Cells as a Biofactory: Parallels between Biopharmaceutical Manufacturing and Industrial Biotechnology

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10

11 Abstract

12 Industrial biotechnology and biopharmaceutical manufacturing leverage biology to enable cellular

13 systems to serve as factories to produce molecules of value to humankind. These biotechnological

14 processes utilize diverse host organisms and address applications from biofuel, polymer building

15 blocks, antibiotics, and whole cell therapies. Industrial biotechnology can address environmental and

16 sustainability goals in addition to chemical production. In a similar fashion, the field of

17 biopharmaceutical manufacturing has and continues to produce life-saving medicines. Despite these

18 diverse applications, these fields rely on common biological themes and require similar approaches

19 for genetic and metabolic engineering as discussed in this review. Through advances in synthetic

20 biology, targeted genetic engineering, DNA sequencing, adaptation and high-throughput screening,

21 industrial biotechnology and biopharmaceutical manufacturing utilize the same framework for

22 efficient biochemical production which can be leveraged in current and future collaborations to

23 enable rapid innovation.

25 1 Introduction

26 The power of recombinant DNA technology has enabled society to harness biotechnology toward a 27 wide variety of applications, and humanity is still in the early days of realizing these benefits. Even 28 in these early days, different types of cells have demonstrated an ability to solve specific types of 29 problems. For example, microbes, which are diverse in their environments, genes, metabolism, and 30 growth, are particularly useful in addressing applications that benefit from diverse biochemistry and 31 the ability for robust growth. Engineered mammalian cells have very sophisticated abilities to 32 synthesize complex products – from monoclonal antibodies (mAbs) and vaccines to gene therapy 33 vectors. Additionally, mammalian cells can produce complex and human-like post-translational 34 modifications such as glycosylation which are critical for appropriate pharmacological activity. In 35 addition to serving as a biofactory, the cells used in biopharmaceutical applications have gone 36 beyond the factory and are also the medicinal product themselves such as in CAR-T 37 immunotherapies.

38 Industrial biotechnology, the application of biotechnology to produce commodity and 39 specialty chemicals or recycle waste and plastics, utilizes a broad set of microorganisms as cellular 40 factories. These applications are often (but not always) characterized by high volume, low margin 41 products. Most commonly using bacteria, yeast or fungi, industrial biotechnology leverages central 42 carbon metabolic pathways to enable and enhance production of desired compounds with 43 applications such as biofuels, commodity chemicals and polymer precursors (Curran and Alper, 44 2012). In addition to chemical production, the use of these organisms extends the possible carbon 45 feedstocks which can be utilized including lignocellulosic biomass and waste oils (Kommoji et al., 46 2021; Lad et al., 2022). These microbes can help achieve goals in greenhouse gas emission and 47 waste management with potentially concurrent biochemical production (Cordova et al., 2020; 48 Gordillo Sierra et al., 2022; Wongsirichot et al., 2022). Microbes, isolated from nature or engineered within research labs, can tolerate and sometimes flourish in environments such as high temperature,
high pressure, high salt, and the presence of toxic chemicals which are beneficial characteristics for
commercial manufacturing (Satyanarayana et al., 2013; Yin et al., 2015; Brabender et al., 2018; Chen
and Jiang, 2018; Cordova et al., 2020).

53 Like industrial biotechnology, biopharmaceutical manufacturing relies on cellular systems 54 toward the goal of producing medicines. Here, however, these processes are often characterized by 55 low volume, high margin products. The resulting compounds can range from small proteins and 56 antibodies to vaccines and even whole cells as the delivery vehicle or therapy. In the case of these 57 biomedicines, extensive clinical studies and regulatory approvals are involved to protect patient 58 outcomes. The complexity of the desired product drives host selection with simpler products 59 produced in bacteria and yeast and more complex proteins, especially those requiring glycosylation, 60 produced in mammalian cell lines. Proper glycosylation is a critical attribute of the drug product and 61 has impacts on drug targeting, *in vivo* activity, and half-life (Ebersbach et al., 2012). Due to the 62 growth in the number of approved monoclonal antibody drugs, Chinese Hamster Ovary (CHO) cells 63 are the most common host with myeloma NS0 and Sp2, BHK-21, and Human Embryonic Kidney 64 (HEK293) cells also leveraged for specific product classes (Lindskog et al., 2018). In addition to 65 monoclonal antibodies, vaccines and cell/gene therapies represent the most established and the 66 newest biopharmaceutical products, respectively (Jagschies, 2018a). Vaccine production uses various 67 host cells depending on the classification and complexity while cell and gene therapies are typically 68 reserved for specialized cell types (Jagschies, 2018b). The use of mammalian cell types, which have 69 slower growth rates as compared to bacteria and yeast, extends the length of experimental design 70 which can be compounded with challenges in application of synthetic biology tools. Nonetheless, the 71 biopharmaceutical manufacturing field has enabled production of diverse medicinal products with at

72 least four monoclonal antibody products reaching blockbuster status, greater than 1 billion in sales

73 within the first year of release, as of 2016 (Jagschies, 2018b; Spahn et al., 2022).

74 In both industrial biotechnology and biopharmaceutical manufacturing, post-production 75 processing is a critical step in isolating the desired product from the bioreactor environment of cells 76 and supernatant. These processes can vary widely depending on the characteristics and application of 77 the biochemical produced which requires additional considerations for process scale-up and final 78 economic viability. Unit operations used for downstream processing can include filtration, 79 chromatography, viral inactivation, liquid-liquid extraction, and/or distillation, with several 80 purification steps required to achieve desired purity. Downstream purifications, in either industrial 81 biotechnology or biopharmaceutical manufacturing, represent an entirely separate but related field 82 and are reviewed extensively elsewhere (Cheng et al., 2012; Jungbauer, 2013; Kumar et al., 2019; 83 Mehta, 2019; Datar and Rosén, 2020; Sengupta et al., 2020).

84 Industrial biotechnology and biopharmaceutical manufacturing represent applications within 85 biotechnology which rely on a biological basis and use the same techniques and approaches (Figure 86 1). Each field has unique characteristics in the production of useful biomolecules as shown in Table 87 1. Specifically, similarities in tools and screening approaches unite industrial biotechnology and 88 biopharmaceutical manufacturing. The synthetic biology toolbox brings genetic engineering closer to 89 an ideal 'plug and play' system where parts can be used interchangeably with predictable function 90 across host organisms (Litcofsky et al., 2012). Additionally, genetic engineering techniques including 91 CRISPR and sequencing technologies have drastically improved over the past 20 years enabling 92 more efficient cellular manipulation. With these new techniques for genetic modification, rapid 93 screening has been required to complete the design, build, test, learn cycle to enhance biomolecule 94 production (Petzold et al., 2015; Carbonell et al., 2018). Robotics and automation in addition to assay 95 development have enabled this rapid screening to more rapidly identify top producing strains or

96 clones (Houston and Banks, 1997; Carbonell et al., 2020; Gurdo et al., 2022). In cases where less 97 information is available, especially in non-conventional hosts, adaptation has been leveraged to 98 enable higher chemical production or tolerance to strenuous environments (Thorwall et al., 2020). 99 Together, these techniques enable successes in both industries and serve as common ground for 100 innovation. Additionally, these industries rely on the same basis of economic feasibility and efficient 101 metabolism which adds to complexity of using biological production systems (Zhang and Hua, 2016; 102 Perin and Jones, 2019; Yang et al., 2020; Nielsen et al., 2022). Balancing the risk of culture 103 contamination with efficient and stable production, biomolecules for chemical or medicinal use 104 require complex understanding and control of biological systems. For successful development of 105 future medicines and biochemicals, continued and additional collaboration efforts can promote 106 innovation toward addressing global challenges of the 21st century related to food, fuel and human 107 health. Industrial biotechnology enables use of non-edible carbon for biofuel processes and can create 108 many commodity chemicals required to replace dependence on non-renewable fossil fuels 109 (Moshelion and Altman, 2015; Dupont-Inglis and Borg, 2018; Yuan et al., 2022). While 110 biopharmaceutical manufacturing has a more targeted range of applications, these still span diverse 111 medical treatments such as life-saving insulin proteins, high-specificity monoclonal antibodies, and 112 even serve as a cure for cancer and genetic diseases (Assidi et al., 2022). This review provides a 113 concise summary of several areas related to cell line/strain development and engineering across both 114 industrial biotechnology and biopharmaceutical manufacturing providing motivation for continued 115 and additional collaboration and innovation between these fields.

116 2 Parallels between Biopharmaceutical Manufacturing and Industrial Biotechnology

Industrial biotechnology and biopharmaceutical manufacturing rely heavily on cellular systems to serve as 'biofactories' which create useful compounds with diverse applications. Regardless of the organism and molecule chosen, production at industrially relevant scales relies on harnessing biological control at the DNA or RNA level to make genetic modifications. These systems also rely
on the same metabolic pathways which govern the movement of carbon from feedstocks to the
desired product.

