

1 **Theoretical design of a space bioprocessing system to produce recombinant proteins**

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12 **Abstract**

13 Space-based biomanufacturing has the potential to improve the sustainability of deep space
14 exploration. To advance biomanufacturing, bioprocessing systems need to be developed for
15 space applications. Here, commercial technologies were assessed to design space bioprocessing
16 systems to supply a liquid amine carbon dioxide scrubber with active carbonic anhydrase
17 produced recombinantly. Design workflows encompassed biomass dewatering of 1 L
18 *Escherichia coli* cultures through to recombinant protein purification. Equivalent system mass
19 (ESM) analyses had limited utility for selecting specific technologies. Instead, bioprocessing
20 system designs focused on minimizing complexity and enabling system versatility. Three
21 designs that differed in biomass dewatering and protein purification approaches had nearly
22 equivalent ESM of 357-522 kg eq. Values from the system complexity metric (SCM), technology
23 readiness level (TRL), and degree of crew assistance metric identified a simpler, less costly, and
24 easier to operate design for automated biomass dewatering, cell lysis, and protein affinity
25 purification.

26

27 Introduction

28 Liquid amine scrubbing is a promising technology to capture CO₂ produced during
29 crewed extraterrestrial missions^{1,2}. In this system, a CO₂-rich gas stream is passed over an
30 organic liquid amine which absorbs the CO₂. Pure CO₂ is recovered by raising the solution
31 temperature, which regenerates the amine for subsequent capture at low temperature³. An
32 efficient liquid amine system should have fast absorption kinetics to reduce system size as well
33 as a low desorption temperature to minimize energy inputs. Different liquid amines either have
34 fast absorption kinetics or low desorption temperature but not both simultaneously⁴. Carbonic
35 anhydrase is an enzyme that catalyzes the interconversion of CO₂ and HCO₃⁻ to increase the CO₂
36 sequestration in some liquid amine systems. Addition of carbonic anhydrase enhances the
37 absorption kinetics of liquid amines with a low desorption temperature enabling both reduced
38 size and improved energy efficiency of CO₂ scrubbing⁵⁻⁷.

39 Implementing an enzyme-assisted liquid amine CO₂ scrubber requires a time-course
40 supply of carbonic anhydrase. On long-duration space missions close to Earth, this requirement
41 could be met by resupply or long-term storage. However, resupply is not an economical option
42 for many deep space missions like those planned for Mars. Purified enzymes are typically
43 sensitive to room temperature conditions and require ultra low storage temperatures to retain
44 activity long-term. Not all enzymes retain activity in low temperature storage and in situ
45 production of enzymes would mitigate risks of relying solely on low temperature storage of
46 proteins with limited stability. Space biomanufacturing systems have the potential to produce
47 enzymes and other biological materials using in situ resources during a Mars mission⁸⁻¹³. Space

48 systems must minimize cost and crew time, while assuring astronaut safety and addressing
49 effects of increased radiation and reduced gravity¹⁴⁻¹⁷.

50 Previous space biomanufacturing studies and reviews evaluated large-scale mission
51 design^{8,18,19}, microbial growth kinetics²⁰, and bioreactor design²⁰⁻²². Extracting products of
52 interest at sufficient quality is equally essential to develop biomanufacturing. Systems such as
53 Wetlab-2 or the Gene Expression Measurement Module (GEMM) illustrate the challenge of
54 adapting biological sample processing for RNA extraction and molecular analysis in the
55 microgravity environment^{23,24}. In these systems, the sample mass and volume processed was
56 small with the goal of providing biological inputs for analytical experiments^{23,24}. Future space
57 biomanufacturing systems need to address post-growth processing at larger scales to extract
58 products for in situ use.

59 In this study, we compared commercial technologies and potential designs for in space
60 biomanufacturing systems. Our operational scenario was post-growth bioprocessing to produce
61 recombinant carbonic anhydrase from *Escherichia coli* during a Mars mission. Since carbonic
62 anhydrase is unlikely to be the only useful product in deep space missions, the ability to
63 produce a variety of recombinant proteins from multiple chassis organisms was a key
64 consideration for the designs. The designs were compared using equivalent system mass (ESM)
65 analysis^{14,25}, a system complexity metric (SCM)¹⁶, technology readiness level (TRL)²⁶, and crew-
66 mediated steps to guide future prototype development efforts.

67 **Results**

68 Bioprocessing technology comparisons were based on a production scenario that
69 required thermostable and high-pH tolerant carbonic anhydrase for a liquid amine CO₂ capture

70 system during 600 days of surface operations on Mars^{27,28}. In this system, enzyme activity will
71 decay with heating-cooling cycles, and will require intermittent addition of recombinant protein
72 to supply sufficient enzyme activity throughout the surface operations. Protein purification was
73 assumed to be required to reduce side reactions with the liquid amine; however, multiple
74 chromatography steps to produce highly purified protein are not required for this application⁵.
75 Active enzyme can be produced in *E. coli* as an intracellular recombinant protein with a His-tag
76 for affinity purification. A prior study reported 180 mg/L of recombinant carbonic anhydrase
77 yield²⁹. A total of 14.4 g of active enzyme was estimated to be required to supply a crew of six
78 for 600 days, and 100 cultures at 1 L volume is estimated to be sufficient.

