. Furthermore, they demonstrated the production of more than 50 compounds, including vaccines, antibodies, antimicrobial peptides, and small molecules, using the same approach [\[168\]](#page-8-9). Recently, the Jewett group managed to provide another example of protective conjugate vaccines [\[169\].](#page-8-25) These products can be created outside of the laboratory setting and have the potential to revolutionize the field of bio-manufacturing.

Because of the limited amount of proteinogenic or canonical amino acids, the engineering of proteins with distinct chemical activities has been hampered. Non-canonical amino acids (NCAAs) and amino acid analogs could offer new functionalities to proteins, such as altered activity, enhanced stability, alternative post-translational modifications and more, which is particularly useful in the fields of drug discovery, bio-catalysis, and protein design when site-specific incorporation of NCAAs is possible [\[170\]](#page-8-26). The introduction of an NCAA at a specific position within the protein sequence requires the presence of an aminoacyl-tRNA synthetase specific for the desired NCAA, a tRNA molecule with an anticodon complementary to the NCAA's codon, and a genetically encoded amino acid specific enzyme, such as a codon-specific ribosome  $[171-175]$ . Several groups have done pioneering work [\[176\]](#page-8-28). However, difficulties persist in selecting NCAAs, which must be able to easily traverse membrane barriers. Although CPFS provided an open environment and unique advantages for selective multiplexed inclusion, the development of multidomain proteins or protein complexes would benefit more from the use of this technique [\[177–179\]](#page-8-29).

#### *4.3. New trends in in vitro diagnostics*

In combination with DNA manipulation techniques, in particular the CRISPR/Cas-based system, the CFPS systems could be further developed as molecular diagnostic tools [\[180,181\].](#page-8-30) In a recent case, Collins and co-authors developed a flexible three-layer device using silicone elastomers and cellulose matrices, containing freeze-dried insets with genetic circuits. The circuits were configured to express the lacZ β-galactosidase operon, hydrolyzing a substrate that caused a colorimetric output when exposed to a target analyte [\[182\]](#page-8-31). The authors optimized the device materials and reaction kinetics to complete the colorimetric output in less than 60 min. Using the same principles, they built prototype devices with freeze-dried circuits for the detection of anhydrotetracycline, Ebola virus RNA, and small molecules [\[183\].](#page-8-10) Jung et al. developed a cell-free biosensor for water contamination via RNA output sensors activated by ligand induction [\[184\]](#page-8-32). Such a system consisted of highly processive RNA polymerase, allosteric protein transcription factors and synthetic DNA templates, which contained a fluorescence-activation RNA aptamer sequence. The binding of a target contaminant could trigger the release of allosteric transcription factors and allow the transcription of the synthetic DNA template. The resulting product, which contained a fluorescence activation RNA aptamer, could be detected via its florescence. The further development of various

sensors for small molecules has been reviewed elsewhere [\[166,180,185\]](#page-8-33).

#### **5. Summary and perspectives**

With continuous effort to improve the efficiency of the CFPS system, a new higher record of 4 mg/mL was achieved with an *E. coli*  lysate-based batch CFPS system [\[59\]](#page-6-13) and up to 6 mg/mL with continuous exchange configurations [\[186\].](#page-8-34) In the case of a complete reconstituted PURE system, the productivity of a continuous exchange setup reached around 30 % of the total protein contained in the optimized PURE system, comparable to the level of overexpressed protein in *E. coli* cells [\[60\].](#page-6-14) However, one would still wonder: Is the current productivity upper limit of the CFPS system catching up to the efficiency within a living cell? It would be challenging to directly answer this question due to the lack of accurate data on the overall performance of a cell. Nevertheless, we could get a close estimate. During the 20-minute doubling time of an active growing *E. coli* cell, an average ribosome would need to synthesize around 55,000 peptide bonds, which is at least 1–2 orders of magnitude higher than the current performance of CFPS systems [\[25,187\]](#page-6-3). Taking into account the rate of synthesis, current CFPS systems are even less efficient, considering the highest protein synthesis rate at around 5000 peptide bonds per hour per ribosome [\[188\].](#page-9-0) Therefore, further efforts are still needed to improve overall efficiency. This would require a more efficient energy regeneration system and a homeostatic environment to maintain the efficiency of ribosomes [\[25\]](#page-6-3). A set of systematic studies have revealed the limiting factors for the overall yield of the corresponding CFPS system, including fast depletion of substrates (energy precursors, NTPs and certain amino acids) [\[22\]](#page-5-8), degradation of DNA templates, transcribed mRNAs and target proteins [\[190\]](#page-9-1) and accumulation of inhibitory biproducts, such as free inorganic phosphates, which cause the fast decay of ribosomes [\[189\].](#page-9-2) Furthermore, optimizations based on the fully reconstituted PURE system revealed certain transcription and translation factors would be benefit for improving the final yield [\[191,192\].](#page-9-3) In addition, molecular crowding agents and chaperons also showed beneficial effects on the overall yields [\[53,193\].](#page-6-12) Finally, recent proteomic analysis could give valuable information of limiting factors for extract-based CFPS systems, which might vary depending on the individual strains and preparation procedures [\[194–196\]](#page-9-4). As stated above, ribosome, as the core translational apparatus, plays a vital role in the overall performance of the CFPS system. Therefore, achieving ribosome biogenesis in cell-free environment not only reveals the fundamental principles but also has many potential applications in synthetic biology. Pioneering work from Jewett's group in ribosome synthesis, namely integrated synthesis, assembly, and translation (iSAT), has shown the generation of functional 30 S, 50 S subunits with in vitro transcribed rRNAs [\[197\].](#page-9-5) Moreover, individual purified ribosomal proteins that form the 30 s and 50 s subunits could be assembled with native rRNAs into a functional ribosome [\[187,198\].](#page-9-6) Furthermore, such iSAT process could be validated within a double emulsion templated vesicle [\[199\].](#page-9-7) However, despite the successful assembly of functional ribosomes with in vitro transcribed rRNA for 30 S subunits, post-translational modifications of 23 S rRNA might be crucial  $[200]$ , which certainly need to be further investigated to generate full reconstituted ribosomes. Despite the rapid development and expansion of CFPS technique, it is still not a straight forward lab routine, which might require certain optimization work to establish the best suitable system for particular applications. Commercially available CFPS kits, together with a set of detailed protocols [\[42,201–203\]](#page-6-27), might be a good starting point.

The current fast development of different compartmentalization methods and materials for the formation of different cell membrane mimicries. The functional membranes are essential for a minimal cell, including selective permeability, responsive to different

# membrane proteins [\[204,205\].](#page-9-9) Even before application in the field of synthetic biology, CFPS system was intensively tuned to express membrane proteins, which were difficult to overexpress in vivo, due to their cytotoxicity. Devoid of living cells, CFPS system possess unique advantages for membrane proteins and has successfully overexpressed a large number of membrane proteins for both functional and structural characterization, prepared with different hydrophobic reagents, such as detergent, lipids (i.e., liposomes, nanodiscs or other model lipid bilayers) [\[206–208\].](#page-9-10) The main effort in membrane protein expression using CFPS system shifts towards the optimization of co-translational hydrophobic environments, which is certainly target dependent [\[209\].](#page-9-11) In sum, such advantage of CFPS system on membrane protein expression will certainly be beneficial for minimal cell projects, as exemplified in our recent effort to reconstitute a reversible membrane switch direct on the supported lipid bilayers [\[90\].](#page-7-16) Furthermore, efforts to improve encapsulation efficiency are still needed, especially when a protein-rich and highly viscous solution is used [\[210–213\].](#page-9-12) As noted above, the current CFPS system is still far less efficient than the cellular system. The encapsulation process would further challenge the performance of the CPFS system. Parameters and conditions optimized from bulk solutions would need to be curated and validated in the microcompartment, taking into account the molecular crowding effect and stochasticity therein [\[214–216\]](#page-9-13). Taken together, these factors would have a direct impact if we move towards an autonomous self-reproduction system, which would require the self-replication of genetic materials, the *de novo* synthesis of ribosomes, the minimal unit for protein production, phospholipids, and the minimal divisome [\[154,217,218\].](#page-8-35) In this regard, the research toward a minimal cell has just begun.

environmental signals, which are fulfilled by a large group of integral

Despite the fact that sustainable and ecologically friendly biomaterials have a clear benefit in the product-driven sector of synthetic biology, they nonetheless cost more than the material obtained by conventional chemical refining techniques. Therefore, there is a continuous demand to reduce the overall cost, which is certainly critical for the application of CFPS systems. Although there have been ongoing efforts to reduce the price of CFPS systems, only a small number of high-value protein products have been successfully produced using this method so far. There is still some uncertainty about the issue. How far does the CFPS method go beyond prototyping in the realm of synthetic biology? The development of CFPS pathways for certain metabolites would also benefit from a quantitative model [\[219\].](#page-9-14) However, the one of the current barriers is the lack of standardized data that quantitatively explain the performance of the in vitro metabolic network. Another factor making standardization difficult is the wide variety of host strain backgrounds. Recent results from proteome analysis on multiple *E. coli*  lysates may offer broad directions for a possible metabolic network [\[194–196\].](#page-9-4) In addition, the convergence of technological advancements in artificial intelligence will accelerate the process of constructing mathematical and computational models as a corollary. As previously stated, the CFPS system is rapidly growing into a valuable production tool for protein-based drugs and in vitro diagnostics. Real-time on-demand protein synthesis could be particularly beneficial in instances with limited resources, such as the current global SARS-Cov-2 outbreak.