123 **2.1** Advances in Synthetic Biology

124 Development of synthetic biology tools have enabled a variety of organisms to be used for bio-125 production. From the building blocks of gene expression (toolbox of parts) to gene editing and DNA 126 sequencing, advances in synthetic biology have enabled enhanced product development for both 127 biopharmaceutical manufacturing and industrial biotechnology applications.

128 2.1.1 Synthetic Biology Toolkit

129 At the core of recombinant chemical and biologic production is the genetic engineering of organisms 130 to enable or enhance production. This engineering relies on a toolbox of synthetic biology parts 131 (promoters, terminators, enhancers, etc.) as building blocks to enable efficient gene and protein 132 expression, and ultimately proper protein folding and localization. It is also desirable for these 133 toolbox components to function independently to enable mix-and-match of parts directly 'off the 134 shelf'. As these building blocks serve a critical role across biotechnology applications, significant 135 research has been performed to identify native sequences as well as to create synthetic versions by 136 combining smaller functional units together (Curran et al., 2013; Redden and Alper, 2015; Cheng and 137 Alper, 2016; Cheng et al., 2019). In the case of promoters, transcription factor binding sites and 138 efficient ribosome binding sites have served as the basis for promoter design across all evolutionary 139 scales from *Escherichia. coli* (Chen et al., 2018) and yeast (Redden and Alper, 2015) to CHO cells 140 (Johari et al., 2019) and human cell lines (Cheng and Alper, 2016). As a second most important core 141 element following the target gene, terminators enable fine-tuning of expression often through 142 sequence modification to achieve optimal expression.

143 Promoters are perhaps the most well studied component of the synthetic biology toolbox. 144 Engineering of these systems leads to dramatic changes in gene expression. The ability for induction 145 and tuning of gene expression has been critical in finding a balance between conflicting needs of 146 growth and protein or chemical production. As such, discovery and development of promoters is 147 required in both industrial biotechnology and biopharmaceutical manufacturing applications across a 148 variety of host organisms (Table 2). The length and structural complexity of promoters increases 149 with evolutionary complexity with several key features outlined for bacteria, yeast, and mammalian 150 production hosts (Table 2). Mining of native promoter sequences has been applied to microbial and 151 mammalian cultures to leverage innate transcription factor binding motifs (Cheng and Alper, 2016; 152 Johari et al., 2019; McGraw et al., 2020). The conserved presence of these factors enables a pipeline 153 approach which can be applied to any organism of interest for any application (Redden and Alper, 154 2015; Cheng and Alper, 2016; Johari et al., 2019). Specifically, in mammalian cells the transcription 155 factor, Nuclear Factor KB (NF- kappaB) is present within the CMV promoter routinely used in 156 biopharmaceutical applications (McGraw et al., 2020). While this factor is absent in yeast, a similar 157 function is completed through retrograde response genes (Srinivasan et al., 2010). In addition to 158 conserved binding motifs, features including inducibility and multi-expression cassettes are required 159 and desired in all production hosts for biochemical production. In many cases, a core promoter 160 sequence can be multiplexed with upstream activating sequences from other promoter sequences to 161 generate novel sequences. Continued study and development of promoter sequences, especially for 162 mammalian cells, is essential for expanding the synthetic biology toolbox to achieve tighter 163 expression control with shorter sequences to ultimately improve production.

Similar approaches building up from various motifs have been applied to terminator
 development. Although these regions are less studied, they are critical in fine-tuning mRNA half-life
 to achieve optimal gene expression and have been engineered across all production hosts (Morse et

167 al., 2017; Cheng et al., 2019). In deploying the same sequence structure, a range of terminators have 168 been developed within Saccharomyces cerevisiae and human cell line lines in parallel demonstrating 169 a wide range of activity (Morse et al., 2017; Cheng et al., 2019). These examples highlight the DNA 170 molecular basis of synthetic biology parts which is conserved across applications in industrial 171 biotechnology and biopharmaceutical manufacturing. While promoters and terminators are 172 considered most critical in controlling gene expression, they represent only two parts of the synthetic 173 biology toolbox. For brevity, repressors, insulators, activators and enhancers are not discussed here 174 and are reviewed extensively elsewhere (Gaszner and Felsenfeld, 2006; Moore et al., 2014; Shlyueva 175 et al., 2014; Engstrom and Pfleger, 2017; Hafner and Boettiger, 2022). With continued development 176 of diverse synthetic biology tools, open-source projects have sought to provide standardization in 177 storage of data, organization of tools, and reference software for routine analysis (Decoene et al., 178 2017). These efforts including the Synthetic Biology Open Language (SBOL) (Decoene et al., 2017), 179 SynBioHub (McLaughlin et al., 2018), and SynBiopython (Yeoh et al., 2021) provide tools and 180 information across laboratories to speed progress as accessibility enables researchers to build upon 181 the work of others. Continued sharing of synthetic biology toolbox knowledge will be beneficial for 182 both industrial biotechnology and biopharmaceutical manufacturing applications.

183 2.1.2 Gene Editing including CRISPR

Genetic engineering for industrial biotechnology or biopharmaceutical manufacturing applications relies on efficient delivery of the desired genetic cargo often into a known location within the genome. Discovery of site-specific tools including Zinc Finger Nucleases (ZFN), transcription activator like effector nucleases (TALEN) and CRISPR have enabled this level of precise genetic engineering (Urnov et al., 2010; Copeland et al., 2014; Doudna and Charpentier, 2014; Wright et al., 2014). By leveraging DNA interactions for these approaches, they are broadly applicable across all domains of life with applications in both industrial biotechnology and biopharmaceutical manufacturing. Specific applications of CRISPR span a large body of literature and genetic editing of *E. coli, S. cerevisiae*, and CHO cells are extensively reviewed elsewhere (Peters et al., 2015; Stovicek
et al., 2017; Deaner and Alper, 2019; McGraw et al., 2020; Cai et al., 2022).

194 In addition to direct gene editing, the CRISPR/Cas system has been modified and repurposed in a 195 myriad of ways to serve as a 'molecular Swiss army knife' (Mans et al., 2015). Partial or full 196 deactivation of Cas function has been applied to fine tune behavior for enhanced gene editing (Ran et 197 al., 2013), for tighter control of gene expression or repression (Deaner et al., 2017) and for various 198 RNAi strategies (Schultenkämper et al., 2019) across all cellular workhorses and product 199 applications. Additionally, CRISPR based approaches generating DNA nicks have been used for 200 enhanced site-specific integration and mutation generation for screening purposes (Halperin et al., 201 2018; Hamaker and Lee, 2023). Gene editing tools are central to all biotechnology applications and 202 serve as a common thread between the industrial biotechnology and biopharmaceutical 203 manufacturing fields.

204 2.1.3 DNA Sequencing

205 Closely tied to genetic editing innovation, advancement of DNA sequencing technology over the past 206 20 years has propelled biochemical production across all scales of life. Conventional production host 207 genomes such as E. coli (4.6 million base pairs) and S. cerevisiae (12 million base pairs) were first 208 sequenced and published in 1996 and 1997, respectively, while the Human Genome Project released 209 the first human genome in 2000 (Saccharomyces Genome Database | SGD, n.d.; Blattner et al., 1997; 210 Engel et al., 2014; Nurk et al., 2022). The complete sequence and assembly required another 20 years 211 to complete in part due to additional technological advances enabling longer, high-fidelity 212 sequencing reads (Nurk et al., 2022). Development of sequencing technologies using parallel 213 reactions have enabled high fidelity and longer read lengths with lower costs. Traditional Sanger 214 sequencing is useful for projects where short reads are sufficient, typically less than 1kb (McCombie

215 et al., 2019). By deploying a sequencing by synthesis approach, detection of the newly added 216 nucleotide can be quantified using direct fluorescence or post-synthesis detection via released 217 phosphate groups or pH changes as used in Illumina and Ion Torrent technology (McCombie et al., 218 2019). For read lengths exceeding 500 base pairs, single molecule sequencing techniques use 219 nanoscale surfaces for DNA synthesis in PacBio instruments or direct detection in the case of Oxford 220 Nanopore sequencing (McCombie et al., 2019). These technological advances and various methods 221 from Sanger sequencing to Next-Generation Sequencing approaches merit their own independent 222 review which can be found elsewhere in the literature (Grada and Weinbrecht, 2013; Slatko et al., 223 2018; McCombie et al., 2019; Hu et al., 2021). Specifically, within applications utilizing adaptation, 224 such as adaptive laboratory evolution, DNA sequencing provides key insights and can provided 225 causative mutations for the desired phenotype which can apply to both industrial biotechnology and 226 biopharmaceutical manufacturing (Phaneuf et al., 2019; Sandberg et al., 2019). Likewise, in the case 227 of non-conventional organisms, microbial communities or even those which cannot be cultured in 228 vivo, sequencing enables genome mining providing critical insight and potentially novel enzymes 229 (Seppälä et al., 2017; Panaiotov et al., 2021). Specifically, within biopharmaceuticals, full genome 230 assembly has been challenging for the main workhorse, CHO cells. Within the past 5 years, small 231 molecule real time sequencing paired with extensive scaffolding has generated the most up-to-date 232 Chinese Hamster genome assembly with 97% sequence coverage for direct use in CHO cell 233 applications (Rupp et al., 2018; Hilliard et al., 2020). Continued development of DNA sequencing 234 technology will speed data collection, reduce analysis times, and enable more robust annotation and 235 assembly to enable rapid studies of cellular systems for biochemical production.

