Establishing a cell-free *Vibrio natriegens* expression system

Authors: Daniel J. Wiegand[1,2], Henry H. Lee[1], Nili Ostrov[1*], George M. Church[1,2*]

Author affiliation:
[1] Department of Genetics, Harvard Medical School, Boston, MA 02115
[2] Wyss Institute for Biologically Inspired Engineering, Boston, MA 02115

[*] Correspondence to: nili_ostrov@hms.harvard.edu, gchurch@genetics.med.harvard.edu

Abstract

The fast growing bacterium *Vibrio natriegens* is an emerging microbial host for biotechnology. Harnessing its productive cellular components may offer a compelling platform for rapid protein production and prototyping of metabolic pathways or genetic circuits. Here, we report the development of a *V. natriegens* cell-free expression system. We devised a simplified crude extract preparation protocol and achieved >260µg/mL of super-folder GFP in a small-scale batch reaction after three hours. Culturing conditions, including growth media and cell density, significantly affect translation kinetics and extract protein yield. We observed maximal protein yield at incubation temperatures of 26°C or 30°C, and show improved yield by tuning ions crucial for ribosomal stability. This work establishes an initial *V. natriegens* cell-free expression system, enables probing of *V. natriegens* biology, and will serve as a platform to accelerate metabolic engineering and synthetic biology applications.

Keywords: *Vibrio natriegens*, crude cell extract, cell-free system, TX-TL, *in-vitro* protein synthesis

With the shortest doubling time of all known organisms, *Vibrio natriegens* has garnered considerable interest as a promising microbial host to accelerate research and biotechnology [1–4]. Its rapid growth rate, which has been linked to high rates of protein synthesis [5] and metabolic efficiency [6,7] suggests that this host may be harnessed as a powerful cell-free expression system. Cell-free bioproduction of protein and chemicals has been extensively demonstrated in *E. coli*, with recent work in several other bacteria [8–13]. Accordingly, we assessed *V. natriegens* crude cell extract productivity in small-scale batch reactions using super-folder GFP (sfGFP) controlled by a T7 promoter. We systematically explored culturing conditions and extract additives to provide an initial *V. natriegens* cell-free system which produces a comparable protein yield to that of cell-free *E. coli* similarly tuned in this work. Our calibration offers conditions for cell-free protein expression in *V. natriegens* and sheds light on critical factors for future process engineering [14,15]

Since a cell-free preparation protocol has not yet been described for *V. natriegens* to date, we evaluated established methods for extract preparation for *E.coli* and other bacterial systems [10,16–18]. Overall, we aimed for general accessibility and reproducibility by opting at each step for commonly available equipment while considering ease of user operation and cost reduction. Our preparation protocol utilizes one liter cultures in shake flasks, cell lysis by pulse sonication, and small-scale (10 µL) batch reactions in a 96- or 384-well format to maximize parallelization and screening throughput [17].

We first assessed the effect of *V. natriegens* culturing conditions on extract productivity. We tested commonly available microbiological media, supplemented with salt as needed to maintain robust growth [1,2,5,19]. Crude cell extracts were prepared from *V. natriegens* cultures growing in the following six media: LB with 3% (w/v) NaCl (LB3), LB with V2 salts (LB-V2), LB with Ocean Salts (LBO), Nutrient Broth with Ocean Salts (NBO), Brain Heart Infusion Broth with Ocean Salts (BHIO), and Marine Broth (MB). Cultures were grown at 30°C and harvested at OD_{600} of 1.0 (**Methods**).

We found that the choice of growth media significantly effects cell extract productivity. Extracts cultured in LB-V2 produced the highest protein yield (196 ± 12.46 µg/mL), followed by extracts cultured in BHIO (58.86 ± 2.61 µg/mL) and LB3 (33.18 ± 5.57 µg/mL) (**Figure 1a, Supplementary Figure 1a**). Low protein yield was observed from extracts cultured in NBO and LBO media, with no significant protein expression observed from extracts cultured in MB media. We thus elected to use LB-V2 extracts for all further investigations.