Despite the hurdles that now exist, the rapid advancement in synthetic biology via CFPS has gained widespread interest from the scientific communities, which will surely result in a more diverse application and may soon be a game-changer in the area.

#### **CRediT authorship contribution statement**

All authors contributed to the conceptualization, writing, reviewing and editing this manuscript.

#### **Declaration of Competing Interest**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

#### **Acknowledgments**

L.K. is thankful for the support of the Natural Science Research of Jiangsu Higher Education Institutions of China, China (Grant No. 17KJB180003), the Natural Science Foundation of Jiangsu Normal University, China (Grant No. 17XLR037), Priority Academic Program Development of Jiangsu Higher Education Institutions, China, and the Jiangsu Specially-Appointed Professor program, China.

#### **References**

- <span id="page-5-0"></span>[1] Clarke L, Kitney R. Developing synthetic biology for industrial biotechnology applications. 113-22 Biochem Soc Trans 2020;48. https://doi.org/10.1042 ST20190349
- [2] Cubillos-Ruiz A, Guo T, Sokolovska A, Miller PF, Collins JJ, et al. Engineering living therapeutics with synthetic biology. 941-60 Nat Rev Drug Disco 2021;20. https://doi.org/10.1038/s41573-021-002
- [3] Mccarty NS, Ledesma-Amaro R. Synthetic biology tools to engineer microbial communities for biotechnology. 181-97 Trends Biotechnol 2019;37. https://doi. org/10.1016/j.tibtech.2018.11.002
- <span id="page-5-1"></span>[4] Doudna JA, Charpentier E. The new frontier of genome engineering with CRISPR-Cas9. Science 2014;346:1258096. https://doi.org/10.1126/science.
- 1258096 [5] Doudna JA. The promise and challenge of therapeutic genome editing. Nature 2020;578:229–36. https://doi.org/10.1038/s41586-020-1978-5
- [6] Cox DB, Platt RJ, Zhang F. Therapeutic genome editing: prospects and challenges. Nat Med 2015;21:121–31. https://doi.org/10.1038/nm.3793
- <span id="page-5-2"></span>[7] Kai L, Schwille P. Cell-free protein synthesis and its perspectives for assembling cells from the bottom-up. Adv Biosyst 2019;3:e1800322. https://doi.org/10. 1002/adbi.201800322
- <span id="page-5-3"></span>[8] Li J, Zhang L, Liu W. Cell-free synthetic biology for in vitro biosynthesis of pharmaceutical natural products. Synth Syst Biotechnol 2018;3:83–9. https:// doi.org/10.1016/j.synbio.2018.02.002
- [9] Harris DC, Jewett MC. Cell-free biology: exploiting the interface between synthetic biology and synthetic chemistry. Curr Opin Biotechnol 2012;23:672–8. https://doi.org/10.1016/j.copbio.2012.02.002
- [10] Jiang L, Zhao J, Lian J, Xu Z. Cell-free protein synthesis enabled rapid prototyping for metabolic engineering and synthetic biology. Synth Syst Biotechnol 2018;3:90–6. https://doi.org/10.1016/j.synbio.2018.02.003
- [11] Perez JG, Stark JC, Jewett MC. Cell-free synthetic biology: engineering beyond the cell. Cold Spring Harb Perspect Biol 2016;8:a023853. https://doi.org/10.  $+1022853$
- <span id="page-5-4"></span>[12] Gao W, Bu N, Lu Y. Efficient incorporation of unnatural amino acids into proteins with a robust cell-free system. Methods Protoc 2019;2:16. https://doi.org/ 10.3390/mps2010016
- [13] Kohno T, Endo Y. Production of protein for nuclear magnetic resonance study using the wheat germ cell-free system. Methods Mol Biol 2007;375:257–72. //doi.org/10.1007/978-1-59745-388-2\_13
- <span id="page-5-5"></span>[14] Lu Y. Cell-free synthetic biology: engineering in an open world. Synth Syst Biotechnol 2017;2:23–7. https://doi.org/10.1016/j.synbio.2017.02.003
- <span id="page-5-7"></span>[15] Roos C, Kai L, Proverbio D, Ghoshdastider U, Filipek S, et al. Co-translational association of cell-free expressed membrane proteins with supplied lipid bilayers. Mol Membr Biol 2013;30:75–89. https://doi.org/10.3109/09687688. 012.693212
- <span id="page-5-6"></span>[16] Nirenberg MW, Matthaei JH. The dependence of cell-free protein synthesis in E. coli upon naturally occurring or synthetic polyribonucleotides. Proc Natl Acad Sci U S A 1961;47:1588–602. https://doi.org/10.1073/pnas.47.10.1588
- [17] Matthaei JH, Nirenberg MW. Characteristics and stabilization of DNAase-sensitive protein synthesis in E. coli extracts. Proc Natl Acad Sci U S A 1961;47:1580–8. https://doi.org/10.1073/pnas.47.10.1580
- [18] Matthaei H, Nirenberg MW. The dependence of cell-free protein synthesis in E. coli upon RNA prepared from ribosomes. Biochem Biophys Res Commun 1961;4:404–8. https://doi.org/10.1016/0006-291x(61)90298-4
- [19] Smolskaya S, Logashina YA, Andreev YA. Escherichia coli extract-based cell-free expression system as an alternative for difficult-to-obtain protein biosynthesis. Int J Mol Sci 2020;21:928. https://doi.org/10.3390/ijms21030928
- [20] Kimura-Soyema T, Shirouzu M, Yokoyama S. Cell-free membrane protein expression. Methods Mol Biol 2014;1118:267–73. https://doi.org/10.1007/978-1- .<br>62703-782-2\_18
- [21] Ramm F, Jack L, Kaser D, Schlosshauer JL, Zemella A, et al. Cell-free systems enable the production of AB(5) toxins for diagnostic applications. Toxins (Basel) 2022;14:233. https://doi.org/10.3390/toxins14
- <span id="page-5-8"></span>[22] Carlson ED, Gan R, Hodgman CE, Jewett MC. Cell-free protein synthesis: applications come of age. Biotechnol Adv 2012;30:1185–94. https://doi.org/10. 1016/j.biotechadv.2011.09.016
- [23] Schneider B, Junge F, Shirokov VA, Durst F, Schwarz D, et al. Membrane protein expression in cell-free systems. Methods Mol Biol 2010;601:165–86. https:// doi.org/10.1007/978-1-60761-344-2\_11
- <span id="page-6-0"></span>[24] Laohakunakorn N, Grasemann L, Lavickova B, Michielin G, Shahein A, et al. Bottom-up construction of complex biomolecular systems with cell-free synthetic biology. Front Bioeng Biotechnol 2020;8:213. https://doi.org/10.3389/ fbioe.2020.0021
- <span id="page-6-3"></span>[25] Jia H, Heymann M, Bernhard F, Schwille P, Kai L. Cell-free protein synthesis in micro compartments: building a minimal cell from biobricks. N Biotechnol 2017;39:199–205. https://doi.org/10.1016/j.nbt.2017.06.014
- [26] Schwille P, Spatz J, Landfester K, Bodenschatz E, Herminghaus S, et al. MaxSynBio: avenues towards creating cells from the bottom up. Angew Chem Int Ed Engl 2018;57:13382–92. https://doi.org/10.1002/anie.201802288
- Matsubayashi H, Ueda T. Purified cell-free systems as standard parts for synthetic biology. Curr Opin Chem Biol 2014;22:158–62. https://doi.org/10.1016/j. cbpa.2014.09.031
- <span id="page-6-1"></span>[28] Szostak JW, Bartel DP, Luisi PL. Synthesizing life. Nature 2001;409:387–90. https://doi.org/10.1038/35053176
- [29] Luisi PL, Ferri F, Stano P. Approaches to semi-synthetic minimal cells: a review. Naturwissenschaften 2006;93:1-13. 0056-z
- <span id="page-6-2"></span>[30] Luisi PL. Toward the engineering of minimal living cells. Anat Rec 2002;268:208–14. https://doi.org/10.1002/ar.10155
- [31] Stano P, Luisi PL. Semi-synthetic minimal cells: origin and recent developments. Curr Opin Biotechnol 2013;24:633–8. https://doi.org/10.1016/j.copbio. 2013.01.002
- <span id="page-6-4"></span>[32] Guindani C, Da Silva LC, Cao S, Ivanov T, Landfester K. Synthetic cells: from simple bio-inspired modules to sophisticated integrated systems. Angew Chem Int Ed Engl 2022;61:e202110855. https://doi.org/10.1002/anie.202110855
- <span id="page-6-5"></span>[33] Zawada JF, Burgenson D, Yin G, Hallam TJ, Swartz JR, et al. Cell-free technologies for biopharmaceutical research and production. Curr Opin Biotechnol 2022;76:102719. https://doi.org/10.1016/j.copbio.2022.102719
- [34] Swartz J. Developing cell-free biology for industrial applications. J Ind Microbiol Biotechnol 2006;33:476–85. https://doi.org/10.1007/s10295-006- 0127-y