236 2.2 Strain/Clone Development

A critical aspect of the metabolic engineering design, build, test cycle is evaluation of strains orclones to identify the best producer. This process can be called strain development for microbial

239 hosts or clone development for mammalian hosts and leverages adaptation and high-throughput 240 screening. These tools find the 'needle in a haystack' cell which may have the appropriate genetic 241 modification, desired enzyme mutation, or even higher tolerance to process impurities. From 242 traditional approaches utilizing random integration of transgenes to more targeted point mutations, 243 screening is required to isolate the desired phenotype and corresponding cell(s). In both industrial 244 biotechnology and biopharmaceutical manufacturing, single cell/strain cloning is critical for 245 consistent growth and biochemical reproducibility. Specifically, within biopharmaceutical 246 manufacturing, clone screening is needed to isolate a homogenous population of favorable product 247 quality attributes such as glycosylation or charge variants. In addition to finding desired rare events, 248 strain/clone development is required to ensure an optimal production host. While traditional 249 strain/cell line development is performed in vivo, recent work is leveraging cell-free or hybrid 250 approaches for biomolecule production (Luro et al., 2019; Silverman et al., 2019). These systems 251 enable construction of complex pathway networks using cell lysates which can be rapidly 252 multiplexed via mixing as compared to extensive cellular engineering (Luro et al., 2019; Silverman et 253 al., 2019). Whether performed in vivo or in vitro, development of cell lines/strains is critical to 254 creating platforms for biomolecule production.

255 2.2.1 Adaptation

Adaptation is a widely used technique which leverages natural or induced mutations to create diverse cellular populations and achieve desired behaviors in industrial biotechnology and biopharmaceutical manufacturing. Often employed when direct mechanisms are not known, adaptation enables cells to be selected based on an externally desirable phenotype. Regularly employed in industrial biotechnology applications, adaptation or adaptive laboratory evolution (ALE) utilizes growth-based selection to improve growth or tolerance to inhibitory compounds. Adaptation is typically performed on shorter time frames with longer studies (30+ growth cycles) designated as ALE. Inhibitory

263 compounds can range from metabolic overflow products to by-products of lignocellulosic biomass 264 and waste carbon sources for recycling (Walker et al., 2019; Wang et al., 2020; Coleman et al., 2023; 265 Mavrommati et al., 2023). Implementation of ALE has increased ethanol tolerance for higher 266 production yields within S. cerevisiae and improved methanol tolerance/conversion in the methanol-267 dependent methylotroph Corynebacterium glutamicum (Walker et al., 2019; Wang et al., 2020). In a 268 similar approach, tolerance to toxic compounds such as phenol and furfural has been achieved in a 269 variety of organism hosts including Escherichia coli, Kluyveromyces marxianus, Yarrowia lipolytica, 270 and Zymomonas mobilis (Shui et al., 2015; Hemansi et al., 2022; Zheng et al., 2022; Coleman et al., 271 2023). In situations where additional mechanisms are known, directed evolution can be applied 272 where targeted mutations are introduced rather than relying on genome wide, random modifications. 273 Directed evolution is commonly deployed for enzymes or other small molecule screening to improve 274 or diversify function (Romero and Arnold, 2009; Arnold, 2018). Regardless of the approach, 275 industrial biotechnology has and continues to leverage the benefits of evolution-based approaches 276 toward achieving production goals.

277 In a parallel manner, the biopharmaceutical manufacturing industry has a long history of 278 applying adaptation to identify cell lines with fast growth in suspension culture and the appropriate 279 selection markers (Dahodwala and Lee, 2019). Specifically, within CHO cells, adaptation schemes 280 with random and chemical mutagenesis have enabled methotrexate and glutamine synthase selection 281 systems which enrich for cell lines with higher expression of the target protein (Dahodwala and Lee, 282 2019; Szkodny and Lee, 2022). In these cases, adaptation created cell lines which can be further 283 manipulated using selection markers and the synthetic biology tools discussed above. For high level 284 production, various cell line types including but not limited to CHO, HEK293, and Vero cells, have 285 been adapted from adherent to suspension growth conditions to support high cell densities (Shridhar 286 et al., 2017; Rourou et al., 2019; Lomba et al., 2021). Adaptation has been deployed to achieve a

287 wide variety of cellular phenotypes in biopharmaceutical manufacturing and industrial

288 biotechnology.

289 2.2.2 High-Throughput Screening

290 Following genetic editing and/or adaptation, screening is required to identify the best production 291 clone or strain. With advances in genetic editing and tools, the population size for screening efforts 292 has dramatically increased while a shorter time from discovery to market is desired requiring the 293 deployment of high-throughput approaches. High-throughput screening includes miniaturization of 294 cell cultures with rapid analytics to measure all appropriate parameters (Leavell et al., 2020). Across 295 biopharmaceutical manufacturing and industrial biotechnology, high product titer, yield and 296 productivity are critical parameters for optimization. Product quality attributes such as post-297 translational modifications are also important parameters for biopharmaceutical screening while 298 industrial biotechnology applications may focus on robust growth using non-traditional substrates as 299 another screening metric. Considering the miniaturization of cell culture, new technologies can 300 monitor cells from μ L to 250 mL scale conditions utilizing microfluidic devices and unique geometry 301 to create accurate scale-down models (Long et al., 2014; Totaro et al., 2021). In a similar fashion, 302 parallelization and development of process analytical technology has enabled screening of larger 303 populations providing additional depth of data critical for making informed decisions (Long et al., 304 2014; Leavell et al., 2020). For rapid analytics, microtiter plates were historically used with 305 fluorescence or spectroscopic measurements (Lai et al., 2013; Long et al., 2014; Zeng et al., 2020). 306 Newer data analytics have enabled biosensor detection, electrochemical based sensors and mass 307 spectrometry approaches depending on the size and characteristics of the analyte. Robotics and 308 advanced automation including liquid handler systems have revolutionized the capacity and speed of 309 high-throughput screening (Zeng et al., 2020). The use of simple, modular components enables these 310 devices to be readily deployed in industrial biotechnology applications to measure online parameters

311 such as temperature, cell density and fluorescence (Wong et al., 2018; Steel et al., 2020). Operating 312 at a 12-25 mL scale, the Chi. Bio system paired with eVOLVER technology can monitor and control 313 multiple miniature reactor vessels from a single computer (Wong et al., 2018; Steel et al., 2020). 314 While this technology has been deployed for continuous evolution applications, it can also be utilized 315 for high-throughput analysis of other parameters critical in strain development (Wong et al., 2018; 316 Steel et al., 2020). In addition, deployment of microfluidics has enabled a variety of screening 317 approaches including live-cell fluorescence imaging (Luro et al., 2019; Bowman et al., 2021). 318 Advanced microfluidic devices can monitor growth of individual cells with isolation of desired 319 clones for both industrial biotechnology and biopharmaceutical applications. These devices use 320 carefully controlled fluid movement to screen and select E. coli in the case of the SIFT system and 321 mammalian cell lines in the Berkeley Lights Beacon system (Delivering digital cell biology at light 322 speed, n.d.; Luro et al., 2019). These developments in high-throughput screening have improved 323 biotechnological production in both industrial and biopharmaceutical manufacturing applications 324 using a variety of production hosts. Bringing detection of key product attributes to real or near-real 325 time enables more rapid and informed decision making about the screening process, from how many 326 clones to keep to identifying the optimal conditions. Adaptation and high-throughput screening serve as critical upstream development techniques which are ubiquitously employed across the industrial 327 328 biotechnology and biopharmaceutical manufacturing industries to identify the most effective cell 329 factories.