Previous studies have suggested that higher cellular ribosomal content is required to support faster growth rates [5,20]. To test whether extract productivity could be used as a proxy for active ribosomes in each growth medium, we assessed the correlation between the culture generation time and extract protein yield (**Figure 1b, Supplementary Figure 1c**). Our data shows no

relationship between generation time and cell extract productivity. The three shortest generation times at at 30°C were MB, LB-V2, and LB3 (20.14 ± 2.16, 20.55 ± 0.63 and 22.14 ± 1.13 minutes, respectively). However, extracts from LB-V2 cultures produced significantly more protein than extract from all other culture media (~6-fold more than LB3).

To gain deeper insight into the difference between growth media, we assessed translation kinetics for each growth media type by examining the rate of accumulating sfGFP (**Supplementary Figure 1b, Methods**). As expected, LB-V2 extracts had the maximum rate of protein synthesis, which was achieved after ~30 minutes. However, NBO extracts reached its maximum synthesis rate in only ~15 minutes, though the rate was 2.6-fold lower, and the total protein yield was 19.6-fold lower. Intriguingly, though their rate and total yield were significantly lower than that of LB-V2 extract, BHIO and LB3 extracts appear to sustain protein synthesis more robustly compared to other extracts, as evidenced by the protracted time constants for maximum and minimal rates. Overall, all extracts demonstrated a decay in rate of protein expression after 60 minutes, indicating consumption of input building blocks, buildup of inhibitory byproducts, or depletion of the sfGFP template. Overall, these results indicate significant variation in the fraction of active translation between media types. Specifically, potassium and magnesium ions, which are present in LB-V2 but not LB3, may enhance the stability of translation components in crude cell extract. Given the significant impact of culture media on extract yield, further investigation and development of customized cell-free growth medium for extract preparation may be required.

Active cell-free extracts are routinely produced using exponentially growing cells[17,21] . We thus tested the impact of *V. natriegens* cell density at harvest on extract productivity. Cells were grown in LB-V2 media, harvested at OD_{600} of 0.5, 1.0 or 3.0 and the corresponding sfGFP yield was measured (**Figure 1c, Supplementary Figure 2**). We found the most productive extracts were obtained from mid-logarithmic cultures (OD_{600} = 1.0), compared to 6.2-fold lower yield from late-logarithmic cultures (OD_{600} = 3.0). We were unable to detect sfGFP production from extracts obtained from early-logarithmic cultures (OD_{600} = 0.5). These effects of cell density on extract performance are consistent with those reported for other cell-free systems [17].

Cell-free extracts uniquely allow cellular components to operate decoupled from their culturing conditions. We thus turned to calibrating cell-free reaction conditions. We examined incubation temperatures ranging 18-37°C and observed maximal protein expression at 26°C and 30°C (262.28 ± 8.13 and 265.01 ± 8.15 µg/mL, respectively) (**Figure 2a**). While *in vivo* growth rate for *V. natriegens* increases with temperature and is maximal at 37°C [1,19], extracts incubated at 30°C produced 3-fold more protein than those incubated at 37°C. These results support the hypothesis that *V. natriegens'* rapid growth at higher temperature is aided by a larger number of ribosomes, rather than more efficient ones [5]. It may also be the case that more functional ribosomes are present at lower temperatures despite a higher total number at higher temperature

as observed in *E. coli* [22]. Further investigation of ribosome content and availability is warranted to elucidate the underlying biology. In addition, the reduced protein yields at temperatures higher than 30°C may be artifactual due to our choice of T7 polymerase. Due to its high processivity, T7 polymerase has been shown to reduce protein yield in a bacterial cell-free system by disrupting the coupling of transcription and translation [23]. Further improvements may be made by using mutant T7 polymerases or endogenous promoters. For further investigations, we chose to incubate all *V. natriegens* cell-free reactions at 26°C.