- <span id="page-6-6"></span>[35] Karim AS, Jewett MC. A cell-free framework for rapid biosynthetic pathway prototyping and enzyme discovery. Metab Eng 2016;36:116–26. https://doi. org/10.1016/j.ymben.2016.03.002
- <span id="page-6-7"></span>[36] Miller OJ, Bernath K, Agresti JJ, Amitai G, Kelly BT, et al. Directed evolution by in vitro compartmentalization. Nat Methods 2006;3:561–70. https://doi.org/10. 1038/nmeth897
- [37] Hestericova M, Heinisch T, Alonso-Cotchico L, Marechal JD, Vidossich P, et al. Directed evolution of an artificial imine reductase. Angew Chem Int Ed Engl 2018;57:1863–8. https://doi.org/10.1002/anie.201711016
- [38] Dodevski I, Markou GC, Sarkar CA. Conceptual and methodological advances in cell-free directed evolution. Curr Opin Struct Biol 2015;33:1–7. https://doi.org/ 10.1016/j.sbi.2015.04.008
- [39] Wang Y, Xue P, Cao M, Yu T, Lane ST, et al. Directed evolution: methodologies and applications. Chem Rev 2021;121:12384-444. https://doi.org/10.1021 chemrev.1c00260
- <span id="page-6-8"></span>[40] Chen Z, Kibler RD, Hunt A, Busch F, Pearl J, et al. De novo design of protein logic gates. Science 2020;368:78-84. https://doi.org/10.1126/science.aay
- <span id="page-6-9"></span>[41] Zubay G. In vitro synthesis of protein in microbial systems. Annu Rev Genet 1973;7:267–87. https://doi.org/10.1146/annurev.ge.07.120173.001411
- <span id="page-6-27"></span>[42] Schwarz D, Junge F, Durst F, Frolich N, Schneider B, et al. Preparative scale expression of membrane proteins in Escherichia coli-based continuous exchange cell-free systems. Nat Protoc 2007;2:2945–57. https://doi.org/10.1038/ nprot.2007.426
- <span id="page-6-25"></span>[43] Kigawa T, Yabuki T, Matsuda N, Matsuda T, Nakajima R, et al. Preparation of Escherichia coli cell extract for highly productive cell-free protein expression. J Struct Funct Genom 2004;5:63–8. https://doi.org/10.1023/B:JSFG.0000029204. 57846.7d
- [44] Kwon YC, Jewett MC. High-throughput preparation methods of crude extract for robust cell-free protein synthesis. Sci Rep 2015;5:8663. https://doi.org/10. 1038/srep08663
- [45] Kim TW, Keum JW, Oh IS, Choi CY, Park CG, et al. Simple procedures for the construction of a robust and cost-effective cell-free protein synthesis system. J Biotechnol 2006;126:554–61. https://doi.org/10.1016/j.jbiotec.2006.05.014
- [46] Yamane T, Ikeda Y, Nagasaka T, Nakano H. Enhanced cell-free protein synthesis using a S30 extract from Escherichia coli grown rapidly at 42 degrees C in an amino acid enriched medium. Biotechnol Prog 2005;21:608–13. https://doi. org/10.1021/bp0400238
- <span id="page-6-10"></span>[47] Haberstock S, Roos C, Hoevels Y, Dotsch V, Schnapp G, et al. A systematic approach to increase the efficiency of membrane protein production in cell-free expression systems. Protein Expr Purif 2012;82:308–16. https://doi.org/10. 1016/j.pep.2012.01.018
- [48] Mureev S, Kovtun O, Nguyen UT, Alexandrov K. Species-independent translational leaders facilitate cell-free expression. Nat Biotechnol 2009;27:747–52. https://doi.org/10.1038/nbt.1556
- [49] Endo Y, Sawasaki T, High-throughput, genome-scale protein production method based on the wheat germ cell-free expression system. Biotechnol Adv 2003;21:695–713. https://doi.org/10.1016/s0734-9750(03)00105-8
- <span id="page-6-11"></span>[50] Kim DM, Swartz JR. Prolonging cell-free protein synthesis with a novel ATP regeneration system. Biotechnol Bioeng 1999;66:180–8.
- [51] Kim DM, Swartz JR. Regeneration of adenosine triphosphate from glycolytic intermediates for cell-free protein synthesis. Biotechnol 2001;74:309–16.
- [52] Calhoun KA, Swartz JR. Energizing cell-free protein synthesis with glucose metabolism. Biotechnol Bioeng 2005;90:606–13. https://doi.org/10.1002/bit. 20449
- <span id="page-6-12"></span>[53] Jewett MC, Swartz JR. Mimicking the Escherichia coli cytoplasmic environment activates long-lived and efficient cell-free protein synthesis. Biotechnol Bioeng 2004;86:19–26. https://doi.org/10.1002/bit.20026
- [54] Liu Y, Fritz BR, Anderson MJ, Schoborg JA, Jewett MC. Characterizing and alleviating substrate limitations for improved in vitro ribosome construction. ACS Synth Biol 2015;4:454–62. https://doi.org/10.1021/sb5002467
- [55] Caschera F, Karim AS, Gazzola G, D'aquino AE, Packard NH, et al. Highthroughput optimization cycle of a cell-free ribosome assembly and protein synthesis system. ACS Synth Biol 2018;7:2841–53. https://doi.org/10.1021/ cssynbio.8b00276
- [56] Rasor BJ, Chirania P, Rybnicky GA, Giannone RJ, Engle NL, et al. Mechanistic insights into cell-free gene expression through an integrated -omics analysis of extract processing methods. ACS Synth Biol 2023. https://doi.org/10.1021/  $c$ ssynbio.2 $c$ 00339
- [57] Jewett MC, Calhoun KA, Voloshin A, Wuu JJ, Swartz JR. An integrated cell-free metabolic platform for protein production and synthetic biology. Mol Syst Biol 2008;4:220. https://doi.org/10.1038/msb.2008.57
- [58] Spirin AS, Baranov VI, Ryabova LA, Ovodov SY, Alakhov YB. A continuous cellfree translation system capable of producing polypeptides in high yield. Science 1988;242:1162–4. https://doi.org/10.1126/science.3055301
- <span id="page-6-13"></span>[59] Garenne D, Thompson S, Brisson A, Khakimzhan A, Noireaux V. The all-E. coliTXTL toolbox 3.0: new capabilities of a cell-free synthetic biology platform. Synth Biol (Oxf) 2021;6:ysab017. https://doi.org/10.1093/synbio/ysab017
- <span id="page-6-14"></span>[60] Kazuta Y, Matsuura T, Ichihashi N, Yomo T. Synthesis of milligram quantities of proteins using a reconstituted in vitro protein synthesis system. J Biosci Bioeng 2014;118:554–7. https://doi.org/10.1016/j.jbiosc.2014.04.019
- <span id="page-6-15"></span>[61] Smith MT, Berkheimer SD, Werner CJ, Bundy BC. Lyophilized Escherichia colibased cell-free systems for robust, high-density, long-term storage. Biotechniques 2014;56:186–93. https://doi.org/10.2144/000114158
- [62] Wilding KM, Zhao EL, Earl CC, Bundy BC. Thermostable lyoprotectant-enhanced cell-free protein synthesis for on-demand endotoxin-free therapeutic production. N Biotechnol 2019;53:73–80. https://doi.org/10.1016/j.nbt.2019.07.004
- [63] Yang J, Cui Y, Cao Z, Ma S, Lu Y. Strategy exploration for developing robust lyophilized cell-free systems. Biotechnol Notes 2021;2:44–50. https://doi.org/ 10.1016/j.biotno.2021.08.004
- [64] Endo Y, Sawasaki T. Cell-free expression systems for eukaryotic protein pro-duction. Curr Opin Biotechnol 2006;17:373–80. https://doi.org/10.1016/j. copbio.2006.06.009
- <span id="page-6-26"></span>[65] Pardee K. Perspective: Solidifying the impact of cell-free synthetic biology through lyophilization. Biochem Eng J 2018;138:91–7. https://doi.org/10.1016/j. bej.2018.07.008
- [66] Lu Y. Textile-embedded cell-free biosensors. Nat Biomed Eng 2022;6:225–6. https://doi.org/10.1038/s41551-022-00869-3
- <span id="page-6-16"></span>[67] Borkowski O, Bricio C, Murgiano M, Rothschild-Mancinelli B, Stan GB, et al. Cell-free prediction of protein expression costs for growing cells. Nat Commun 2018;9:1457. https://doi.org/10.1038/s41467-018-03970-
- <span id="page-6-17"></span>[68] Kelwick R, Webb AJ, Macdonald JT, Freemont PS. Development of a Bacillus subtilis cell-free transcription-translation system for prototyping regulatory elements. Metab Eng 2016;38:370–81. https://doi.org/10.1016/j.ymben.2016. 09.008
- <span id="page-6-18"></span>[69] Hodgman CE, Jewett MC. Optimized extract preparation methods and reaction conditions for improved yeast cell-free protein synthesis. Biotechnol Bioeng 2013;110:2643–54. https://doi.org/10.1002/bit.24942
- <span id="page-6-19"></span>[70] Ezure T, Suzuki T, Higashide S, Shintani E, Endo K, et al. Cell-free protein synthesis system prepared from insect cells by freeze-thawing. Biotechnol Prog 2006;22:1570–7. https://doi.org/10.1021/bp060110v