79 *Potential workflows for the operational scenario*

80 Figure 1 shows five potential bioprocessing workflows (a, b, c, d, and e) starting from a
81 common cell growth and production step. Each workflow considers sub-processes of biomass
82 processing, protein extraction, and storage. These sub-processes were split into steps that
83 could have multiple alternate methods. For the sub-process of biomass processing, dewatering
84 and drying steps were the primary options considered. The stated use case will produce
85 recombinant protein intracellularly and will require protein extraction sub-process including cell
86 lysis, protein purification, and buffer exchange/desalting steps. Finally, protein product could
87 have a storage sub-process, either as biomass or as a purified product.

88 Workflow-a was selected as best aligned with the operational scenario of supplying
89 purified carbonic anhydrase on a 6 to 8-day cycle. This workflow moves from growth and
90 production steps to dewatering, cell lysis, protein purification, and buffer exchange to end with

91 product utilization, cleaning, and disposal. Although storage and drying steps were considered,
92 they were not included and deemed unnecessary based on the selected scenario.

93 *Biomass processing*

94 Dewatering cultures greatly reduces processing volumes for protein extraction or
95 biomass storage sub-processes. However, it may be feasible to complete protein extraction
96 without a dewatering step. We modeled the impact of dewatering on cell lysis and protein
97 purification steps by scaling processing time for flow-through methods including bead beater
98 lysis (L-1), flow cell sonication (L-3), affinity resin column purification (P-1), and crude lysate
99 column purification (P-2) methods (Fig. 2, Supplementary data 1). This analysis showed that
100 processing cultures without dewatering would require multiple days using flow-through
101 methods.

102 Other methods could be completed in batch including enzyme lysis (L-2), large-volume
103 probe sonication (L-4), batch affinity resin purification (P-3), magnetic bead affinity purification
104 (P-4), and affinity membrane purification (P-5). These were scaled by increasing materials to
105 limit impacts on processing duration (Fig. 2). However, most protein purification methods were
106 developed for cell lysates from concentrated biomass suspensions. It is unknown whether
107 cultures could be lysed directly, or if large-scale batch purification would yield sufficiently
108 concentrated purified protein. We concluded that dewatering would help ensure feasibility for
109 batch methods and allow flow methods to be considered as options in the bioprocessing
110 designs.

111 ESM is a metric to estimate the flown mass required to implement a space technology
112 and can help guide selection of alternative technologies^{14,25,30}. The metric is a linear model to

113 estimate mass of the system along with mass equivalences for providing volume and other
114 infrastructure within a spacecraft (Supplementary data 1). Table 1 gives the 2015 and 2022
115 equivalency factors used to calculate ESM^{31,32}, and Table 2 reports total ESM for the methods
116 and bioprocessing designs. These calculations were highly correlated ($r = 0.992$), and the 2015
117 equivalency factors are reported in the figures to enable comparisons to prior technology
118 proposals. Due to the variability in calculating ESM for preliminary designs, the metric is only
119 used for selection of competing technologies when ESM estimates approach a 5- to 10-fold
120 difference^{25,33}. Figure 3a shows ESM calculations for dewatering methods. Batch and
121 countercurrent centrifugation have ~5-fold higher ESM than a tangential flow filter. Despite the
122 similar ESM, a countercurrent centrifuge is easier to automate and can potentially reduce crew
123 time requirements. Based on these considerations, we removed batch centrifugation from
124 further consideration.

Parameter	2015 Equivalency factor	2022 Equivalency factor
Shielded Volume (V)	215.5 kg _{eq} /m ³	79.3 kg _{eq} /m ³
Power (P)	87 kg _{eq} /kW	162 kg _{eq} /kW
Thermal Control (C)	146 kg _{eq} /kW	96 kg _{eq} /kW
Cold Storage (CS)	0.79 kg _{eq} /kg	0.21 kg _{eq} /kg
Water Treatment (W)	0.12 kg _{eq} /kg	0.3 kg _{eq} /kg
Waste Storage (WS)	0.83 kg _{eq} /kg	0.93 kg _{eq} /kg

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Table 2. Total ESM for the methods and designs reported in this study.

Method/design	2015 factors	2022 factors	Designation
Tangential flow filter	50	40	D-1
Countercurrent centrifuge	290	220	D-2
Batch centrifuge	120	90	D-3
Bead beating	14.2	14.4	L-1
Enzyme lysis	4.1	2.6	L-2
Sonicator (flow cell)	189	201	L-3
Sonicator (large volume probe)	182	197	L-4
Affinity resin column	43	32	P-1
Crude lysate column	16	18	P-2
Batch resin purification	46	66	P-3
Magnetic beads	41	46	P-4
Affinity membrane	44	32	P-5
Design 1	460	400	
Design 2	360	340	
Design 3	520	450	

126 *Protein extraction*

127 ESM models for lysis eliminated sonication due to high power and cooling requirements

128 (Fig. 3b). Although enzyme lysis has a low ESM in this analysis, there are several concerns for

129 implementation of an enzyme-only method that could not be easily modeled via ESM.

130 Lysozyme is only effective as a lysis method for a limited number of microbial host species. The

131 enzyme is most effective when combined with chelators, detergent, or sonication to disrupt the

132 outer membrane of gram-negative bacteria like *E. coli*³⁴. The chelators and detergents required

133 for more effective enzyme lysis also create wastewater treatment challenges. Finally, enzyme
134 lysis is not as effective as mechanical lysis³⁵ and would likely require greater biomass growth to
135 achieve equivalent recombinant protein yield.