Having set an incubation temperature for optimal extract productivity, we then tuned the range of potassium and magnesium ions in the extract reaction [10,18]. In general, we found the additional of potassium ions (K^+) had a significant effect on both yield and rate of protein expression, while magnesium ions (Mg^{2+}) had only moderate effect at the tested conditions (**Figure 2b-c, Supplementary Figure 3**). We set our assay conditions at 80 mM K^+ and 3.5 mM Mg^{2+}, which yielded the highest reaction productivity for sfGFP expression (248.75 ± 6.82 μg/mL and 217.87 ± 23.40 μg/mL, respectively). It is worth noting, that when performing this calibration on both a plate reader and thermocycler, we observed an 1.25-fold average increase in protein yield using a thermocycler; likely due to uniform heat distribution (**Supplementary Figure 3**).

We then sought to determine if the total amount of crude extract needed per sample could be lowered while retaining reaction productivity. The percent of cell free reaction that comprises crude cell extract varies between different bacterial systems [12,17] and titration of the cellular components has been shown to improve protein yield [9]. We thus tested reactions where the percent of extract was varied, ranging 35% to 15%, and monitored the kinetics of sfGFP accumulation. Surprisingly, we found that decreasing the extract from 35% to 30% of the total reaction volume resulted in significant improvement in protein yield (43% increase) with no significant change in expression rate (**Figure 2d**, **Supplementary Figure 4**). Further decrease in extract amount (25% to 20%) resulted in a decreased rate of protein expression without significant change in protein yield. These results indicate up to half of the original extract volume can be used with increased or equal reaction productivity, which greatly increases the number of cell-free reactions produced from a single culture batch. It is worth also noting that the lowering the total extract percentage per reaction volume yielded sustained protein production for the duration of the reaction (**Supplementary Figure 4**).

The use of linear DNA as template in cell-free expression systems is desirable for high-throughput and rapid testing without requiring cloning of plasmids [18]. We thus evaluated protein production using either circular plasmid or linear PCR product (**Figure 2e**). In addition to sfGFP under T7 promoter, our PCR amplicon also contained 98bp of non-coding DNA at the 3' end of the construct. We observed protein production from the PCR amplicon to be 13.5-fold lower than an equimolar amount of circular plasmid, suggesting rapid DNA degradation by cellular nucleases. To test whether a linear template could be protected from nuclease digestion, we

assessed sfGFP expression using a PCR product with two phosphorothioated bonds on each end [24]. Notably, this modified linear template was also shorter, carrying only 40bp of non-coding sequence at the 3'. We observed no improvement in protein yield using protected linear template (**Figure 2e**), suggestive of endonuclease, rather than exonuclease, activity. In fact, the modified short template had 2-fold lower yield compared with longer, non-modified template. Padding of linear templates with non-coding sequences [24] or inactivation of endogenous nucleases by genome engineering will likely improve protein yield significantly and warrants further investigation.

To monitor the kinetics of linear DNA template degradation, we used a linear DNA template labeled with fluorescent nucleotides (**Methods**) [24]. We found that more than 50% of template was degraded in the first 10 minutes of cell-free reaction (**Figure 2f**). No significant difference in degradation was observed using the shorter phosphorothioated template, corroborating our previous observations that protecting the 5' ends of linear DNA does not improve template stability and that less non-coding padding decreases protein yield. Further work is required to address linear template stability in *V. natriegens* extracts. Promising directions may include template modifications or reduction of host nuclease activity by inclusion of a gam-like protein [24,25]. Alternatively, engineering of the host genome may provide facile production of highly active extracts free from these considerations [26].