- [71] Kubick S, Schacherl J, Fleischer-Notter H, Royall E, Roberts LO, Stiege W. In vitro translation in an insect-based cell-free system. Cell-Free Protein Expr 2003:209-17. https://doi.org/10.1007/978-3-6
- <span id="page-6-20"></span>[72] Schweet R, Lamfrom H, Allen E. The synthesis of hemoglobin in a cell-free system. Proc Natl Acad Sci USA 1958;44:1029–35. https://doi.org/10.1073/pnas. 44.10.1029
- <span id="page-6-21"></span>[73] Roberts BE, Paterson BM. Efficient translation of tobacco mosaic virus RNA and rabbit globin 9S RNA in a cell-free system from commercial wheat germ. Proc Natl Acad Sci USA 1973;70:2330–4. https://doi.org/10.1073/pnas.70.8.2330
- [74] Anderson CW, Straus JW, Dudock BS. Preparation of a cell-free protein-synthesizing system from wheat germ. Methods Enzym 1983;101:635–44. https:// doi.org/10.1016/0076-6879(83)01044-7
- [75] Takai K, Sawasaki T, Endo Y. Practical cell-free protein synthesis system using purified wheat embryos. Nat Protoc 2010;5:227–38. https://doi.org/10.1038/ nprot.2009.207
- <span id="page-6-22"></span>[76] Buntru M, Vogel S, Stoff K, Spiegel H, Schillberg S. A versatile coupled cell-free transcription-translation system based on tobacco BY-2 cell lysates. Biotechnol Bioeng 2015;112:867–78. https://doi.org/10.1002/bit.25502
- <span id="page-6-23"></span>[77] Suzuki K, Inoue H, Matsuoka S, Tero R, Hirano-Iwata A, et al. Establishment of a cell-free translation system from rice callus extracts. Biosci Biotechnol Biochem 2020;84:2028–36. https://doi.org/10.1080/09168451.2020.17
- <span id="page-6-24"></span>[78] Brodel AK, Sonnabend A, Kubick S. Cell-free protein expression based on extracts from CHO cells. Biotechnol Bioeng 2014;111:25–36. https://doi.org/10. 1002/bit.25013
- [79] Martin RW, Majewska NI, Chen CX, Albanetti TE, Jimenez RBC, et al. Development of a CHO-based cell-free platform for synthesis of active monoclonal antibodies. ACS Synth Biol 2017;6:1370–9. https://doi.org/10.1021/ acssynbio.7b00001
- <span id="page-7-7"></span>[80] Mikami S, Masutani M, Sonenberg N, Yokoyama S, Imataka H. An efficient mammalian cell-free translation system supplemented with translation factors. Protein Expr Purif 2006;46:348–57. https://doi.org/10.1016/j.pep.2005.09.
- <span id="page-7-8"></span>021 [81] Endoh T, Kanai T, Sato YT, Liu DV, Yoshikawa K, et al. Cell-free protein synthesis at high temperatures using the lysate of a hyperthermophile. J Biotechnol
- <span id="page-7-9"></span>2006;126:186–95. https://doi.org/10.1016/j.jbiotec.2006.04.010 [82] Yang C, Yang M, Zhao W, Ding Y, Wang Y, et al. Establishing a Klebsiella pneumoniae-based cell-free protein synthesis system. Molecules 2022;27:4684. https://doi.org/10.3390/molecules27154684
- <span id="page-7-10"></span>[83] Des Soye BJ, Davidson SR, Weinstock MT, Gibson DG, Jewett MC. Establishing a high-yielding cell-free protein synthesis platform derived from vibrio natriegens. ACS Synth Biol 2018;7:2245–55. https://doi.org/10.1021/acssynbio. 8b00252
- <span id="page-7-11"></span>[84] Cui J, Stevenson D, Korosh T, Amador-Noguez D, Olson DG, et al. Developing a cell-free extract reaction (CFER) System in clostridium thermocellum to identify metabolic limitations to ethanol production. Front Energy Res 2020:8. ://doi.org/10.3389/fenrg.2020.00
- <span id="page-7-12"></span>[85] Xu H, Yang C, Tian X, Chen Y, Liu WQ, et al. Regulatory part engineering for high-yield protein synthesis in an all-streptomyces-based cell-free expression system. ACS Synth Biol 2022;11:570–8. https://doi.org/10.1021/acssynbio. 1c00587
- <span id="page-7-13"></span>[86] Zemella A, Thoring L, Hoffmeister C, Kubick S. Cell-free protein synthesis: pros and cons of prokaryotic and eukaryotic systems. Chembiochem 2015;16:2420–31. https://doi.org/10.1002/cbic.201500340
- <span id="page-7-14"></span>[87] Katsura K, Tomabechi Y, Matsuda T, Yonemochi M, Mikuni J, et al. Phosphorylated and non-phosphorylated HCK kinase domains produced by cell-free protein expression. Protein Expr Purif 2018;150:92–9. https://doi.org/ 10.1016/j.pep.2018.05.005
- [88] Oza JP, Aerni HR, Pirman NL, Barber KW, Ter Haar CM, et al. Robust production of recombinant phosphoproteins using cell-free protein synthesis. Nat Commun 2015;6:8168. https://doi.org/10.1038/ncomms9168
- <span id="page-7-15"></span>[89] Jaroentomeechai T, Stark JC, Natarajan A, Glasscock CJ, Yates LE, et al. Single-pot glycoprotein biosynthesis using a cell-free transcription-translation system enriched with glycosylation machinery. Nat Commun 2018;9:2686. https://doi. org/10.1038/s41467-018-05110-x
- <span id="page-7-16"></span>[90] Kai L, Sonal, Heermann T, Schwille P. Reconstitution of a reversible membrane switch via prenylation by one-pot cell-free expression. ACS Synth Biol<br>2023;12:108–19.https://doi.org/10.1021/acssynbio.2c00406
- <span id="page-7-17"></span>[91] Schaerli Y, Jimenez A, Duarte JM, Mihajlovic L, Renggli J, et al. Synthetic circuits reveal how mechanisms of gene regulatory networks constrain evolution. Mol Syst Biol 2018;14:e8102. https://doi.org/10.15252/msb.20178102
- <span id="page-7-18"></span>[92] Shin J, Noireaux V. Efficient cell-free expression with the endogenous E. coli RNA polymerase and sigma factor 70. J Biol Eng 2010;4:8. https://doi.org/10. 1186/1754-1611-4-8
- [93] Mcmanus JB, Emanuel PA, Murray RM, Lux MW. A method for cost-effective and rapid characterization of engineered T7-based transcription factors by cellfree protein synthesis reveals insights into the regulation of T7 RNA polymerase-driven expression. Arch Biochem Biophys 2019;674:108045. htt doi.org/10.1016/j.abb.2019.07.010
- <span id="page-7-19"></span>[94] Senda N, Enomoto T, Kihara K, Yamashiro N, Takagi N, et al. Development of an expression-tunable multiple protein synthesis system in cell-free reactions using T7-promoter-variant series. Synth Biol (Oxf) 2022;7:ysac029. https://doi. org/10.1093/synbio/ysac029
- <span id="page-7-20"></span>[95] Shin J, Noireaux V, An E. coli cell-free expression toolbox: application to synthetic gene circuits and artificial cells. ACS Synth Biol 2012;1:29–41. https:// 0.1021/sb200016s
- <span id="page-7-21"></span>[96] Mattick JS. RNA regulation: a new genetics. Nat Rev Genet 2004;5:316–23. https://doi.org/10.1038/nrg1321
- [97] Takahashi MK, Chappell J, Hayes CA, Sun ZZ, Kim J, et al. Rapidly characterizing the fast dynamics of RNA genetic circuitry with cell-free transcription-translation (TX-TL) systems. ACS Synth Biol 2015;4:503–15. https://doi.org/10.1021/ sb400206c
- [98] Debroy S, Gebbie M, Ramesh A, Goodson JR, Cruz MR, et al. Riboswitches. A riboswitch-containing sRNA controls gene expression by sequestration of a response regulator. Science 2014;345:937–40. https://doi.org/10.1126/science. 1255091
- [99] Rhea KA, Mcdonald ND, Cole SD, Noireaux V, Lux MW, et al. Variability in cellfree expression reactions can impact qualitative genetic circuit characterization. Synth Biol (Oxf) 2022;7:ysac011. https://doi.org/10.1093/synbio/ysac011
- [100] Jia H, Sun X, Sun H, Li C, Wang Y, et al. Intelligent microbial heat-regulating engine (IMHeRE) for improved thermo-robustness and efficiency of bioconversion. ACS Synth Biol 2016;5:312–20. https://doi.org/10.1021/acssynbio. 5b00158
- [101] Chappell J, Takahashi MK, Lucks JB. Creating small transcription activating RNAs. Nat Chem Biol 2015;11:214–20. https://doi.org/10.1038/nchembio.1737
- <span id="page-7-22"></span>[102] Chushak Y, Harbaugh S, Zimlich K, Alfred B, Chavez J, et al. Characterization of synthetic riboswitch in cell-free protein expression systems. RNA Biol 2021;18:1727–38. https://doi.org/10.1080/15476286.2020.1868149
- [103] Lins MRDCR, Correa GG, Amorim LADS, Franco RAL, Ribeiro NV, et al. Characterization of five purine riboswitches in cellular and cell-free expression