330 3 Discussion

Leveraging a strong biological basis, industrial biotechnology and biopharmaceutical manufacturing
 rely on similar concepts, methods and techniques. Additionally, advances in synthetic biology,
 sequencing technology and high-throughput screening have enabled rapid progress in the past 20

334 years resulting in a variety of new products. The biochemicals or even cells themselves which come

335 out of genetic engineering projects have diverse applications related to food, fuel, and human health.

336 3.1 Mechanisms for Cross-Disciplinary Innovation

337 For continued advancement of biotechnology, interdisciplinary collaborations between academics 338 and industry partners are becoming more common. These projects or groups expand the available 339 expertise and enable participants to leverage skills and equipment they might not otherwise be able to 340 access. Within the industrial biotechnology realm, several consortia groups have been created in the 341 past five years to promote and further develop technology. These include the Agile BioFoundry 342 which is a collection of national laboratories focused on bioenergy technologies and BioMADE 343 which is focused on US-based bioindustrial manufacturing (About BioMADE — BioMADE, n.d.; 344 About the Agile BioFoundry, n.d.). The Agile BioFoundry hosts centralized equipment for 345 automated strain building and screening at national laboratories to support academic and industry 346 research projects. These efforts are designed to forward research progress but can also be leveraged 347 as technology and expertise hubs during pandemic crises (Vickers and Freemont, 2022). Unification 348 of several biofoundries into the Global Biofoundry Alliance network connects the Agile BioFoundry 349 and other US-based laboratories with worldwide facilities in Europe, Asia, and Australia (Hillson et 350 al., 2019; Vickers and Freemont, 2022). Likewise, within the biopharmaceutical manufacturing 351 space, two consortia groups known as the Advanced Mammalian Biomanufacturing Innovation 352 Center (AMBIC) and the National Institute for Innovation in Manufacturing Biopharmaceuticals 353 (NIIMBL) were formed within the past eight years (About NIIMBL, n.d.; What is AMBIC? -354 AMBIC, n.d.). Despite variation in size and key stakeholders, these consortia groups host dedicated 355 platforms for innovation and connect research groups across multiple biotechnology subfields. More 356 specifically, toward the goal of improving biomanufacturing and the transition of technologies from 357 ideation to practice, BioMADE and NIIMBL have each released detailed information about

358 Technology Readiness Levels (Kedia et al., 2022; Smanski et al., 2022). These documents create a 359 standard across the industrial biotechnology and biopharmaceutical manufacturing fields which 360 enables clear communication and highlights the steps required to bring new technologies to market 361 (Kedia et al., 2022; Smanski et al., 2022). Additionally, these two sister consortia groups are focused 362 on increasing American manufacturing of biochemicals and biopharmaceuticals while expanding the 363 specialized workforce needed in biotechnological applications. Efforts such as the Agile BioFoundry, 364 AMBIC, BioMADE, and NIIMBL provide a connection between academic and industry researchers 365 to drive faster innovation in biotechnology.

366 The examples provided here represent just a fraction of the activity by organizations and consortia around the globe. While these groups represent tremendous progress in connection of 367 368 academic and industrial researchers, few connect progress in industrial biotechnology and 369 biopharmaceutical manufacturing together despite the commonalities outlined here. Sharing of 370 technologies and best practices for cell line/strain screening across projects would enable more 371 efficient processes for both biopharmaceutical manufacturing and industrial biotechnology 372 applications. The general process development steps are maintained and can be automated in nearly 373 identical ways. Likewise, discovery and construction of synthetic biology tools can be shared for 374 more efficient protein expression, whether as the direct product or key catalyst in biochemical 375 production. With additional collaboration through these groups and new partnerships, future 376 innovation can bridge industrial biotechnology and biopharmaceutical manufacturing to more rapidly 377 engineer cells as efficient biofactories.

379 **3.2 Figures**

- 380 Figure 1: Contributions from advances in the synthetic biology toolbox and strain/clone development
- 381 *enable cellular systems to be used as a biological-based factory spanning products within industrial*
- 382 *biotechnology and biopharmaceutical manufacturing*. Additional collaboration and innovation
- 383 between these two fields can leverage similarities to achieve ambitious goals in biochemical
- 384 production.
- 385
- 386 **3.3 Tables**
- 387 Table 1: Characteristics of industrial biotechnology and biopharmaceutical manufacturing in

388 producing useful biomolecules

Industrial Biotechnology	Biopharmaceuticals				
Extensive synthetic biology tools available	Viral based synthetic biology tools available				
Achieved using bacterial and yeast hosts	Achieved using bacterial, yeast and				
	mammalian hosts				
Well established genome sequences for	Human and CHO genome sequences				
conventional hosts	available within the past 20 years				
Product is small molecules and proteins	Product is large proteins and/or cells (higher				
(lower sale price)	sale price)				
Ability to use and/or detoxify waste carbon	Established production from chemically-				
sources	defined growth media				
Faster growth rates, shorter process length,	Generate complex human-like glycosylation				
Lower risk of contamination	patterns				
Can address global challenges in food, fuel,	Can address global challenges in medicine				
and commodity chemicals					
Selected Examples:	Selected Examples:				
1,3-propanediol, citric acid, biofuels,	Recombinant insulin, monoclonal				
succinic acid, itaconic acid	antibodies, vaccines, cell & gene therapies				

390 Table 2: *Characteristics of selected promoters available within the synthetic biology toolbox for genetic engineering across production hosts*

	Bacterial			Fungal			Mammalian		
	Promoter engineering for native or synthetic promoters leverages transcription factor binding motifs								
<u>Promoter</u> <u>Characteristics</u>	Shorter in sequence			Sequence length can vary			Longer in sequence		
	Poly-cistronic operons			Multi-expression cassette possible using 2A linker sites			Dual expression possible: IRES for small proteins, large proteins require independent cassettes		
	Tunable & inducible expression readily achieved			Tunable & inducible expression readily achieved in <i>S. cerevisisae</i> , more challenging in non-conventional hosts			Limited options for tuning & induction capability		
<u>Selected</u> examples:	T7 promoter	Lac	Trp	SV40	GPD	Eflα (TEF)	Cytomegalovirus (CMV-IE variant)	SV40	Eflα (TEF)
Host organisms	Bacteriophage	Escherichia coli	Escherichia coli	Simian virus expressed in Saccharomyces pombe	Saccharomyces cerevisiae	Yarrowia lipolytica	Cytomegalovirus	Simian Virus	Cricetulus griseus (CHO)
Sequence length	18	61	86	420	655	404	2105	420	1335
Viral or Native Origin	Viral	Native	Native	Viral	Native	Native	Viral	Viral	Native
Reference	(T7 Promoter System, n.d.)	(Czarniecki et al., 1997)	(Bass and Yansura, 2000)	(Jones et al., 1988)	(Redden and Alper, 2015)	(Blazeck et al., 2011)	(Cheng and Alper, 2016)	(Das et al., 1985)	(Wang et al., 2017)

393 4 Additional Requirements

394 Number of Figures: 1

395 Number of Tables: 2

396 Contribution to the field statement:

397 Industrial biotechnology and biopharmaceutical manufacturing leverage biology to enable cellular 398 systems to serve as factories to produce molecules of value to humankind. These biotechnological 399 processes utilize diverse host organisms and address applications from biofuel, polymer building 400 blocks, antibiotics, monoclonal antibodies, and whole cell therapies. In this review, areas of 401 foundational research which are used in both industrial biotechnology and biopharmaceutical 402 manufacturing are discussed. Development of synthetic biology tools, DNA editing, and next 403 generation sequencing has enabled genetic engineering across a variety of production organisms. 404 Likewise, strain and clone development aids in identification of the optimal cells for a given 405 application and utilizes approaches in adaptation, high-throughput screening and automation. 406 Together these methods, tools, and techniques enable cellular systems to be used as biological based 407 factories. While many consortia groups have formed in the past 10 years to support innovation with 408 specific focus areas, more collaboration is needed at the intersection of biopharmaceutical 409 manufacturing and industrial biotechnology to share technological advances and best practices.

410 **5 Conflict of Interest**

The authors declare that the research was conducted in the absence of any commercial or financialrelationships that could be construed as a potential conflict of interest.

413 **6** Author Contributions

414 LC and KL conceptualized the idea. LC wrote the manuscript. All authors contributed to manuscript
415 revision and approved the submitted version.