Finally, to place our *V. natriegens* system in context of other cell-free expression systems, we compared our protein yield to that of *E. coli* strain A19, an RNase I- deficient strain that is traditionally used for preparation of cell free reactions [27,28]. Crude cell extract was prepared from *E.coli* cultured in rich media (YPG) at 37°C [21] and harvested at OD_{600} 1.0 (**Methods**). We then performed similar calibration of reaction conditions for *E.coli* as described above for *V. natriegens* (**Supplementary Figure 5**). Under their respective optimal reaction conditions, we observed *E.coli* A19 to have comparable protein yield to wild type *V. natriegens* (**Supplementary Figure 6**). Our results are also comparable with previously reported GFP yield for strain A19 using small-batch conditions [29]. Kinetic analysis shows that *V. natriegens* extracts sustained elevated protein expression rates over 60 minutes, while *E. coli* extracts only sustains elevated rates for 20 minutes.

These are promising results given the use of wild type *V. natriegens*, which can direct enhancement of designated cell free strains. Higher protein yield could be achieved by further optimization of culturing and preparation conditions and may include: semi-continuous extract reactions to allow for energy regeneration, resupplying of amino acids, and the removal of waste products [12,30]. In addition, engineering of *Vibrio natriegens,* for example using DNAse- or RNAse-deficient strains, removal of deleterious and competing metabolic pathways, and expression of additional tRNAs will likely further enhance protein yield [31]. These additional improvements will also enable the use of linear DNA to facilitate rapid prototyping and high-

throughput screens. Our work establishes an initial cell-free system in *V. natriegens* and sheds light on important factors for further development.

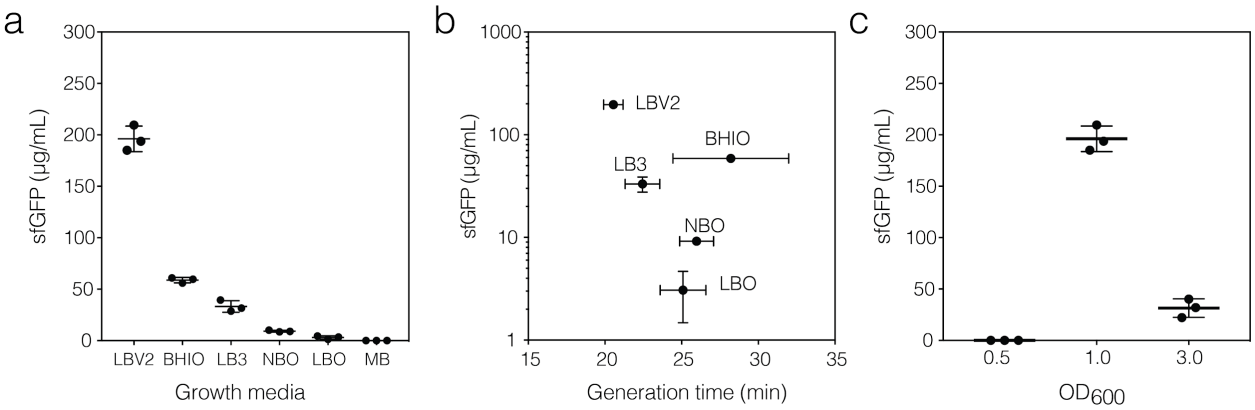

Figure 1. *V. natriegens* culture conditions impact extract protein yield. (a) Effect of culture growth media on cell-free extract protein yield. *V. natriegens* cells were grown in the indicated media at 30°C to OD_{600} = 1.0. Crude cell extract was prepared and production of sfGFP measured over three hours. (LB3 - LB with 3% (w/v) NaCl; LB-V2 - LB with V2 salts; LBO - LB with Ocean Salts, NBO - Nutrient Broth with Ocean Salts; BHIO - Brain Heart Infusion with Ocean Salts; and MB - Marine Broth). (b) Generation time and sfGFP yield for each media type tested. (c) Optical density at the time of cell harvest. Unless otherwise indicated, cell free reactions were incubated at 26°C in a thermocycler using 500 ng of plasmid DNA, 80 mM K-glutamate and 3.5 mM Mg-glutamate. sfGFP yield was measured after 3 hours. The mean and standard deviations are shown (N=3).