systems. Curr Microbiol 2022;79:207. https://doi.org/10.1007/s00284-022- 02902-9

- [104] Espah Borujeni A, Mishler DM, Wang J, Huso W, Salis HM. Automated physicsbased design of synthetic riboswitches from diverse RNA aptamers. Nucleic
- Acids Res 2016;44:1–13. https://doi.org/10.1093/nar/gkv1289 [105] Weigand JE, Suess B. Aptamers and riboswitches: perspectives in biotechnology. Appl Microbiol Biotechnol 2009;85:229–36. https://doi.org/10. 1007/s00253-009-2194-2
- [106] Wieland M, Hartig JS. Artificial riboswitches: synthetic mRNA-based regulators of gene expression. Chembiochem 2008;9:1873–8. https://doi.org/10.1002/cbic. 200800154
- [107] Grundy FJ, Henkin TM. From ribosome to riboswitch: control of gene expression in bacteria by RNA structural rearrangements. Crit Rev Biochem Mol Biol 2006;41:329–38. https://doi.org/10.1080/10409230600914294
- <span id="page-7-23"></span>[108] Martini L, Mansy SS. Cell-like systems with riboswitch controlled gene expression. Chem Commun (Camb) 2011;47:10734–6. https://doi.org/10.1039/ c1cc13930d
- <span id="page-7-0"></span>[109] Yue K, Zhu Y, Kai L. Cell-free protein synthesis: chassis toward the minimal cell. Cells 2019;8:315. https://doi.org/10.3390/cells8040315
- <span id="page-7-24"></span>[110] Li M, Huang X, Tang TY, Mann S. Synthetic cellularity based on non-lipid microcompartments and protocell models. Curr Opin Chem Biol 2014;22:1–11.  $:$ //doi.org/10.1016/j.cbpa.2014.05.018
- <span id="page-7-1"></span>[111] Buddingh BC, Van Hest JCM. Artificial cells: synthetic compartments with lifelike functionality and adaptivity. Acc Chem Res 2017;50:769–77. https://doi.  $org/10.1021/acs.accounts.6b005$
- <span id="page-7-25"></span>[112] Kita-Tokarczyk K, Grumelard J, Haefele T, Meier W. Block copolymer vesicles—using concepts from polymer chemistry to mimic biomembranes. Polymer 2005;46:3540–63. https://doi.org/10.1016/j.polymer.2005.02.083
- <span id="page-7-2"></span>[113] Discher DE, Eisenberg A. Polymer vesicles. Science 2002;297:967–73. https:// doi.org/10.1126/science.1074972
- <span id="page-7-26"></span>[114] Ma L, Eisenberg A. Relationship between wall thickness and size in block copolymer vesicles. Langmuir 2009;25:13730–6. https://doi.org/10.1021/ la9012729
- <span id="page-7-27"></span>[115] Rodríguez-García R, Mell M, López-Montero I, Netzel J, Hellweg T, et al. Polymersomes: smart vesicles of tunable rigidity and permeability. Soft Matter 2011;7:1532. https://doi.org/10.1039/c0sm00823k
- <span id="page-7-28"></span>[116] Egli S, Schlaad H, Bruns N, Meier W, Functionalization of block copolymer vesicle surfaces. Polymers 2011;3:252–80. https://doi.org/10.3390/polym3010252
- <span id="page-7-29"></span>[117] Fu Z, Ochsner MA, De Hoog HP, Tomczak N, Nallani M. Multicompartmentalized polymersomes for selective encapsulation of biomacromolecules. Chem Commun (Camb) 2011;47:2862–4. https://doi.org/10.1039/c0cc03971c
- <span id="page-7-30"></span>[118] Le Meins JF, Schatz C, Lecommandoux S, Sandre O. Hybrid polymer/lipid vesicles: state of the art and future perspectives. Mater Today 2013;16:397–402. https://doi.org/10.1016/j.mattod.2013.09.002
- [119] Kleineberg C, Wolfer C, Abbasnia A, Pischel D, Bednarz C, et al. Light-driven ATP regeneration in diblock/grafted hybrid vesicles. Chembiochem 2020;21:2149–60. https://doi.org/10.1002/cbic.201900774
- <span id="page-7-3"></span>[120] Huang X, Patil AJ, Li M, Mann S. Design and construction of higher-order structure and function in proteinosome-based protocells. J Am Chem Soc 2014;136:9225–34. https://doi.org/10.1021/ja504213m
- [121] Huang X, Li M, Mann S. Membrane-mediated cascade reactions by enzymepolymer proteinosomes. Chem Commun (Camb) 2014;50:6278–80. https://doi. org/10.1039/c4cc02256d
- <span id="page-7-4"></span>[122] Torre P, Xiao Q, Buzzacchera I, Sherman SE, Rahimi K, et al. Encapsulation of hydrophobic components in dendrimersomes and decoration of their surface with proteins and nucleic acids. Proc Natl Acad Sci USA 2019;116:15378–85. https://doi.org/10.1073/pnas.1904868116
- [123] Percec V, Wilson DA, Leowanawat P, Wilson CJ, Hughes AD, et al. Self-assembly of Janus dendrimers into uniform dendrimersomes and other complex architectures. Science 2010;328:1009–14. https://doi.org/10.1126/science.1185547
- [124] Wagner AM, Eto H, Joseph A, Kohyama S, Haraszti T, et al. Dendrimersome synthetic cells harbor cell division machinery of bacteria. Adv Mater 2022;34:e2202364. https://doi.org/10.1002/adma.202202364
- <span id="page-7-5"></span>[125] Jones JA, Giessen TW. Advances in encapsulin nanocompartment biology and engineering. Biotechnol Bioeng 2021;118:491-505. https://doi.org/10.100 27564
- [126] Sutter M, Boehringer D, Gutmann S, Gunther S, Prangishvili D, et al. Structural basis of enzyme encapsulation into a bacterial nanocompartment. Nat Struct Mol Biol 2008;15:939–47. https://doi.org/10.1038/nsmb.1473
- <span id="page-7-6"></span>[127] Tavano L, De Cindio B, Picci N, Ioele G, Muzzalupo R. Drug compartmentalization as strategy to improve the physico-chemical properties of diclofenac sodium loaded niosomes for topical applications. Biomed Micro 2014;16:851–8. https://doi.org/10.1007/s10544-014
- [128] Baillie AJ, Florence AT, Hume LR, Muirhead GT, Rogerson A. The preparation and properties of niosomes–non-ionic surfactant vesicles. J Pharm Pharm 1985;37:863–8. https://doi.org/10.1111/j.2042-7158.1985.tb04990.x
- <span id="page-7-31"></span>[129] Park N, Um SH, Funabashi H, Xu J, Luo D. A cell-free protein-producing gel. Nat Mater 2009;8:432–7. https://doi.org/10.1038/nmat2419
- [130] Allen ME, Hindley JW, Baxani DK, Ces O, Elani Y. Hydrogels as functional components in artificial cell systems. Nat Rev Chem 2022;6:562–78. https:// doi.org/10.1038/s41570-022-00404-7
- <span id="page-7-32"></span>[131] Ghosh B, Bose R, Tang TYD. Can coacervation unify disparate hypotheses in the origin of cellular life. Curr Opin Colloid Interface Sci 2021;52:101415. https:// doi.org/10.1016/j.cocis.2020.101415
- [132] Gao N, Mann S. Membranized coacervate microdroplets: from versatile protocell models to cytomimetic materials. Acc Chem Res 2023;56:297–307. https:// doi.org/10.1021/acs.accounts.2c00696
- <span id="page-8-11"></span>[133] Kato S, Garenne D, Noireaux V, Maeda YT. Phase separation and protein partitioning in compartmentalized cell-free expression reactions.<br>Biomacromolecules 2021;22:3451–9. https://doi.org/10.1021/acs.biomac. 1c00546