136 Mechanical lysis with bead beating is a well-established cell disruption technique for a
137 large variety of organisms and developmental stages including spores³⁶. A small footprint, flow-
138 through bead beater has been used on the ISS for biology research, demonstrating technology
139 feasibility²³. Based on these factors, flow-through bead beating was selected as the lysis method
140 for design comparisons.

141 ESM estimates for the protein purification step compared five commercial affinity
142 purification methods. ESM estimates were within a 3-fold range for all technologies (Fig. 3c).
143 Like the cell lysis step, we considered feasibility of implementation to select three methods for
144 bioprocessing system design comparisons. The affinity resin column and crude lysate column
145 use equivalent flow-through approaches, but the affinity resin column required a clarified lysate
146 with minimal cell debris. The crude lysate column was selected for increased reliability and
147 reduced complexity. Batch affinity purification using magnetic beads requires a crew-assisted
148 step. By contrast, the batch affinity resin “tea bag” method would be simpler to automate and
149 was selected. The affinity membrane was selected to analyze design requirements for an
150 alternate solid matrix.

151 *Bioprocessing system integrated designs*

152 Figure 4 shows the steps and methods eliminated and retained to design integrated
153 bioprocessing systems. Table 3 summarizes key decisions and the rationale for selection of
154 specific steps and methods. Biomass storage, product storage, and drying steps were

155 eliminated. For dewatering, the counter current centrifuge and filtration methods were
 156 retained. For cell lysis, only a flow-through bead beater was retained. For protein purification,
 157 crude lysate column, batch resin purification, and affinity membrane purification were retained.

Table 3. Summary of workflow method decisions and rationales.

	Decision	Rationale	Issues/concerns
1	No long-term biomass storage	<ul style="list-style-type: none"> • Reduce complexity 	
2	No long-term product storage	<ul style="list-style-type: none"> • Reduce complexity 	<ul style="list-style-type: none"> • Increases mission risk in case of anomalies
3	No drying	<ul style="list-style-type: none"> • Reduce complexity 	
4	Any component in contact with biological material will be single use	<ul style="list-style-type: none"> • Reduce crew time for cleaning • Reduce complexity • Reduce chemical safety concerns 	
5	Include dewatering	<ul style="list-style-type: none"> • Shorten processing time 	<ul style="list-style-type: none"> • Adds complexity
6	Use tangential flow filters or countercurrent centrifuge	<ul style="list-style-type: none"> • Batch centrifuge requires crew assisted steps 	<ul style="list-style-type: none"> • Countercurrent centrifuge may require modification for microbial applications
7	Use bead beating for lysis	<ul style="list-style-type: none"> • Applicable for multiple chassis organisms • Demonstrated in space 	<ul style="list-style-type: none"> • May require modification to process large volumes
8	Use affinity purification	<ul style="list-style-type: none"> • Product specific • Produces relatively pure protein after a single purification step 	<ul style="list-style-type: none"> • Must supply affinity binding competitors for elution
9	Exclude affinity column and magnetic beads	<ul style="list-style-type: none"> • Crude lysate column may increase reliability • Magnets increase complexity 	
10	May or may not include a buffer exchange and desalting step	<ul style="list-style-type: none"> • Insufficient data to either include or eliminate this step 	

158 We developed three integrated designs using the methods selected from the trade
 159 study (Fig. 5). Design 1 uses a countercurrent centrifugation system to dewater biomass, lyse
 160 cells, and purify the protein with a batch resin method. Material flow is mediated by a

161 peristaltic pump (1) and automated pinch valves (2). Cells from the biomass reservoir (3) are fed
162 into the centrifuge (4) and concentrated. Supernatant media is collected in a spent media
163 reservoir (5). Concentrated biomass is pumped through a bead beater (6) for lysis and the
164 lysate is returned to the biomass reservoir. The lysate is then pumped into the affinity resin
165 reservoir (7) for protein binding. Protein-bound resin is separated from the lysate using the
166 centrifuge, while the spent lysate is collected in a waste reservoir (8). The resin is washed with
167 buffer (9). Wash buffer is separated by the centrifuge and collected into the waste reservoir.
168 The bound protein is eluted from the resin using elution buffer (10), separated by the
169 centrifuge, and collected in the product reservoir (11).

170 Design 2 assumes a peristaltic pump (1) from the growth and production step will pump
171 fluids through a tangential flow filter (12) to dewater and concentrate biomass. Concentrated
172 biomass is returned to the biomass reservoir (3), and clarified media is collected in the spent
173 media reservoir (5). The concentrated biomass is lysed by the bead beater (6), and crude lysate
174 is returned to the biomass reservoir. The lysate is transferred to the purification system by the
175 crew. The purification system uses a separate pump (1) and pinch-valve module (2) to load
176 lysate into a crude lysate column (13). The column is washed with buffer (9), and recombinant
177 protein is eluted into the product reservoir (11).

178 Design 3 uses an identical dewatering and lysis system as in design 2, but with a
179 different protein purification system. Crew will transfer the lysate to the lysate chamber (14) of
180 a continuous loop affinity membrane purification system (15). Rollers (17) move the affinity
181 membrane through buffer chambers for protein binding (14), wash (9), and elution (10). A

182 second wash chamber equilibrates the membrane for multiple cycles of protein binding. The
183 crew transfers the eluted protein to a product reservoir (11).