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418 8 References

- 419 About BioMADE BioMADE (n.d.). Available at: https://www.biomade.org/about-biomade
 420 [Accessed February 18, 2023].
- About NIIMBL (n.d.). Available at: https://niimbl.force.com/s/about-niimbl [Accessed February 18, 2023].
- 423 About the Agile BioFoundry (n.d.). Available at: https://agilebiofoundry.org/about/ [Accessed
 424 February 18, 2023].
- Arnold, F. H. (2018). Directed Evolution: Bringing New Chemistry to Life. *Angewandte Chemie International Edition* 57, 4143–4148. doi: 10.1002/ANIE.201708408.
- Assidi, M., Buhmeida, A., and Budowle, B. (2022). Medicine and health of 21st Century: Not just a
 high biotech-driven solution. *npj Genomic Medicine 2022 7:1* 7, 1–7. doi: 10.1038/s41525-02200336-7.
- Bass, S. H., and Yansura, D. G. (2000). Application of the E. coli trp promoter. *Applied Biochemistry and Biotechnology Part B Molecular Biotechnology* 16, 253–260. doi:
 10.1385/MB:16:3:253/METRICS.
- Blattner, F. R., Plunkett, G., Bloch, C. A., Perna, N. T., Burland, V., Riley, M., et al. (1997). The
 complete genome sequence of Escherichia coli K-12. *Science (1979)* 277, 1453–1462. doi:
 10.1126/SCIENCE.277.5331.1453/ASSET/5AE101DE-877C-44DD-B1763A8D1DA63BFE/ASSETS/GRAPHIC/SE3275565002.JPEG.
- Blazeck, J., Liu, L., Redden, H., and Alper, H. (2011). Tuning Gene Expression in Yarrowia
 lipolytica by a Hybrid Promoter Approach. *Appl Environ Microbiol* 77, 7905. doi:
 10.1128/AEM.05763-11.
- Bowman, E. K., Wagner, J. M., Yuan, S.-F., Deaner, M., Palmer, C. M., D'Oelsnitz, S., et al. (2021).
 Sorting for secreted molecule production using a biosensor-in-microdroplet approach. *Proc Natl Acad Sci U S A* 118. doi: 10.1073/pnas.2106818118.
- Brabender, M., Hussain, M. S., Rodriguez, G., and Blenner, M. A. (2018). Urea and urine are a
 viable and cost-effective nitrogen source for Yarrowia lipolytica biomass and lipid
 accumulation. *Appl Microbiol Biotechnol* 102, 2313–2322. doi: 10.1007/S00253-018-8769Z/TABLES/4.
- Cai, G., Lin, Z., and Shi, S. (2022). Development and expansion of the CRISPR/Cas9 toolboxes for
 powerful genome engineering in yeast. *Enzyme Microb Technol* 159, 110056. doi:
 10.1016/J.ENZMICTEC.2022.110056.
- 450 Carbonell, P., Jervis, A. J., Robinson, C. J., Yan, C., Dunstan, M., Swainston, N., et al. (2018). An
 451 automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine
 452 chemicals. *Communications Biology 2018 1:1*, 1–10. doi: 10.1038/s42003-018-0076-9.

- 453 Carbonell, P., le Feuvre, R., Takano, E., and Scrutton, N. S. (2020). In silico design and automated
- learning to boost next-generation smart biomanufacturing. *Synth Biol* 5. doi:
 10.1093/SYNBIO/YSAA020.
- Chen, G. Q., and Jiang, X. R. (2018). Next generation industrial biotechnology based on
 extremophilic bacteria. *Curr Opin Biotechnol* 50, 94–100. doi: 10.1016/J.COPBIO.2017.11.016.
- Chen, Y., Ho, J. M. L., Shis, D. L., Gupta, C., Long, J., Wagner, D. S., et al. (2018). Tuning the
 dynamic range of bacterial promoters regulated by ligand-inducible transcription factors. *Nature Communications 2017 9:1 9*, 1–8. doi: 10.1038/s41467-017-02473-5.
- Cheng, J. K., and Alper, H. S. (2016). Transcriptomics-Guided Design of Synthetic Promoters for a
 Mammalian System. ACS Synth Biol 5, 1455–1465. doi: 10.1021/ACSSYNBIO.6B00075.
- 463 Cheng, J. K., Morse, N. J., Wagner, J. M., Tucker, S. K., and Alper, H. S. (2019). Design and
 464 Evaluation of Synthetic Terminators for Regulating Mammalian Cell Transgene Expression.
 465 ACS Synth Biol 8, 1263–1275. doi:
- 466 10.1021/ACSSYNBIO.8B00285/ASSET/IMAGES/LARGE/SB-2018-00285Y_0004.JPEG.
- Cheng, K. K., Zhao, X. B., Zeng, J., Wu, R. C., Xu, Y. Z., Liu, D. H., et al. (2012). Downstream
 processing of biotechnological produced succinic acid. *Appl Microbiol Biotechnol* 95, 841–850.
 doi: 10.1007/S00253-012-4214-X/FIGURES/1.
- 470 Coleman, S. M., Cordova, L. T., Lad, B. C., Ali, S. A., Ramanan, E., Collett, J. R., et al. (2023).
 471 Evolving tolerance of Yarrowia lipolytica to hydrothermal liquefaction aqueous phase waste.
 472 Appl Microbiol Biotechnol, 1–15. doi: 10.1007/S00253-023-12393-8/TABLES/2.
- 473 Copeland, M. F., Politz, M. C., and Pfleger, B. F. (2014). Application of TALEs, CRISPR/Cas and
 474 sRNAs as trans-acting regulators in prokaryotes. *Curr Opin Biotechnol* 29, 46–54. doi:
 475 10.1016/J.COPBIO.2014.02.010.
- 476 Cordova, L. T., Lad, B. C., Ali, S. A., Schmidt, A. J., Billing, J. M., Pomraning, K., et al. (2020).
 477 Valorizing a hydrothermal liquefaction aqueous phase through co-production of chemicals and
 478 lipids using the oleaginous yeast Yarrowia lipolytica. *Bioresour Technol* 313. doi:
 479 10.1016/j.biortech.2020.123639.
- 480 Curran, K. A., and Alper, H. S. (2012). Expanding the chemical palate of cells by combining systems
 481 biology and metabolic engineering. *Metab Eng* 14, 289–297. doi:
 482 10.1016/J.YMBEN.2012.04.006.
- 483 Curran, K. A., Karim, A. S., Gupta, A., and Alper, H. S. (2013). Use of expression-enhancing
 484 terminators in Saccharomyces cerevisiae to increase mRNA half-life and improve gene
 485 expression control for metabolic engineering applications. *Metab Eng* 19, 88–97. doi:
 486 10.1016/J.YMBEN.2013.07.001.
- 487 Czarniecki, D., Noel, R. J., and Reznikoff, W. S. (1997). The -45 region of the Escherichia coli lac
 488 promoter: CAP-dependent and CAP-independent transcription. *J Bacteriol* 179, 423. doi:
 489 10.1128/JB.179.2.423-429.1997.

- 490 Dahodwala, H., and Lee, K. H. (2019). The fickle CHO: a review of the causes, implications, and
 491 potential alleviation of the CHO cell line instability problem. *Curr Opin Biotechnol* 60, 128–
 492 125 Line 1016/L COPPLO 2010 01 011
- 492 137. doi: 10.1016/J.COPBIO.2019.01.011.
- 493 Das, G. C., Niyogi, S. K., and Salzan, N. P. (1985). SV40 Promoters and Their Regulation. *Prog* 494 *Nucleic Acid Res Mol Biol* 32, 217–236. doi: 10.1016/S0079-6603(08)60349-9.
- 495 Datar, R., and Rosén, C.-G. (2020). Downstream Process Economics. Separation Processes in
 496 Biotechnology, 741–794. doi: 10.1201/9781003066392-25.
- 497 Deaner, M., and Alper, H. S. (2019). Enhanced scale and scope of genome engineering and
 498 regulation using CRISPR/Cas in Saccharomyces cerevisiae. *FEMS Yeast Res* 19, 76. doi:
 499 10.1093/FEMSYR/FOZ076.
- Deaner, M., Mejia, J., and Alper, H. S. (2017). Enabling Graded and Large-Scale Multiplex of
 Desired Genes Using a Dual-Mode dCas9 Activator in Saccharomyces cerevisiae. ACS Synth
 Biol 6, 1931–1943. doi:
- 503 10.1021/ACSSYNBIO.7B00163/SUPPL_FILE/SB7B00163_SI_001.PDF.
- 504 Decoene, T., De Paepe, B., Maertens, J., Coussement, P., Peters, G., De Maeseneire, S. L., et al.
 505 (2017). Standardization in synthetic biology: an engineering discipline coming of age.
 506 https://doi.org/10.1080/07388551.2017.1380600 38, 647–656. doi:
 507 10.1080/07388551.2017.1380600.
- 508 Delivering digital cell biology at light speed (n.d.). Available at:
 509 https://www.nature.com/articles/d43747-020-00770-5 [Accessed April 17, 2023].
- Doudna, J. A., and Charpentier, E. (2014). The new frontier of genome engineering with CRISPR Cas9. *Science (1979)* 346. doi: 10.1126/SCIENCE.1258096.
- 512 Dupont-Inglis, J., and Borg, A. (2018). Destination bioeconomy The path towards a smarter, more
 513 sustainable future. *N Biotechnol* 40, 140–143. doi: 10.1016/J.NBT.2017.05.010.
- 514 Ebersbach, H., Geisse, S., Vincent, K. J., Zurini, M., Mcneely, P. M., Naranjo, A. N., et al. (2012).
 515 The sweet tooth of biopharmaceuticals: Importance of recombinant protein glycosylation
 516 analysis. *Biotechnol J* 7, 1462–1472. doi: 10.1002/BIOT.201200078.
- 517 Engel, S. R., Dietrich, F. S., Fisk, D. G., Binkley, G., Balakrishnan, R., Costanzo, M. C., et al.
 518 (2014). The Reference Genome Sequence of Saccharomyces cerevisiae: Then and Now. *G3*:
 519 *Genes, Genomes, Genetics* 4, 389–398. doi: 10.1534/G3.113.008995/-/DC1/TABLES1.XLS.
- Engstrom, M. D., and Pfleger, B. F. (2017). Transcription control engineering and applications in
 synthetic biology. *Synth Syst Biotechnol* 2, 176–191. doi: 10.1016/J.SYNBIO.2017.09.003.
- Gaszner, M., and Felsenfeld, G. (2006). Insulators: exploiting transcriptional and epigenetic
 mechanisms. *Nature Reviews Genetics 2006 7:9* 7, 703–713. doi: 10.1038/nrg1925.
- Gordillo Sierra, A. R., Amador-Castro, L. F., Ramírez-Partida, A. E., García-Cayuela, T., Carrillo Nieves, D., and Alper, H. S. (2022). Valorization of Caribbean Sargassum biomass as a source