- [134] Chen Y, Yuan M, Zhang Y, Liu S, Yang X, et al. Construction of coacervate-incoacervate multi-compartment protocells for spatial organization of enzymatic reactions. Chem Sci 2020;11:8617–25. https://doi.org/10.1039/d0sc03849k
- [135] Aufinger L, Simmel FC. Artificial gel-based organelles for spatial organization of cell-free gene expression reactions. Angew Chem Int Ed Engl 2018:17245–8. https://doi.org/10.1002/anie.201809374
- <span id="page-8-12"></span>[136] Noireaux V, Libchaber A. A vesicle bioreactor as a step toward an artificial cell assembly. Proc Natl Acad Sci USA 2004;101:17669–74. https://doi.org/10.1073/ pnas.0408236101
- <span id="page-8-13"></span>[137] Ryabova LA, Vinokurov LM, Shekhovtsova EA, Alakhov YB, Spirin AS. Acetyl phosphate as an energy source for bacterial cell-free translation systems. Anal Biochem 1995;226:184–6. https://doi.org/10.1006/abio.1995.1208
- <span id="page-8-0"></span>[138] Berhanu S, Ueda T, Kuruma Y. Artificial photosynthetic cell producing energy for protein synthesis. Nat Commun 2019;10:1325. https://doi.org/10.1038/ s41467-019-09147-4
- [139] Biner O, Fedor JG, Yin Z, Hirst J. Bottom-up construction of a minimal system for cellular respiration and energy regeneration. ACS Synth Biol 2020;9:1450–9. https://doi.org/10.1021/acssynbio.0c00110
- <span id="page-8-1"></span>[140] Miller TE, Beneyton T, Schwander T, Diehl C, Girault M, et al. Light-powered CO<sub>2</sub> fixation in a chloroplast mimic with natural and synthetic parts. Science 2020;368:649-54. https://doi.org/10.1126/scienc
- <span id="page-8-2"></span>[141] Van Nies P, Westerlaken I, Blanken D, Salas M, Mencia M, et al. Self-replication of DNA by its encoded proteins in liposome-based synthetic cells. Nat Commun 2018;9:1583. https://doi.org/10.1038/s41467-018-03926-1
- <span id="page-8-3"></span>[142] Libicher K, Hornberger R, Heymann M, Mutschler H. In vitro self-replication and multicistronic expression of large synthetic genomes. Nat Commun 2020;11:904. https://doi.org/10.1038/s41467-020-146
- <span id="page-8-14"></span>[143] Exterkate M, Driessen AJM. Synthetic minimal cell: self-reproduction of the boundary layer. ACS Omega 2019;4:5293–303. https://doi.org/10.1021/ acsomega.8b02955
- <span id="page-8-4"></span>[144] Blanken D, Foschepoth D, Serrao AC, Danelon C. Genetically controlled membrane synthesis in liposomes. Nat Commun 2020;11:4317. https://doi.org/10. 1038/s41467-020-17863-5
- <span id="page-8-15"></span>[145] Deshpande S, Spoelstra WK, Van Doorn M, Kerssemakers J, Dekker C. Mechanical division of cell-sized liposomes. ACS Nano 2018;12:2560-8. https:// doi.org/10.1021/acsnano.7b08411
- <span id="page-8-16"></span>[146] Canman JC, Cabernard C. Mechanics of cell division and cytokinesis. Mol Biol Cell 2018;29:685–6. https://doi.org/10.1091/mbc.E17-11-0671
- <span id="page-8-17"></span>[147] Micali G, Grilli J, Osella M, Cosentino Lagomarsino M, Concurrent processes set E. coli cell division. Sci Adv 2018;4:eaau3324. https://doi.org/10.1126/sciadv. aau3324
- [148] Gray AN, Egan AJ, Van't Veer IL, Verheul J, Colavin A, et al. Coordination of peptidoglycan synthesis and outer membrane constriction during Escherichia coli cell division. Elife 2015;4:e07118. https://doi.org/10.7554/eLife.07118
- [149] Bisson-Filho AW, Hsu YP, Squyres GR, Kuru E, Wu F, et al. Treadmilling by FtsZ filaments drives peptidoglycan synthesis and bacterial cell division. Science 2017;355:739–43. https://doi.org/10.1126/science.aak9973
- [150] Yang X, Lyu Z, Miguel A, Mcquillen R, Huang KC, et al. GTPase activity-coupled treadmilling of the bacterial tubulin FtsZ organizes septal cell wall synthesis. Science 2017;355:744-7. https://doi.org/10.1126/science.aak999.
- <span id="page-8-18"></span>[151] Jia H, Schwille P. Bottom-up synthetic biology: reconstitution in space and time. Curr Opin Biotechnol 2019;60:179–87. https://doi.org/10.1016/j.copbio. 2019.05.008
- [152] Loose M, Kruse K, Schwille P. Protein self-organization: lessons from the min system. Annu Rev Biophys 2011;40:315–36. https://doi.org/10.1146/annurev-.<br>iophys-042910-15533
- [153] Kretschmer S, Schwille P. Pattern formation on membranes and its role in bacterial cell division. Curr Opin Cell Biol 2016;38:52–9. https://doi.org/10. 1016/j.ceb.2016.02.005
- <span id="page-8-35"></span>[154] Martos A, Jimenez M, Rivas G, Schwille P. Towards a bottom-up reconstitution of bacterial cell division. Trends Cell Biol 2012;22:634–43. https://doi.org/10. 1016/j.tcb.2012.09.003
- <span id="page-8-5"></span>[155] Kohyama S, Merino-Salomon A, Schwille P. In vitro assembly, positioning and contraction of a division ring in minimal cells. Nat Commun 2022;13:6098. https://doi.org/10.1038/s41467-022-33679-x
- <span id="page-8-6"></span>[156] Dubuc E, Pieters PA, Van Der Linden AJ, Van Hest JC, Huck WT, et al. Cell-free microcompartmentalised transcription-translation for the prototyping of synthetic communication networks. Curr Opin Biotechnol 2019;58:72-80. https:// doi.org/10.1016/j.copbio.2018.10.006
- <span id="page-8-19"></span>[157] Bartelt SM, Steinkuhler J, Dimova R, Wegner SV. Light-guided motility of a minimal synthetic cell. Nano Lett 2018;18:7268–74. https://doi.org/10.1021/acs. nanolett.8b03469
- <span id="page-8-20"></span>[158] Fallah-Araghi A, Baret JC, Ryckelynck M, Griffiths AD, A completely in vitro ultrahigh-throughput droplet-based microfluidic screening system for protein engineering and directed evolution. Lab Chip 2012;12:882-91. https://doi.org/ 10.1039/c2lc21035e
- <span id="page-8-21"></span>[159] Dudley QM, Karim AS, Jewett MC. Cell-free metabolic engineering: biomanufacturing beyond the cell. Biotechnol J 2015;10:69–82. https://doi.org/10.1002/ biot.201400330
- <span id="page-8-22"></span>[160] Suresh A, Shravan Ramgopal D, Panchamoorthy Gopinath K, Arun J, Sundarrajan P, et al. Recent advancements in the synthesis of novel thermostable biocatalysts and their applications in commercially important chemoenzymatic conversion processes. Bioresour Technol 2021;323:124558. https://doi.org/10. 1016/j.biortech.2020.124558
- [161] Thompson MP, Peñafiel I, Cosgrove SC, Turner NJ. Biocatalysis using immobilized enzymes in continuous flow for the synthesis of fine chemicals. Org Process Res Dev 2018;23:9–18. https://doi.org/10.1021/acs.oprd.8b00305