184 *Comparative analysis of designs*

185 Each design integrates different methods to complete the same bioprocessing steps
186 (Fig. 5b). Multiple systems parameters including ESM, SCM, TRL, and degree of crew assistance
187 were used to assess the three designs. SCM estimates complexity of life support systems by
188 summing all the components and proposed interconnections of a specific design¹⁶. Larger SCM
189 values are interpreted as more complex systems with potentially lower reliability. Figure 6
190 depicts the major components and interconnections used to calculate SCM values for each of
191 the three designs. We also analyzed the degree of crew assistance because crew time was not
192 incorporated into ESM calculations. Crew-assisted steps are highlighted in red or pink in Figures
193 5 and 6. TRL assesses technology maturity using a 9-point scale with TRL 9 being spaceflight-
194 proven technologies²⁶.

195 Figure 7 compares ESM, SCM, and degree of crew assistance for the integrated designs,
196 while Table 4 reports TRL for the dewatering, cell lysis, and protein purification steps
197 (Supplementary data 2). ESM was comparable for all three designs. Design 1 had the lowest
198 SCM due to the multifunctional commercial countercurrent centrifuge that integrates
199 dewatering, cell lysis, and protein purification. The ease of integration and automation in design
200 1 is also reflected in the low degree of crew assistance and higher TRL for dewatering and
201 purification compared to the other designs. Although these metrics suggest design 1 will be
202 more practical to implement, the differences in the metrics between the designs were not large
203 enough to eliminate specific methods without experimental testing.

Table 4. TRL for each bioprocessing step of the integrated designs			
Step	Design 1	Design 2	Design 3
Dewatering	4	3	3
Lysis	9	9	9
Protein purification	3	3	2

204 Discussion

205 Carbonic anhydrase improves the efficiency of liquid amine CO₂ capture systems⁵⁻⁷,
206 which is a candidate technology for deep space missions^{1,2}. Application of these liquid amine
207 systems requires a steady supply of carbonic anhydrase that may be met by long term storage,
208 resupply or in situ bioproduction. Long term storage of active enzyme requires low temperature
209 storage conditions, and frequent resupply is not possible for surface missions to Mars.

210 Bioprocessing system designs for space applications need to optimize mass, efficiency,
211 power consumption, complexity, reliability, and ease of operation^{37,38}. The initial space design
212 process largely focuses on ESM to ascertain feasibility either in comparison to existing state of
213 the art or other comparable technologies^{12,14,25,39-44}. In this study, we employed ESM along with
214 processing duration, SCM, TRL, and degree of crew assistance metrics to estimate reliability,
215 potential for implementation, and ease of operation. Although carbonic anhydrase production
216 was the use case scenario, the designs would be useful to purify any soluble recombinant
217 protein with an affinity tag from a microbial chassis organism.

218 ESM comparisons were able to eliminate batch centrifugation and sonication as
219 methods for integrated designs. However, the integrated bioprocessing designs have a narrow
220 range of 357-522 kg eq ESM. Given these differences are not large enough for system selection,

221 this metric cannot be used to prioritize designs for implementation. The ESM estimates are
222 comparable to a proposed monoclonal antibody production system at 300-1,700 kg eq⁴⁵ as well
223 as a plant biomass system for food production at 300-1,300 kg eq per kg¹⁰. For theoretical
224 designs such as the proposed biomanufacturing systems, a difference of less than 10-fold
225 suggests similar infrastructure costs. On a mission-wide basis, the recombinant protein
226 bioprocessing system may be reasonable for a Mars mission. The bioprocessing system adds
227 only 2-3% to the physio-chemical-biological life support system proposed by ESA for a full Mars
228 mission (~18,000 kg eq)⁴⁶.

229 Crew time and system complexity are important factors in space system design^{16,47}.
230 Design 1 ranked best for number of crew assisted steps and SCM, which primarily reflects the
231 level of integration for automated fluid handling in the commercial counterflow centrifuge.
232 Additional engineering to integrate pumps and controllers would reduce both SCM and crew-
233 assisted steps for designs 2 and 3. Design 1 also has higher TRL components indicating this
234 design may be easier to implement for space, but a limitation of the study is a lack of empirical
235 validation. All components were assumed to operate as intended and to be compatible within a
236 design and many components have not been tested for the specific use case of recombinant
237 protein purification. For example, the counterflow centrifuge in design 1 has not been used for
238 bioprocessing of microbes. Empirical tests are needed to determine the relative efficiency of
239 the selected technologies when integrated.

240 Although closed-loop systems and reusability are attractive long-term goals in space,
241 they require increased crew time and system reliability^{38,48,49}. On Earth, biomanufacturing often
242 employs single-use technology for various reasons including improved safety as well as reduced

243 contamination, footprint, and cost by eliminating cleaning and sterilization of components that
244 contact biological material^{50,51}. Single-use materials for bioprocessing is predicted to reduce
245 crew time and to increase reliability. Consequently, the proposed bioprocessing designs use
246 disposable components in the ESM calculations.