- of alginate and sugars for de novo biodiesel production. *J Environ Manage* 324, 116364. doi:
 10.1016/J.JENVMAN.2022.116364.
- Grada, A., and Weinbrecht, K. (2013). Next-Generation Sequencing: Methodology and Application.
 Journal of Investigative Dermatology 133, 1–4. doi: 10.1038/JID.2013.248.
- Gurdo, N., Volke, D. C., and Nikel, P. I. (2022). Merging automation and fundamental discovery into
 the design-build-test-learn cycle of nontraditional microbes. *Trends Biotechnol* 40, 1148–1159.
 doi: 10.1016/J.TIBTECH.2022.03.004.
- Hafner, A., and Boettiger, A. (2022). The spatial organization of transcriptional control. *Nature Reviews Genetics 2022 24:1* 24, 53–68. doi: 10.1038/s41576-022-00526-0.
- Halperin, S. O., Tou, C. J., Wong, E. B., Modavi, C., Schaffer, D. V., and Dueber, J. E. (2018).
 CRISPR-guided DNA polymerases enable diversification of all nucleotides in a tunable
 window. *Nature 2018 560:7717 560*, 248–252. doi: 10.1038/s41586-018-0384-8.
- Hamaker, N. K., and Lee, K. H. (2023). High-efficiency and multilocus targeted integration in CHO
 cells using CRISPR-mediated donor nicking and DNA repair inhibitors. *Biotechnol Bioeng*. doi:
 10.1002/BIT.28393.
- Hemansi, Himanshu, Patel, A. K., Saini, J. K., and Singhania, R. R. (2022). Development of multiple
 inhibitor tolerant yeast via adaptive laboratory evolution for sustainable bioethanol production. *Bioresour Technol* 344, 126247. doi: 10.1016/J.BIORTECH.2021.126247.
- Hilliard, W., MacDonald, M. L., and Lee, K. H. (2020). Chromosome-scale scaffolds for the Chinese
 hamster reference genome assembly to facilitate the study of the CHO epigenome. *Biotechnol Bioeng* 117, 2331–2339. doi: 10.1002/BIT.27432.
- 547 Hillson, N., Caddick, M., Cai, Y., Carrasco, J. A., Chang, M. W., Curach, N. C., et al. (2019).
 548 Building a global alliance of biofoundries. *Nature Communications 2019 10:1* 10, 1–4. doi: 549 10.1038/s41467-019-10079-2.
- Houston, J. G., and Banks, M. (1997). The chemical-biological interface: developments in automated
 and miniaturised screening technology. *Curr Opin Biotechnol* 8, 734–740. doi: 10.1016/S09581669(97)80128-0.
- Hu, T., Chitnis, N., Monos, D., and Dinh, A. (2021). Next-generation sequencing technologies: An
 overview. *Hum Immunol* 82, 801–811. doi: 10.1016/J.HUMIMM.2021.02.012.
- Jagschies, G. (2018a). Brief Review of the Biopharmaceutical and Vaccine Industry.
 Biopharmaceutical Processing: Development, Design, and Implementation of Manufacturing Processes, 33–58. doi: 10.1016/B978-0-08-100623-8.00002-5.
- Jagschies, G. (2018b). Selected Biotherapeutics Overview. *Biopharmaceutical Processing: Development, Design, and Implementation of Manufacturing Processes*, 59–72. doi:
 10.1016/B978-0-08-100623-8.00003-7.

- Johari, Y. B., Brown, A. J., Alves, C. S., Zhou, Y., Wright, C. M., Estes, S. D., et al. (2019). CHO
 genome mining for synthetic promoter design. *J Biotechnol* 294, 1–13. doi:
 10.1016/J.JBIOTEC.2019.01.015.
- Jones, R. H., Moreno, S., Nurse, P., and Jones, N. C. (1988). Expression of the SV40 promoter in
 fission yeast: Identification and characterization of an AP-1-like factor. *Cell* 53, 659–667. doi:
 10.1016/0092-8674(88)90581-8.
- Jungbauer, A. (2013). Continuous downstream processing of biopharmaceuticals. *Trends Biotechnol* 31, 479–492. doi: 10.1016/J.TIBTECH.2013.05.011.
- Kedia, S. B., Baker, J. C., Carbonell, R. G., Lee, K. H., Roberts, C. J., Erickson, J., et al. (2022).
 Biomanufacturing readiness levels [BRL]—A shared vocabulary for biopharmaceutical
 technology development and commercialization. *Biotechnol Bioeng* 119, 3526–3536. doi:
 10.1002/BIT.28227.
- Kommoji, S., Gopinath, M., Satya Sagar, P., Yuvaraj, D., Iyyappan, J., Jaya Varsha, A., et al. (2021).
 Lipid bioproduction from delignified native grass (Cyperus distans) hydrolysate by Yarrowia *Bioresour Technol* 324, 124659. doi: 10.1016/J.BIORTECH.2020.124659.
- Kumar, R., Ghosh, A. K., and Pal, P. (2019). Sustainable Production of Biofuels through Membrane Integrated Systems. *https://doi.org/10.1080/15422119.2018.1562942* 49, 207–228. doi:
 10.1080/15422119.2018.1562942.
- Lad, B. C., Coleman, S. M., and Alper, H. S. (2022). Microbial valorization of underutilized and
 nonconventional waste streams. *J Ind Microbiol Biotechnol* 49, 56. doi:
 10.1093/JIMB/KUAB056.
- Lai, T., Yang, Y., and Ng, S. K. (2013). Advances in Mammalian Cell Line Development
 Technologies for Recombinant Protein Production. *Pharmaceuticals 2013, Vol. 6, Pages 579-*603 6, 579–603. doi: 10.3390/PH6050579.
- Leavell, M. D., Singh, A. H., and Kaufmann-Malaga, B. B. (2020). High-throughput screening for
 improved microbial cell factories, perspective and promise. *Curr Opin Biotechnol* 62, 22–28.
 doi: 10.1016/J.COPBIO.2019.07.002.
- Lindskog, E. K., Fischer, S., Wenger, T., and Schulz, P. (2018). Host Cells. *Biopharmaceutical Processing: Development, Design, and Implementation of Manufacturing Processes*, 111–130.
 doi: 10.1016/B978-0-08-100623-8.00006-2.
- Litcofsky, K. D., Afeyan, R. B., Krom, R. J., Khalil, A. S., and Collins, J. J. (2012). Iterative plug and-play methodology for constructing and modifying synthetic gene networks. *Nat Methods* 9, 1077. doi: 10.1038/NMETH.2205.
- Lomba, A. L. O., Tirapelle, M. C., Biaggio, R. T., Abreu-Neto, M. S., Covas, D. T., Picanço-Castro,
 V., et al. (2021). Serum-Free Suspension Adaptation of HEK-293T Cells: Basis for Large-Scale
 Biopharmaceutical Production. *Brazilian Archives of Biology and Technology* 64, 2021. doi:
 10.1590/1678-4324-2021200817.