- [162] Guo W, Sheng J, Feng X. Mini-review: in vitro metabolic engineering for biomanufacturing of high-value products. Comput Struct Biotechnol J 2017;15:161–7. https://doi.org/10.1016/j.csbj.2017.01.006
- <span id="page-8-23"></span>[163] Korman TP, Opgenorth PH, Bowie JU. A synthetic biochemistry platform for cell free production of monoterpenes from glucose. Nat Commun 2017;8:15526. https://doi.org/10.1038/ncomms15526
- <span id="page-8-8"></span>[164] Dudley QM, Anderson KC, Jewett MC. Cell-free mixing of escherichia coli crude extracts to prototype and rationally engineer high-titer mevalonate synthesis. ACS Synth Biol 2016;5:1578–88. https://doi.org/10.1021/acssynbio.6b00154
- <span id="page-8-7"></span>[165] Karim AS, Jewett MC. A cell-free framework for rapid biosynthetic pathway prototyping and enzyme discovery. Metab Eng 2016;36:116-26. https://doi.org 10.1016/j.ymben.2016.03.002
- <span id="page-8-33"></span>[166] Silverman AD, Karim AS, Jewett MC. Cell-free gene expression: an expanded repertoire of applications. Nat Rev Genet 2020;21:151–70. https://doi.org/10. 1038/s41576-019-0186-3
- <span id="page-8-24"></span>[167] Tinafar A, Jaenes K, Pardee K. Synthetic biology goes cell-free. BMC Biol 2019;17:64. https://doi.org/10.1186/s12915-019-0
- <span id="page-8-9"></span>[168] Pardee K, Slomovic S, Nguyen PQ, Lee JW, Donghia N, et al. Portable, on-demand biomolecular manufacturing. Cell 2016;167:248–59. https://doi.org/10. 1016/j.cell.2016.09.013
- <span id="page-8-25"></span>[169] Stark JC, Jaroentomeechai T, Moeller TD, Hershewe JM, Warfel KF, et al. Ondemand biomanufacturing of protective conjugate vaccines. Sci Adv 2021;7:eabe9444. https://doi.org/10.1126/sciadv.abe9444
- <span id="page-8-26"></span>[170] Hohsaka T, Sisido M. Incorporation of non-natural amino acids into proteins. Curr Opin Chem Biol 2002;6(6):809–15. https://doi.org/10.1016/s1367- 5931(02)00376-9
- <span id="page-8-27"></span>[171] Liu DR, Magliery TJ, Pastrnak M, Schultz PG. Engineering a tRNA and aminoacyltRNA synthetase for the site-specific incorporation of unnatural amino acids into proteins in vivo. Proc Natl Acad Sci U S A 1997;94(19):10092–7. https://doi. org/10.1073/pnas.94.19.10092
- [172] Ibba M, Hennecke H. Towards engineering proteins by site-directed incorporation in vivo of non-natural amino acids. Biotechnol (N Y) 1994;12:678–82. https://doi.org/10.1038/nbt0794-678
- [173] Ryu Y, Schultz PG. Efficient incorporation of unnatural amino acids into proteins in Escherichia coli. Nat Methods 2006;3:263–5. https://doi.org/10.1038/ nmeth864
- [174] Young TS, Schultz PG. Beyond the canonical 20 amino acids: expanding the genetic lexicon. J Biol Chem 2010;285:11039–44. https://doi.org/10.1074/jbc. R109.091306
- [175] Benner SA. Expanding the genetic lexicon: incorporating non-standard amino acids into proteins by ribosome-based synthesis. Trends Biotechnol 1994;12:158–63. https://doi.org/10.1016/0167-7799(94)90076-0
- <span id="page-8-28"></span>[176] O'donoghue P, Ling J, Wang YS, Soll D. Upgrading protein synthesis for synthetic biology. Nat Chem Biol 2013;9:594–8. https://doi.org/10.1038/nchembio.1339
- <span id="page-8-29"></span>[177] Ranji Charna A, Des Soye BJ, Ntai I, Kelleher NL, Jewett MC. An efficient cell-free protein synthesis platform for producing proteins with pyrrolysine-based noncanonical amino acids. Biotechnol J 2022;17:e2200096. https://doi.org/10. 1002/biot.202200096
- [178] Martin RW, Des Soye BJ, Kwon YC, Kay J, Davis RG, et al. Cell-free protein synthesis from genomically recoded bacteria enables multisite incorporation of noncanonical amino acids. Nat Commun 2018;9:1203. https://doi.org/10.1038/ s41467-018-03469-5
- [179] Hong SH, Ntai I, Haimovich AD, Kelleher NL, Isaacs FJ, et al. Cell-free protein synthesis from a release factor 1 deficient Escherichia coli activates efficient and multiple site-specific nonstandard amino acid incorporation. ACS Synth Biol 2014;3:398–409. https://doi.org/10.1021/sb400140t
- <span id="page-8-30"></span>[180] Zhang L, Guo W, Lu Y. Advances in cell-free. Biosens: Princ Mech Appl Biotechnol J 2020;15:e2000187. https://doi.org/10.1002/biot.202000187
- [181] Soltani M, Davis BR, Ford H, Nelson JAD, Bundy BC. Reengineering cell-free protein synthesis as a biosensor: Biosensing with transcription, translation, and protein-folding. Biochem Eng J 2018;138:165–71. https://doi.org/10.1016/j.bej. 2018.06.014
- <span id="page-8-31"></span>[182] Nguyen PQ, Soenksen LR, Donghia NM, Angenent-Mari NM, De Puig H, et al. Wearable materials with embedded synthetic biology sensors for biomolecule detection. Nat Biotechnol 2021;39:1366–74. https://doi.org/10.1038/s41587- 021-00950-3
- <span id="page-8-10"></span>[183] Pardee K, Green AA, Ferrante T, Cameron DE, Daleykeyser A, et al. Paper-based synthetic gene networks. Cell 2014;159:940–54. https://doi.org/10.1016/j.cell.  $2014.10.0$
- <span id="page-8-32"></span>[184] Jung JK, Alam KK, Verosloff MS, Capdevila DA, Desmau M, et al. Cell-free biosensors for rapid detection of water contaminants. Nat Biotechnol<br>2020;38:1451–9.https://doi.org/10.1038/s41587-020-0571-7
- [185] Voyvodic PL, Bonnet J. Cell-free biosensors for biomedical applications. Curr Opin Biomed Eng 2020;13:9–15. https://doi.org/10.1016/j.cobme.2019.08.005
- <span id="page-8-34"></span>[186] Kigawa T, Yabuki T, Yoshida Y, Tsutsui M, Ito Y, et al. Cell-free production and stable-isotope labeling of milligram quantities of proteins. FEBS Lett 1999;442:15–9. https://doi.org/10.1016/s0014-5793(98)01620-2
- <span id="page-9-6"></span>[187] Li J, Haas W, Jackson K, Kuru E, Jewett MC, et al. Cogenerating synthetic parts toward a self-replicating system. ACS Synth Biol 2017;6:1327–36. https://doi. org/10.1021/acssynbio.6b00342
- <span id="page-9-0"></span>[188] Jewett MC, Forster AC. Update on designing and building minimal cells. Curr Opin Biotechnol 2010;21:697–703. https://doi.org/10.1016/j.copbio.2010.06. nos
- <span id="page-9-2"></span>[189] Failmezger J, Nitschel R, Sanchez-Kopper A, Kraml M, Siemann-Herzberg M. Site-specific cleavage of ribosomal RNA in Escherichia coli-based cell-free protein synthesis systems. PLoS One 2016;11:e0168764. https://doi.org/10. 1371/journal.pone.0168764
- <span id="page-9-1"></span>[190] Garamella J, Marshall R, Rustad M, Noireaux V. The all E. coli TX-TL Toolbox 2.0: a platform for cell-free synthetic biology. ACS Synth Biol 2016;5:344–55. https://doi.org/10.1021/acssynbio.5b00296