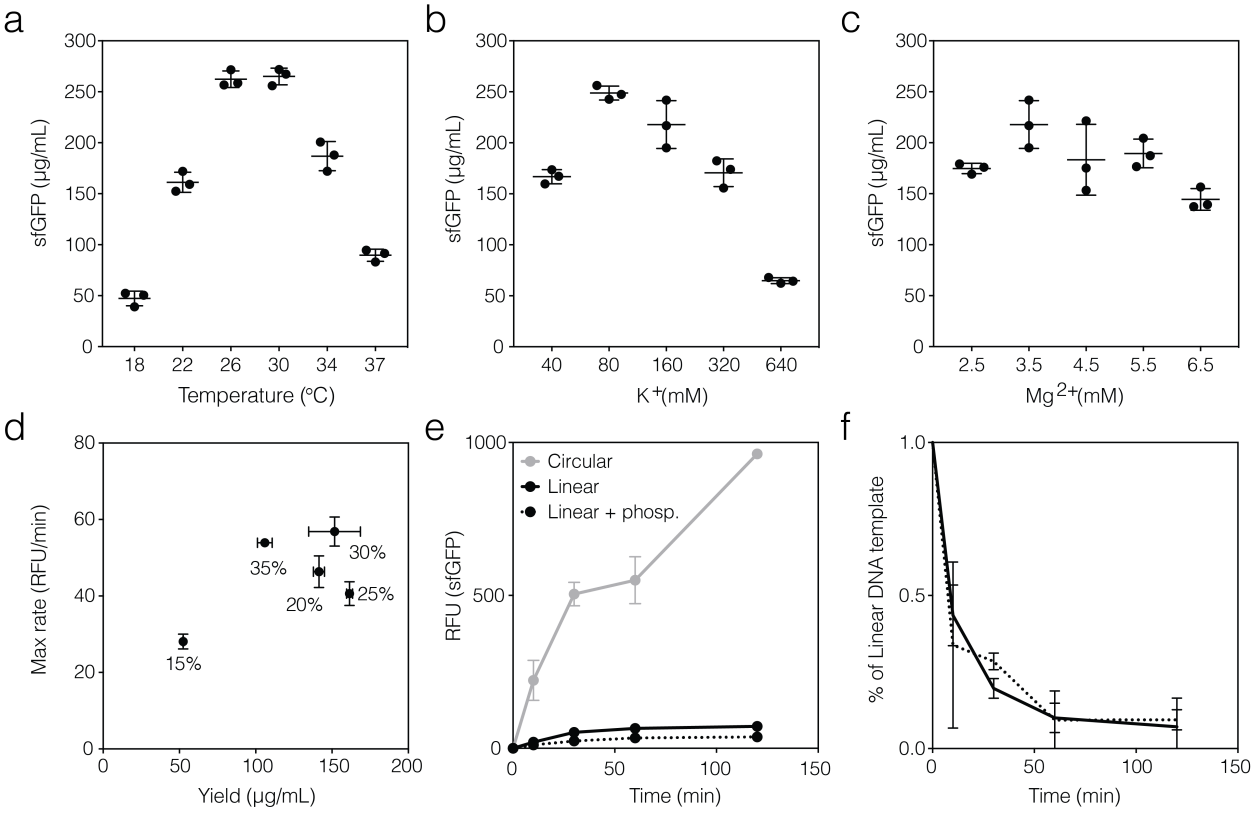

Figure 2. Properties of *V. natriegens* crude cell free extract. (a) Cell-free incubation temperature. (b) Supplemented potassium ions in reaction buffer. (c) Supplemented magnesium ions in reaction buffer. (d) Percent of cell free extract relative to total reaction volume. Yield and rate of reaction are shown. (e) Template DNA used for expression of sfGFP. Equimolar amount of circular plasmid (pJL1, grey), linear DNA (PCR product, black solid line) or linear DNA with two phosphorothioated bonds on each end (PCR product, black dotted line) was used. (f) Degradation of linear DNA template. Fluorescence of AlexaFluor 594-5-dUTP labeled linear template was monitored over two hours. Template with (dotted) or without (solid) two phosphorothioated bonds on each end was used. Unless otherwise indicated, all experiments were performed using *V. natriegens* crude cell extract incubated at 26°C for three hours, supplemented with 80mM K-glutamate and 3.5mM Mg-glutamate. The mean and standard deviations are shown (N=3).