247 We also identified several factors that could influence a recombinant protein
248 bioprocessing design that were difficult to quantify. For example, there are safety and shelf-life
249 concerns for commercial affinity purification products. Affinity resins are stored in ethanol to
250 prevent biological contamination. Ethanol interferes with the current Environmental Control
251 and Life Support Systems on the ISS, creating a safety risk when large amounts of ethanol are in
252 the cabin air or wastewater. The ethanol risk could be mitigated with an affinity membrane that
253 is stored dry. Both commercial resins and affinity membranes have 1-2 year shelf lives, while a
254 Mars mission is expected to require a 5-year shelf life for all systems²⁷. Removing incompatible
255 chemicals and extending the shelf life of the affinity matrix are both critical to advance space
256 biomanufacturing of recombinant proteins.

257 It is possible that using different strategies to express recombinant proteins could
258 reduce complexity and system mass. For instance, an affinity resin “teabag” can purify proteins
259 secreted into the media without dewatering or lysis steps⁵². Although this strategy would
260 simplify bioprocessing, it limits production to recombinant proteins that have activity after
261 secretion. Moreover, *E. coli* secreted proteins are targeted to the periplasmic space and require
262 an osmotic shock step to release protein into the media. Adding an osmotic shock still requires
263 dewatering to concentrate biomass and the osmotic shock step would replace the cell lysis
264 step.

265 This study illustrates multiple approaches to rank technologies for design of new
266 integrated systems intended for space applications. The extreme environment of space, high
267 cost of launching materials, and limited crew time drive systems to be automated and to
268 minimize mass, power, and volume. Further development of space bioprocessing systems is
269 expected to identify technologies that can be integrated and automated reliably, which could
270 be translated to improved efficiency for industrial biomanufacturing on Earth.

271 **Methods**

272 The operational scenario investigated was a six person crew on a 3-year Mars mission
273 with 600 days of surface operations³¹. A total of 14.4 g of recombinant carbonic anhydrase was
274 estimated to be required to maintain a liquid amine CO₂ scrubber with active enzyme
275 throughout surface operations. Affinity purification of the enzyme was assumed to be needed
276 to reduce liquid amine side reactions with cellular debris. Sufficient carbonic anhydrase could
277 be supplied by approximately 80 bioprocessing runs using 1 L cultures with a yield of 180 mg
278 purified enzyme per run. Supplies and power for a total of 100 production runs were assumed
279 to give sufficient redundancy for production runs that failed to meet expected yield.

280 A review of recombinant protein purification from unicellular microorganisms identified
281 sub-process steps (Fig. 1). Essential steps for the operational scenario, such as lysis or
282 purification, were retained. Biomass dewatering was investigated as an optional step. Non-
283 essential steps, such as storage and drying, were eliminated to simplify potential workflows. A
284 trade study of potential methods for each sub-process step was conducted, and ESM was used
285 to evaluate individual technologies for in-space application. Technologies with comparable ESM
286 were used to develop three designs, which were analyzed using four metrics described below.

287 *ESM metric*

288 ESM was calculated using Equation 1 and the equivalency factors in Table 1 based on
289 guidelines from Levri, et al.¹⁴. Parameters for volume (V^{ESM}), power (P^{ESM}), thermal cooling
290 (C^{ESM}), cold storage (CS^{ESM}), water (W^{ESM}), and waste storage (WS^{ESM}) used equivalency factors
291 estimated for a nominal crewed surface mission to Mars³¹. CS^{ESM} assumed that the mass
292 requiring cold storage had a density of 1000 kg/m^3 and was stored in a freezer analogous to
293 that currently used on the International Space Station (ISS)³¹. W^{ESM} and WS^{ESM} values were
294 derived from a prior Mars mission scenario where a crew of six used 30 kg of water per crew
295 member per day, and produced 1.5 kg solid waste per crew member per day^{31,55}. W^{ESM} was
296 based on a water processor similar to the ISS water treatment system and WS^{ESM} assumed that
297 waste was stored within the habitat⁵⁵. Crew time was excluded due to the uncertainties in
298 estimating the practical level of automation that could be achieved after integrating
299 technologies from different commercial manufacturers. Detailed assumptions and calculations
300 of ESM are given in Supplementary data 1 and 2. ESM penalties from both 2015 and 2022
301 Baseline Values and Assumptions Documents were used for comparative calculations shown in
302 Table 2^{31,32}.

$$\begin{aligned} 303 \quad ESM = & \sum M_i + \sum M_t * D + \sum(V_i * V_{eq}) + \sum(V_t * V_{eq}) * D + \sum(P * P_{eq}) + \sum(C * C_{eq}) + \\ 304 \quad & \sum(CT * CT_{eq}) + \sum(CS * CS_{eq}) + \sum(W * W_{eq}) * D + \sum(WS * WS_{eq}) * D \quad (1) \end{aligned}$$

305 Where,

M_i – Initial mass (kg)

M_t – Time dependent mass (kg)

D – Mission duration (number of runs)

V_i – Initial volume (m³)

V_{eq} – Volume equivalency (kg eq/m³)

V_t – Time dependent volume (m³)

P – Power consumed (kW)

P_{eq} – Power equivalency (kg eq/kW)

C – Thermal cooling (kW)

C_{eq} – Thermal cooling equivalency (kg eq/kW)

CT – Crew time (h)

CT_{eq} – Crew time equivalency (kg eq/h)

CS – Cold storage requirement (kg stored)

CS_{eq} – Cold storage equivalency (kg eq/kg stored)

W – Water requirement per run (kg water)

W_{eq} – Water treatment equivalency (kg eq/kg water)

WS – Solid waste generated per run (kg waste)

WS_{eq} – Waste storage equivalency (kg eq/kg waste)

306 *SCM metric*

307 Equation 2 gives the SCM calculation based on the number of components (N) and the

308 number of one-way interactions (I) between components¹⁶.