- <span id="page-9-3"></span>[191] Li J, Gu L, Aach J, Church GM. Improved cell-free RNA and protein synthesis system. PLoS One 2014;9:e106232. https://doi.org/10.1371/journal.pone. 0106232
- [192] Doerr A, Foschepoth D, Forster AC, Danelon C. In vitro synthesis of 32 translation-factor proteins from a single template reveals impaired ribosomal processivity. Sci Rep 2021;11:1898. https://doi.org/10.1038/s41598-020-8082
- [193] Niwa T, Kanamori T, Ueda T, Taguchi H. Global analysis of chaperone effects using a reconstituted cell-free translation system. Proc Natl Acad Sci USA 2012;109:8937–42. https://doi.org/10.1073/pnas.1201380109
- <span id="page-9-4"></span>[194] Foshag D, Henrich E, Hiller E, Schafer M, Kerger C, et al. The E. coli S30 lysate proteome: a prototype for cell-free protein production. N Biotechnol<br>2018;40:245–60.https://doi.org/10.1016/j.nbt.2017.09.005
- [195] Hurst GB, Asano KG, Doktycz CJ, Consoli EJ, Doktycz WL, et al. Proteomics-based tools for evaluation of cell-free protein synthesis. Anal Chem 2017;89:11443–51. https://doi.org/10.1021/acs.analchem.7b02555
- [196] Garenne D, Beisel CL, Noireaux V. Characterization of the all-E. coli transcription-translation system myTXTL by mass spectrometry. Rapid Commun Mass Spectrom 2019;33:1036–48. https://doi.org/10.1002/rcm.8438
- <span id="page-9-5"></span>[197] Jewett MC, Fritz BR, Timmerman LE, Church GM. In vitro integration of ribosomal RNA synthesis, ribosome assembly, and translation. Mol Syst Biol 2013;9:678. https://doi.org/10.1038/msb.2013.31
- [198] Aoyama R, Masuda K, Shimojo M, Kanamori T, Ueda T, et al. In vitro reconstitution of the Escherichia coli 70S ribosome with a full set of recombinant ribosomal proteins. J Biochem 2022;171:227–37. https://doi.org/10.1093/jb/ mvab121
- <span id="page-9-7"></span>[199] Caschera F, Lee JW, Ho KK, Liu AP, Jewett MC. Cell-free compartmentalized protein synthesis inside double emulsion templated liposomes with in vitro synthesized and assembled ribosomes. Chem Commun (Camb) 2016;52:5467–9. https://doi.org/10.1039/c6cc00223d
- <span id="page-9-8"></span>[200] Green R, Noller HF. In vitro complementation analysis localizes 23S rRNA posttranscriptional modifications that are required for Escherichia coli 50S ribosomal subunit assembly and function. RNA 1996;2:1011–21.
- [201] Sun ZZ, Hayes CA, Shin J, Caschera F, Murray RM, et al. Protocols for implementing an Escherichia coli based TX-TL cell-free expression system for synthetic biology. J Vis Exp 2013:e50762. https://doi.org/10.3791/50762
- [202] Kuruma Y, Ueda T. The PURE system for the cell-free synthesis of membrane proteins. Nat Protoc 2015;10:1328–44. https://doi.org/10.1038/nprot.2015.082
- [203] Levine MZ, Gregorio NE, Jewett MC, Watts KR, Oza JP. Escherichia coli-based cell-free protein synthesis: protocols for a robust, flexible, and accessible platform technology. J Vis Exp 2019. https://doi.org/10.3791/58882
- <span id="page-9-9"></span>[204] Sachs JN, Engelman DM. Introduction to the membrane protein reviews: the interplay of structure, dynamics, and environment in membrane protein function. Annu Rev Biochem 2006;75:707–12. https://doi.org/10.1146/annurev. biochem.75.110105.142336
- [205] Cho W, Stahelin RV. Membrane-protein interactions in cell signaling and membrane trafficking. Annu Rev Biophys Biomol Struct 2005;34:119–51. https://doi.org/10.1146/annurev.biophys.33.110502.133337
- <span id="page-9-10"></span>[206] Klammt C, Schwarz D, Lohr F, Schneider B, Dotsch V, et al. Cell-free expression as an emerging technique for the large scale production of integral membrane protein. FEBS J 2006;273:4141–53. https://doi.org/10.1111/j.1742-4658.2006.  $05432.$
- [207] Junge F, Haberstock S, Roos C, Stefer S, Proverbio D, et al. Advances in cell-free protein synthesis for the functional and structural analysis of membrane proteins. N Biotechnol 2011;28:262–71. https://doi.org/10.1016/j.nbt.2010.07.002
- [208] Levin R, Kock Z, Martin J, Zangl R, Gewering T, et al. Cotranslational assembly of membrane protein/nanoparticles in cell-free systems. Biochim Biophys Acta Biomembr 2022;1864:184017. https://doi.org/10.1016/j.bbamem.2022.184017
- <span id="page-9-11"></span>[209] Bernhard F, Tozawa Y. Cell-free expression–making a mark. Curr Opin Struct Biol 2013;23:374–80. https://doi.org/10.1016/j.sbi.2013.03.012
- <span id="page-9-12"></span>[210] De Souza TP, Fahr A, Luisi PL, Stano P. Spontaneous encapsulation and concentration of biological macromolecules in liposomes: an intriguing phenomenon and its relevance in origins of life. J Mol Evol 2014;79:179–92. https://doi. org/10.1007/s00239-014-965
- [211] Sun B, Chiu DT. Determination of the encapsulation efficiency of individual vesicles using single-vesicle photolysis and confocal single-molecule detection. Anal Chem 2005;77:2770–6. https://doi.org/10.1021/ac048439n
- [212] Pereira De Souza T, Steiniger F, Stano P, Fahr A, Luisi PL. Spontaneous crowding of ribosomes and proteins inside vesicles: a possible mechanism for the origin of cell metabolism. Chembiochem 2011;12:2325–30. https://doi.org/10.1002/ cbic.201100306
- [213] Luisi PL, Allegretti M, Pereira De Souza T, Steiniger F, Fahr A, et al. Spontaneous protein crowding in liposomes: a new vista for the origin of cellular metabolism. Chembiochem 2010;11:1989–92. https://doi.org/10.1002/cbic.201000381
- <span id="page-9-13"></span>[214] Elowitz MB, Levine AJ, Siggia ED, Swain PS, Stochastic gene expression in a single cell. Science 2002;297:1183–6. https://doi.org/10.1126/science.1070919
- [215] Karig DK, Jung SY, Srijanto B, Collier CP, Simpson ML. Probing cell-free gene expression noise in femtoliter volumes. ACS Synth Biol 2013;2:497–505. https://doi.org/10.1021/sb400028c
- [216] Nishimura K, Tsuru S, Suzuki H, Yomo T. Stochasticity in gene expression in a cell-sized compartment. ACS Synth Biol 2015;4:566–76. https://doi.org/10. 1021/sb500249g
- [217] Levy M, Falkovich R, Daube SS, Bar-Ziv RH. Autonomous synthesis and assembly of a ribosomal subunit on a chip. Sci Adv 2020;6:eaaz6020. https://doi.org/10. 1126/sciadv.aaz6020
- [218] Luisi PL, Stano P. Synthetic biology: minimal cell mimicry. Nat Chem 2011;3:755–6. https://doi.org/10.1038/nchem.1156
- <span id="page-9-14"></span>[219] Martin JP, Rasor BJ, Debonis J, Karim AS, Jewett MC, et al. A dynamic kinetic model captures cell-free metabolism for improved butanol production. Metab Eng 2023;76:133–45. https://doi.org/10.1016/j.ymben.2023.01.009