Supporting Information

Attached supporting information document includes all materials & methods and supplementary figures for the main text.

Author contribution

DJW and NO designed and performed all experiments. DJW, HHL, and NO analyzed all data and wrote the manuscript. GMC supervised the study.

Acknowledgments

The authors would like to thank Nina Donghia for helpful discussion regarding cell-free extract preparation and Dr. David Thompson for providing sfGFP standards.

Funding

This work was funded by the NIGMS 1U01GM110714-01 and DOE DE-FG02-02ER63445.

Notes

DJW, NO, and GMC has filed a patent related to this work.

References

(1) Lee, H. H., Ostrov, N., Wong, B. G., Gold, M. A., Khalil, A., and Church, G. M. (2016) Vibrio natriegens, a new genomic powerhouse. *bioRxiv*.
(2) Weinstock, M. T., Hesek, E. D., Wilson, C. M., and Gibson, D. G. (2016) Vibrio natriegens as a fast-growing host for molecular biology. *Nat. Methods*.
(3) Fernández-Llamosas, H., Castro, L., Blázquez, M. L., Díaz, E., and Carmona, M. (2017) Speeding up bioproduction of selenium nanoparticles by using Vibrio natriegens as microbial factory. *Sci. Rep. 7*, 16046.
(4) Dalia, T. N., Hayes, C. A., Stolyar, S., Marx, C. J., McKinlay, J. B., and Dalia, A. B. (2017) Multiplex Genome Editing by Natural Transformation (MuGENT) for Synthetic Biology in Vibrio natriegens. *ACS Synth. Biol.*
(5) Aiyar, S. E., Gaal, T., and Gourse, R. L. (2002) rRNA promoter activity in the fast-growing bacterium Vibrio natriegens. *J. Bacteriol. 184*, 1349–1358.
(6) Hoffart, E., Grenz, S., Lange, J., Nitschel, R., Müller, F., Schwentner, A., Feith, A., Lenfers-Lücker, M., Takors, R., and Blombach, B. (2017) High substrate uptake rates empower Vibrio natriegens as production host for industrial biotechnology. *Appl. Environ. Microbiol.*
(7) Long, C. P., Gonzalez, J. E., Cipolla, R. M., and Antoniewicz, M. R. (2017) Metabolism of the fast-growing bacterium Vibrio natriegens elucidated by (13)C metabolic flux analysis. *Metab. Eng. 44*, 191–197.
(8) Li, J., Wang, H., Kwon, Y.-C., and Jewett, M. C. (2017) Establishing a high yielding streptomyces-based cell-free protein synthesis system. *Biotechnol. Bioeng. 114*, 1343–1353.
(9) Wang, H., Li, J., and Jewett, M. C. (2018) Development of a Pseudomonas putida cell-free protein synthesis platform for rapid screening of gene regulatory elements. *Synth. Biol. 3*.
(10) Moore, S. J., Lai, H.-E., Needham, H., Polizzi, K. M., and Freemont, P. S. (2017) Streptomyces venezuelae TX-TL - a next generation cell-free synthetic biology tool. *Biotechnol. J. 12*.
(11) Kim, J. K., Kang, H., Chae, J. S., Park, Y. H., and Choi, Y. J. (2000) Synthesis of cefminox by cell-free extracts of Streptomyces clavuligerus. *FEMS Microbiol. Lett. 182*, 313–317.
(12) Caschera, F., and Noireaux, V. (2014) Synthesis of 2.3 mg/ml of protein with an all Escherichia coli cell-free transcription-translation system. *Biochimie 99*, 162–168.
(13) Carlson, E. D., Gan, R., Hodgman, C. E., and Jewett, M. C. (2012) Cell-free protein synthesis: applications come of age. *Biotechnol. Adv. 30*, 1185–1194.
(14) Forster, A. C., and Church, G. M. (2007) Synthetic biology projects in vitro. *Genome Res.*