309 $SCM = \text{Number of components } (N) + \text{Number of interactions } (I) \text{ (2)}$

310 Components are integrated subsystems that perform one or more bioprocessing steps,

311 such as equipment available from commercial vendors. Auxiliary parts such as valves, ordinary

312 filters, and sensors were excluded with the rationale that integration of major components
313 account for most of the system complexity, cost, and failure modes¹⁶. The number of one-way
314 interactions (I) is derived from a top-level bioprocessing system block diagram based on
315 physical connections between components (Fig. 6).

316 *TRL metric*

317 A TRL was assigned for each of the dewatering, cell lysis, and purification options
318 included in the three designs using existing NASA guidelines²⁶.

319 *Degree of crew assistance metric*

320 The degree of crew assistance was estimated based on whether the commercially
321 available components were integrated and easily automatable. A crew support step was
322 assumed if commercial technology was not readily available to automate a specific step in the
323 proposed workflow of each design. The sum of crew assisted steps was the degree of crew
324 assistance for the design.

325 *Dewatering technologies*

326 Tangential flow filtration, batch centrifugation, and countercurrent centrifugation were
327 three dewatering methods compared for this analysis. The dimensions and mass of the
328 tangential flow filter were based on Xampler cartridge with 1 mm fiber diameter, 500 kDa pore
329 size and 30 cm path length with a 3M housing (Cytiva, Marlborough, MA, USA). To control fluid
330 flow through the tangential flow filter, an Ismatec Reglo ICC Digital Pump with 4-Channels and
331 8-Rollers (Cole-Palmer, Vernon Hills, IL, USA) was included in the ESM calculations. A modified
332 version of the Drucker model 755VES swinging bucket centrifuge (Drucker Diagnostics, Port

333 Matilda, PA, USA) has been approved for operation on the ISS, and the specifications of the
334 commercially available centrifuge were used to calculate the ESM. Twenty disposable 50 mL
335 tubes were assumed to harvest the 1 L culture volume during every run. The countercurrent
336 centrifuge data was based on specifications for the CTS Rotea Counterflow Centrifugation
337 System (Thermo Fisher Scientific, Waltham, MA, USA).

338 *Lysis technologies*

339 The methods considered for lysis were bead beating, enzymatic lysis, a flow-through
340 sonicator, and a large-volume probe sonicator. The bead beater analysis was based on the
341 Claremont Biosolutions LLC (Upland, CA, USA) OmniLyse HL beadbeater flow-through lysis
342 device. Although originally developed for small volumes, the OmniLyse HL unit was assumed to
343 lyse large volumes with equal efficiency using extended processing times. The enzyme lysis
344 protocol assumed that the biomass was incubated for 30 minutes at ambient temperature with
345 0.25 mg/mL lysozyme, 0.1 mL/mL Pierce universal nuclease (Thermo Fisher Scientific, Waltham,
346 MA, USA), and 0.1% w/v Triton X at final concentration. Mass and volumes for ESM were
347 calculated assuming the solid reagents had a density equal to NaCl (2.17 g/cm^3), and liquid
348 reagents had a density equal to water (1 g/cm^3). The QSonica (Newton, CT, USA) ultrasound
349 generator was modeled assuming a 1-inch replaceable tip for a large volume batch method and
350 a Q500 FloCell unit for the flow through method.

351 *Protein purification technologies*

352 Five His-tag affinity purification methods were compared using public domain product
353 information available from commercial vendors. The Sigma Aldrich (St Luis, MO, USA) His-Select
354 Ni affinity gel was used to represent affinity columns requiring clarified lysates. The Cytiva

355 (Marlborough, MA, USA) HisTrap FF was an exemplar of a crude lysate column that does not
356 require clarification before sample loading. Batch resin purification specifications were
357 estimated for the resin “teabag” method from Castaldo, et. al.⁵². Millipore Sigma (Burlington,
358 MA) HIS-Select® Nickel Magnetic Agarose Beads specifications were used to estimate the
359 amount of resin required for batch purification with magnetic beads, while mass and volume of
360 the beads were assumed to be equivalent to affinity resin. For affinity membrane purification,
361 Capturem large volume filters (Takara Bio USA Inc., San Jose, CA, USA) were used to estimate
362 the quantity of membrane required, while mass and volume of the membrane was assumed to
363 be equivalent to Whatman filter paper (200 g/cm²).

364 The buffer composition was 20 mM HEPES, 500 mM NaCl and 20 mM imidazole for the
365 binding buffer, and 20 mM HEPES, 500 mM NaCl and 200 mM imidazole for the elution buffer
366 for all the methods. Buffer volumes were modeled using manufacturer protocols or the resin
367 “teabag” method⁵².

368 *Bioprocessing system designs*

369 All three post-growth bioprocessing system designs assumed a Claremont Biosolutions
370 LLC (Upland, CA, USA) OmniLyse® HL disposable bead beater for in-line cell lysis from the
371 biomass reservoir. The first design included a Thermo Fisher Scientific (Waltham, MA, USA) CTS
372 Rotea Counterflow Centrifugation System with disposable, single use kits for processing. This
373 counterflow centrifuge includes integrated pinch-valves, a peristaltic pump, and a controller for
374 automation. QIAexpressionist Ni-NTA resin (Qiagen Inc., Valencia, CA, USA) was included for
375 affinity purification.