- Long, Q., Liu, X., Yang, Y., Li, L., Harvey, L., McNeil, B., et al. (2014). The development and
 application of high throughput cultivation technology in bioprocess development. *J Biotechnol*192, 323–338. doi: 10.1016/J.JBIOTEC.2014.03.028.
- Luro, S., Potvin-Trottier, L., Okumus, B., and Paulsson, J. (2019). Isolating live cells after highthroughput, long-term, time-lapse microscopy. *Nature Methods 2019 17:1* 17, 93–100. doi: 10.1038/s41592-019-0620-7.
- Mans, R., van Rossum, H. M., Wijsman, M., Backx, A., Kuijpers, N. G. A., van den Broek, M., et al.
 (2015). CRISPR/Cas9: a molecular Swiss army knife for simultaneous introduction of multiple
 genetic modifications in Saccharomyces cerevisiae. *FEMS Yeast Res* 15, 1–15. doi:
 10.1093/FEMSYR/FOV004.
- Mavrommati, M., Papanikolaou, S., and Aggelis, G. (2023). Improving ethanol tolerance of
 Saccharomyces cerevisiae through adaptive laboratory evolution using high ethanol
 concentrations as a selective pressure. *Process Biochemistry* 124, 280–289. doi:
 10.1016/J.PROCBIO.2022.11.027.
- McCombie, W. R., McPherson, J. D., and Mardis, E. R. (2019). Next-Generation Sequencing
 Technologies. *Cold Spring Harb Perspect Med* 9, a036798. doi:
 10.1101/CSHPERSPECT.A036798.
- McGraw, C. E., Peng, D., and Sandoval, N. R. (2020). Synthetic biology approaches: the next tools
 for improved protein production from CHO cells. *Curr Opin Chem Eng* 30, 26–33. doi:
 10.1016/J.COCHE.2020.06.003.
- McLaughlin, J. A., Myers, C. J., Zundel, Z., Mlslrll, G., Zhang, M., Ofiteru, I. D., et al. (2018).
 SynBioHub: A Standards-Enabled Design Repository for Synthetic Biology. ACS Synth Biol 7,
 682–688. doi: 10.1021/ACSSYNBIO.7B00403/ASSET/IMAGES/LARGE/SB-2017004037_0006.JPEG.
- Mehta, A. (2019). Downstream Processing for Biopharmaceuticals Recovery. 163–190. doi:
 10.1007/978-3-030-01881-8_6.
- Moore, R., Chandrahas, A., and Bleris, L. (2014). Transcription activator-like effectors: A toolkit for
 synthetic biology. *ACS Synth Biol* 3, 708–716. doi:
 10.1021/SB400137B/ASSET/IMAGES/LARGE/SB-2013-00137B 0004.JPEG.
- 626 10.1021/SB400137/B/ASSET/IMAGES/LARGE/SB-2013-00137/B_0004.JPEG.
- Morse, N. J., Gopal, M. R., Wagner, J. M., and Alper, H. S. (2017). Yeast Terminator Function Can
 Be Modulated and Designed on the Basis of Predictions of Nucleosome Occupancy. ACS Synth
 Biol 6, 2086–2095. doi:
- 630 10.1021/ACSSYNBIO.7B00138/SUPPL_FILE/SB7B00138_SI_001.PDF.
- Moshelion, M., and Altman, A. (2015). Current challenges and future perspectives of plant and
 agricultural biotechnology. *Trends Biotechnol* 33, 337–342. doi:
 10.1016/J.TIBTECH.2015.03.001.
- Nielsen, J., Tillegreen, C. B., and Petranovic, D. (2022). Innovation trends in industrial
 biotechnology. *Trends Biotechnol* 40, 1160–1172. doi: 10.1016/J.TIBTECH.2022.03.007.

- Nurk, S., Koren, S., Rhie, A., Rautiainen, M., Bzikadze, A. v., Mikheenko, A., et al. (2022). The
 complete sequence of a human genome. *Science (1979)* 376, 44–53. doi:
- 638 10.1126/SCIENCE.ABJ6987.
- Panaiotov, S., Hodzhev, Y., Tsafarova, B., Tolchkov, V., and Kalfin, R. (2021). Culturable and NonCulturable Blood Microbiota of Healthy Individuals. *Microorganisms 2021, Vol. 9, Page 1464*9, 1464. doi: 10.3390/MICROORGANISMS9071464.
- Perin, G., and Jones, P. R. (2019). Economic feasibility and long-term sustainability criteria on the
 path to enable a transition from fossil fuels to biofuels. *Curr Opin Biotechnol* 57, 175–182. doi:
 10.1016/J.COPBIO.2019.04.004.
- Peters, J. M., Silvis, M. R., Zhao, D., Hawkins, J. S., Gross, C. A., and Qi, L. S. (2015). Bacterial
 CRISPR: accomplishments and prospects. *Curr Opin Microbiol* 27, 121–126. doi:
 10.1016/J.MIB.2015.08.007.
- Petzold, C. J., Chan, L. J. G., Nhan, M., and Adams, P. D. (2015). Analytics for metabolic
 engineering. *Front Bioeng Biotechnol* 3, 135. doi: 10.3389/FBIOE.2015.00135/BIBTEX.
- Phaneuf, P. v., Gosting, D., Palsson, B. O., and Feist, A. M. (2019). ALEdb 1.0: a database of
 mutations from adaptive laboratory evolution experimentation. *Nucleic Acids Res* 47, D1164–
 D1171. doi: 10.1093/NAR/GKY983.
- Ran, F. A., Hsu, P. D., Lin, C. Y., Gootenberg, J. S., Konermann, S., Trevino, A. E., et al. (2013).
 XDouble nicking by RNA-guided CRISPR cas9 for enhanced genome editing specificity. *Cell*154, 1380–1389. doi: 10.1016/j.cell.2013.08.021.
- Redden, H., and Alper, H. S. (2015). The development and characterization of synthetic minimal
 yeast promoters. *Nature Communications 2015 6:1* 6, 1–9. doi: 10.1038/ncomms8810.
- Romero, P. A., and Arnold, F. H. (2009). Exploring protein fitness landscapes by directed evolution.
 Nature Reviews Molecular Cell Biology 2009 10:12 10, 866–876. doi: 10.1038/nrm2805.
- Rourou, S., ben Zakkour, M., and Kallel, H. (2019). Adaptation of Vero cells to suspension growth
 for rabies virus production in different serum free media. *Vaccine* 37, 6987–6995. doi:
 10.1016/J.VACCINE.2019.05.092.
- Rupp, O., MacDonald, M. L., Li, S., Dhiman, H., Polson, S., Griep, S., et al. (2018). A reference
 genome of the Chinese hamster based on a hybrid assembly strategy. *Biotechnol Bioeng* 115,
 2087–2100. doi: 10.1002/BIT.26722.
- Saccharomyces Genome Database | SGD (n.d.). Available at: https://www.yeastgenome.org/
 [Accessed January 31, 2023].
- Sandberg, T. E., Salazar, M. J., Weng, L. L., Palsson, B. O., and Feist, A. M. (2019). The emergence
 of adaptive laboratory evolution as an efficient tool for biological discovery and industrial
 biotechnology. *Metab Eng* 56, 1–16. doi: 10.1016/J.YMBEN.2019.08.004.
- Satyanarayana, T., Kawarabayasi, Y., and Littlechild, J. (2013). Thermophilic microbes in
 environmental and industrial biotechnology: Biotechnology of thermophiles. *Thermophilic*