17, 1–6.
(15) Dudley, Q. M., Karim, A. S., and Jewett, M. C. (2015) Cell-free metabolic engineering: biomanufacturing beyond the cell. *Biotechnol. J. 10*, 69–82.
(16) Pratt, M, J. (1984) Coupled transcription-translation in prokaryotic cell-free systems. *Transcription and translation: a practical approach.* 179–209.
(17) Kwon, Y.-C., and Jewett, M. C. (2015) High-throughput preparation methods of crude extract for robust cell-free protein synthesis. *Sci. Rep. 5*, 8663.
(18) Sun, Z. Z., Hayes, C. A., Shin, J., Caschera, F., Murray, R. M., and Noireaux, V. (2013) Protocols for implementing an Escherichia coli based TX-TL cell-free expression system for synthetic biology. *J. Vis. Exp.* e50762.
(19) Eagon, R. G. (1962) Pseudomonas natriegens, a marine bacterium with a generation time of less than 10 minutes. *J. Bacteriol. 83*, 736–737.
(20) Zawada, J., and Swartz, J. (2006) Effects of growth rate on cell extract performance in cell-free protein synthesis. *Biotechnol. Bioeng. 94*, 618–624.
(21) Failmezger, J., Rauter, M., Nitschel, R., Kraml, M., and Siemann-Herzberg, M. (2017) Cell-free protein synthesis from non-growing, stressed Escherichia coli. *Sci. Rep. 7*, 16524.
(22) Yun, H. S., Hong, J., and Lim, H. C. (1996) Regulation of ribosome synthesis in Escherichia coli: effects of temperature and dilution rate changes. *Biotechnol. Bioeng. 52*, 615–624.
(23) Iskakova, M. B., Szaflarski, W., Dreyfus, M., Remme, J., and Nierhaus, K. H. (2006) Troubleshooting coupled in vitro transcription-translation system derived from Escherichia coli cells: synthesis of high-yield fully active proteins. *Nucleic Acids Res. 34*, e135.
(24) Sun, Z. Z., Yeung, E., Hayes, C. A., Noireaux, V., and Murray, R. M. (2014) Linear DNA for rapid prototyping of synthetic biological circuits in an Escherichia coli based TX-TL cell-free system. *ACS Synth. Biol. 3*, 387–397.
(25) Seki, E., Matsuda, N., Yokoyama, S., and Kigawa, T. (2008) Cell-free protein synthesis system from Escherichia coli cells cultured at decreased temperatures improves productivity by decreasing DNA template degradation. *Anal. Biochem. 377*, 156–161.
(26) Michel-Reydellet, N., Calhoun, K., and Swartz, J. (2004) Amino acid stabilization for cell-free protein synthesis by modification of the Escherichia coli genome. *Metab. Eng. 6*, 197–203.
(27) Gesteland, R. F. (1966) Isolation and characterization of ribonuclease I mutants of Escherichia coli. *J. Mol. Biol. 16*, 67–84.
(28) Spirin, A. S., and Swartz, J. R. (2014) Cell-free Protein Synthesis: Methods and Protocols. John Wiley & Sons.
(29) Chen, H., Xu, Z., Wang, C., Liao, Y., and Cen, P. (2008) Preliminary study on preparation of E. coli cell-free system for protein expression. *Front. Chem. Eng. Chin. 2*, 224–229.
(30) Sitaraman, K. (2004) A novel cell-free protein synthesis system. *J. Biotechnol. 110*, 257–263.
(31) Michel-Reydellet, N., Woodrow, K., and Swartz, J. (2005) Increasing PCR fragment stability and protein yields in a cell-free system with genetically modified Escherichia coli extracts. *J. Mol. Microbiol. Biotechnol. 9*, 26–34.