376 The second design uses a MidGee ultrafiltration cartridge UFP-5-C-MM01A (Cytiva,
377 Marlborough, MA, USA) and an Applikon Biotechnology (JG Delft, Netherlands) “my-control”
378 with built in peristaltic pumps for biomass dewatering using tangential flow filtration and
379 subsequent cell lysis. For protein purification, an Automate Scientific (Berkeley, CA, USA)
380 Perfusion System and ValveLink8.2 Perfusion Controller were assumed to integrate with an
381 Masterflex (Gelsenkirchen, Germany) L/S® Digital Drive peristaltic pump with an Easy-Load® 3
382 Pump Head for Precision Tubing. This fluid control system was assumed to automate affinity
383 purification in a Cytiva 5 mL HisTrap FF crude lysate column (Marlborough, MA, USA).

384 Dewatering and lysis components in design 3 were identical to design 2. Protein
385 purification was based on a non-commercial affinity belt system⁵⁷⁻⁵⁹. Rollers were proposed to
386 move an affinity membrane belt continuously through chambers containing the lysate, wash
387 buffers, and elution buffers. The total volume of the system as assumed to be 0.005 m³
388 including the chambers, walls, and rollers. The mass was assumed to be 500 g. One Transmotec
389 Inc. (Burlington, MA, USA) 12 V, 2A DC motor was included to operate the rollers.

390 Disposable materials such as bags, and sterile filters for all three designs were estimated
391 for the system based on commercial options and material properties, while the additional mass
392 of tubing and luers were assumed to be 0.1 kg for all designs.

393 **Data Availability**

394 All source data and ESM calculations needed to replicate the study are provided in the
395 manuscript and Supplementary data 1 and 2.

396 **Acknowledgements**

397 We thank Aditya Hindupur for discussions in the initial phase of the study. This work was
398 funded by the NASA Space Technology Mission Directorate Game Changing Development
399 Program as part of the Space Synthetic Biology Project.

400 **Author Contributions**

401 M.S. and M.B.P. completed the trade study investigation, formal analysis, and wrote the
402 manuscript. M.D. completed data collection, formal analysis, and edited the manuscript. H.W.J.
403 provided systems engineering expertise for formal analysis and edited the manuscript. J.A.H.
404 conceived and supervised the project and edited the manuscript. F.M.D., J.M.G., and A.M.S.
405 contributed to methods development, validation, and visualization of the results, and edited
406 the manuscript.

407

408 **Competing Interests statement**

409 The authors declare no competing interests.

410

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557 **Figure Legends**

558 **Fig. 1.** Flow diagram of potential bioprocessing strategies. Dashed boxes group the primary sub-
559 processes of biomass processing, protein extraction, and product storage. Solid boxes give
560 individual steps with bulleted lists of common methods to complete the step. Methods
561 compared in this analysis have parenthetical designations that are used in Fig. 2 and Fig. 3.
562 Lettered arrows (a, b, c, d, e) give examples of possible workflows for processing *E. coli* cells
563 expressing recombinant carbonic anhydrase.

564

565 **Fig. 2.** Estimated process duration for each run of the lysis (L) and purification (P) based on
566 recommended manufacturer protocols or published literature. Methods included: flow through
567 bead beater (L-1), enzyme lysis (L-2), flow cell sonicator (L-3), large volume probe sonicator (L-
568 4), affinity resin column (P-1), crude lysate column (P-2), batch affinity resin (P-3), batch affinity
569 magnetic beads (P-4), and affinity membrane (P-5). Black bars are process times of 1 L culture

570 and gray bars are process times of 200 mL concentrated biomass. See supplementary data 1 for
571 detailed calculations.

572

573 **Fig. 3.** ESM models assuming 100 bioprocessing runs. **(a)** Dewatering methods included
574 tangential flow filtration (D-1), countercurrent centrifugation (D-2), and batch centrifugation (D-
575 3). **(b)** Cell lysis methods included bead beating (L-1), enzymatic lysis (L-2), flow through
576 sonication (L-3), and large volume probe sonication (L-4). **(c)** Protein purification methods
577 included clarified lysate column (P-1), crude lysate column (P-2), batch resin purification (P-3),
578 magnetic bead purification (P-4), and affinity membrane purification (P-5). Each bar graph
579 shows mass equivalencies for: total mass (M^{ESM}), volume (V^{ESM}), power (P^{ESM}), cooling (C^{ESM}),
580 cold storage (CS^{ESM}), water treatment (W^{ESM}), and solid waste disposal (WD^{ESM}). See Table 2 for
581 total ESM values and Supplementary data 1 for detailed calculations.

582

583 **Fig. 4.** Flow diagram of bioprocessing strategies showing selected methods for integrated, in
584 space designs. Decisions from the trade study are indicated with pink callouts. The rationale for
585 each decision is given in Table 3.