- 673 *Microbes in Environmental and Industrial Biotechnology: Biotechnology of Thermophiles*, 1– 674 956. doi: 10.1007/978-94-007-5899-5/COVER.
- Schultenkämper, K., Brito, L. F., López, M. G., Brautaset, T., and Wendisch, V. F. (2019).
 Establishment and application of CRISPR interference to affect sporulation, hydrogen peroxide
 detoxification, and mannitol catabolism in the methylotrophic thermophile Bacillus
 methanolicus. *Appl Microbiol Biotechnol* 103, 5879–5889. doi: 10.1007/S00253-019-099078/FIGURES/6.
- Sengupta, S., Bhattacharya, D., and Mukhopadhyay, M. (2020). Downstream processing of biofuel.
 Genetic and Metabolic Engineering for Improved Biofuel Production from Lignocellulosic Biomass, 47–62. doi: 10.1016/B978-0-12-817953-6.00004-X.
- Seppälä, S., Wilken, S. E., Knop, D., Solomon, K. v., and O'Malley, M. A. (2017). The importance
 of sourcing enzymes from non-conventional fungi for metabolic engineering and biomass
 breakdown. *Metab Eng* 44, 45–59. doi: 10.1016/J.YMBEN.2017.09.008.
- Shlyueva, D., Stampfel, G., and Stark, A. (2014). Transcriptional enhancers: from properties to
 genome-wide predictions. *Nature Reviews Genetics 2014 15:4* 15, 272–286. doi:
 10.1038/nrg3682.
- 689 Shridhar, S., Klanert, G., Auer, N., Hernandez-Lopez, I., Kańduła, M. M., Hackl, M., et al. (2017).
 690 Transcriptomic changes in CHO cells after adaptation to suspension growth in protein-free
 691 medium analysed by a species-specific microarray. *J Biotechnol* 257, 13–21. doi:
 692 10.1016/J.JBIOTEC.2017.03.012.
- Shui, Z. X., Qin, H., Wu, B., Ruan, Z. yong, Wang, L. shang, Tan, F. R., et al. (2015). Adaptive
 laboratory evolution of ethanologenic Zymomonas mobilis strain tolerant to furfural and acetic
 acid inhibitors. *Appl Microbiol Biotechnol* 99, 5739–5748. doi: 10.1007/S00253-015-6616Z/TABLES/2.
- 697 Silverman, A. D., Karim, A. S., and Jewett, M. C. (2019). Cell-free gene expression: an expanded
 698 repertoire of applications. *Nature Reviews Genetics 2019 21:3* 21, 151–170. doi:
 699 10.1038/s41576-019-0186-3.
- Slatko, B. E., Gardner, A. F., and Ausubel, F. M. (2018). Overview of Next-Generation Sequencing
 Technologies. *Curr Protoc Mol Biol* 122, e59. doi: 10.1002/CPMB.59.
- Smanski, M. J., Aristidou, A., Carruth, R., Erickson, J., Gordon, M., Kedia, S. B., et al. (2022).
 Bioindustrial manufacturing readiness levels (BioMRLs) as a shared framework for measuring and communicating the maturity of bioproduct manufacturing processes. *J Ind Microbiol Biotechnol* 49, 22. doi: 10.1093/JIMB/KUAC022.
- Spahn, P. N., Zhang, X., Hu, Q., Lu, H., Hamaker, N. K., Hefzi, H., et al. (2022). Restoration of
 DNA repair mitigates genome instability and increases productivity of Chinese hamster ovary
 Biotechnol Bioeng 119, 963–982. doi: 10.1002/BIT.28016.
- Srinivasan, V., Kriete, A., Sacan, A., and Michal Jazwinski, S. (2010). Comparing the Yeast
 Retrograde Response and NF-kB Stress Responses: Implications for Aging. *Aging Cell* 9, 933.
 doi: 10.1111/J.1474-9726.2010.00622.X.

- Steel, H., Habgood, R., Kelly, C., and Papachristodoulou, A. (2020). In situ characterisation and
 manipulation of biological systems with Chi.Bio. *PLoS Biol* 18, e3000794. doi:
 10.1371/JOURNAL.PBIO.3000794.
- Stovicek, V., Holkenbrink, C., and Borodina, I. (2017). CRISPR/Cas system for yeast genome
 engineering: advances and applications. *FEMS Yeast Res* 17, 30. doi:
 10.1093/FEMSYR/FOX030.
- Szkodny, A. C., and Lee, K. H. (2022). Biopharmaceutical Manufacturing: Historical Perspectives
 and Future Directions. *https://doi.org/10.1146/annurev-chembioeng-092220-125832* 13, 141–
 165. doi: 10.1146/ANNUREV-CHEMBIOENG-092220-125832.
- T7 Promoter System (n.d.). Available at: https://www.sigmaaldrich.com/US/en/technical documents/technical-article/genomics/cloning-and-expression/t7-promoter-system [Accessed
 February 13, 2023].
- Thorwall, S., Schwartz, C., Chartron, J. W., and Wheeldon, I. (2020). Stress-tolerant non conventional microbes enable next-generation chemical biosynthesis. *Nature Chemical Biology* 2020 16:2 16, 113–121. doi: 10.1038/s41589-019-0452-x.
- Totaro, D., Radoman, B., Schmelzer, B., Rothbauer, M., Steiger, M. G., Mayr, T., et al. (2021).
 Microscale Perfusion-Based Cultivation for Pichia pastoris Clone Screening Enables
 Accelerated and Optimized Recombinant Protein Production Processes. *Biotechnol J* 16,
 2000215. doi: 10.1002/BIOT.202000215.
- Urnov, F. D., Rebar, E. J., Holmes, M. C., Zhang, H. S., and Gregory, P. D. (2010). Genome editing
 with engineered zinc finger nucleases. *Nature Reviews Genetics 2010 11:9* 11, 636–646. doi:
 10.1038/nrg2842.
- Vickers, C. E., and Freemont, P. S. (2022). Pandemic preparedness: synthetic biology and publicly
 funded biofoundries can rapidly accelerate response time. *Nature Communications 2022 13:1*13, 1–4. doi: 10.1038/s41467-022-28103-3.
- Walker, C., Ryu, S., and Trinh, C. T. (2019). Exceptional solvent tolerance in Yarrowia lipolytica is
 enhanced by sterols. *Metab Eng* 54, 83–95. doi: 10.1016/J.YMBEN.2019.03.003.
- Wang, X., Xu, Z., Tian, Z., Zhang, X., Xu, D., Li, Q., et al. (2017). The EF-1α promoter maintains
 high-level transgene expression from episomal vectors in transfected CHO-K1 cells. *J Cell Mol Med* 21, 3044. doi: 10.1111/JCMM.13216.
- Wang, Y., Fan, L., Tuyishime, P., Liu, J., Zhang, K., Gao, N., et al. (2020). Adaptive laboratory
 evolution enhances methanol tolerance and conversion in engineered Corynebacterium
 glutamicum. *Communications Biology 2020 3:1* 3, 1–15. doi: 10.1038/s42003-020-0954-9.
- What is AMBIC? AMBIC (n.d.). Available at: https://www.ambic.org/about-us/ [Accessed
 February 18, 2023].
- Wong, B. G., Mancuso, C. P., Kiriakov, S., Bashor, C. J., and Khalil, A. S. (2018). Precise,
 automated control of conditions for high-throughput growth of yeast and bacteria with
 eVOLVER. *Nature Biotechnology 2018 36*:7 36, 614–623. doi: 10.1038/nbt.4151.

- Wongsirichot, P., Gonzalez-Miquel, M., and Winterburn, J. (2022). Recent advances in rapeseed
 meal as alternative feedstock for industrial biotechnology. *Biochem Eng J* 180, 108373. doi:
 10.1016/J.BEJ.2022.108373.
- Wright, D. A., Li, T., Yang, B., and Spalding, M. H. (2014). TALEN-mediated genome editing:
 prospects and perspectives. *Biochemical Journal* 462, 15–24. doi: 10.1042/BJ20140295.
- Yang, O., Qadan, M., and Ierapetritou, M. (2020). Economic Analysis of Batch and Continuous
 Biopharmaceutical Antibody Production: a Review. *J Pharm Innov* 15, 182–200. doi:
 10.1007/S12247-018-09370-4/FIGURES/3.
- Yeoh, J. W., Swainston, N., Vegh, P., Zulkower, V., Carbonell, P., Holowko, M. B., et al. (2021).
 SynBiopython: an open-source software library for Synthetic Biology. *Synth Biol* 6. doi:
 10.1093/SYNBIO/YSAB001.
- Yin, J., Chen, J. C., Wu, Q., and Chen, G. Q. (2015). Halophiles, coming stars for industrial
 biotechnology. *Biotechnol Adv* 33, 1433–1442. doi: 10.1016/J.BIOTECHADV.2014.10.008.

Yuan, J. S., Pavlovich, M. J., Ragauskas, A. J., and Han, B. (2022). Biotechnology for a sustainable
future: biomass and beyond. *Trends Biotechnol* 40, 1395–1398. doi:
10.1016/j.tibtech.2022.09.020.

- Zeng, W., Guo, L., Xu, S., Chen, J., and Zhou, J. (2020). High-Throughput Screening Technology in
 Industrial Biotechnology. *Trends Biotechnol* 38, 888–906. doi:
 10.1016/J.TIBTECH.2020.01.001.
- Zhang, C., and Hua, Q. (2016). Applications of genome-scale metabolic models in biotechnology and
 systems medicine. *Front Physiol* 6, 413. doi: 10.3389/FPHYS.2015.00413/BIBTEX.

Zheng, Y., Kong, S., Luo, S., Chen, C., Cui, Z., Sun, X., et al. (2022). Improving Furfural Tolerance
of Escherichia coli by Integrating Adaptive Laboratory Evolution with CRISPR-Enabled
Trackable Genome Engineering (CREATE). ACS Sustain Chem Eng 10, 2318–2330. doi:
10.1021/ACSSUSCHEMENG.1C05783/SUPPL FILE/SC1C05783 SI 004.XLSX.