586

587 **Fig. 5.** Bioprocessing system designs integrating selected methods for dewatering, lysis, and
588 purification. **(a)** Design schematics with the following components: peristaltic pump (1), pinch
589 valve (2), biomass reservoir (3), centrifuge cartridge (4), spent media reservoir (5), disposable
590 bead beater (6), affinity resin reservoir (7), waste reservoir (8), wash buffer (9), elution buffer
591 (10), product reservoir (11), tangential flow filter (12), crude lysate column (13), crude lysate

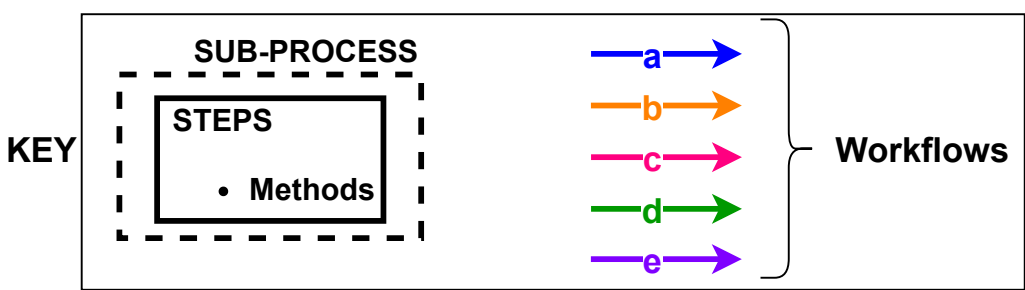
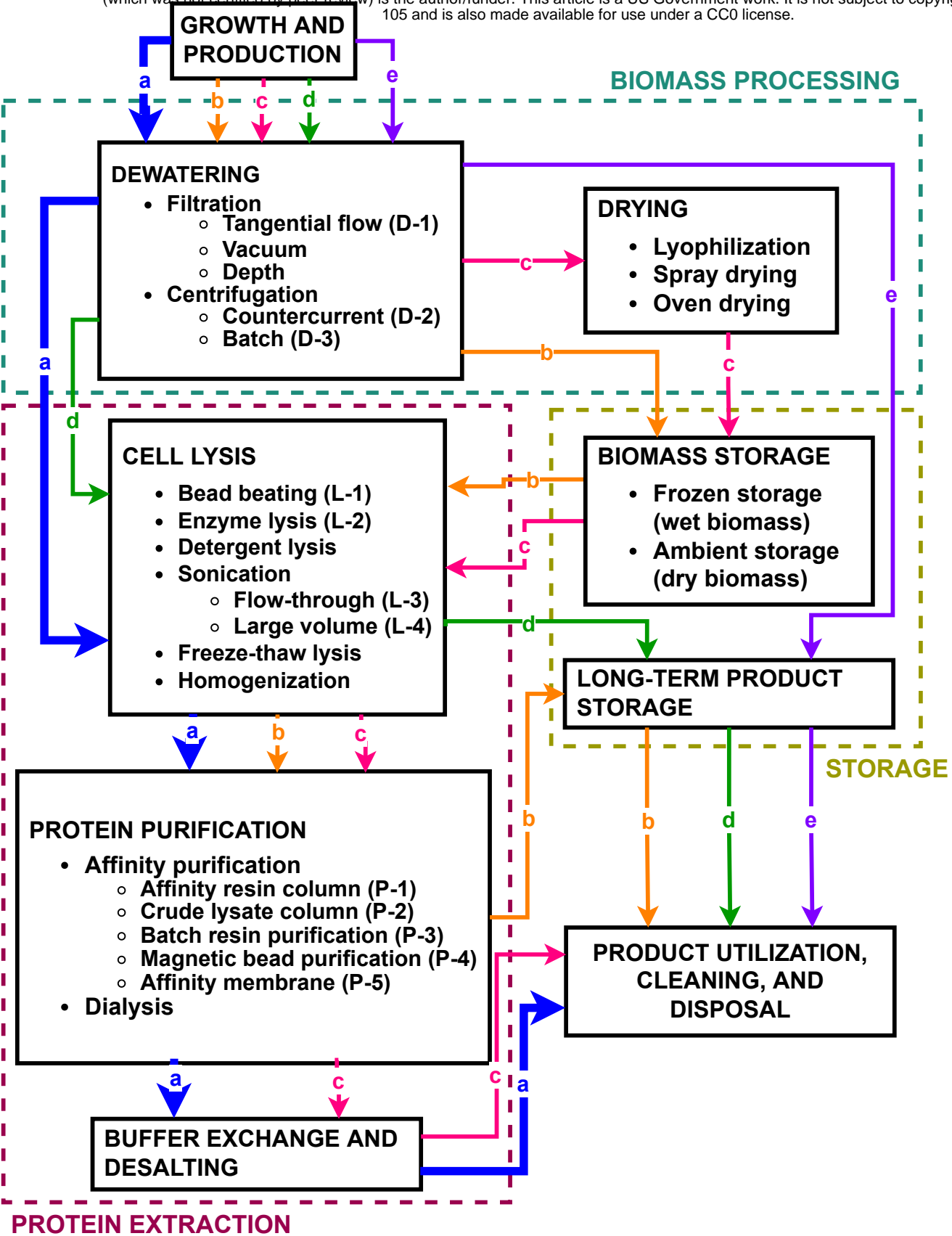
592 chamber (14), affinity purification cartridge (15), affinity membrane (16), rollers (17). Yellow
593 arrows indicate crew-assisted steps. **(b)** Flow diagram comparing the bioprocessing designs.
594 Yellow boxes indicate methods that require crew-assistance to initiate or complete the method.

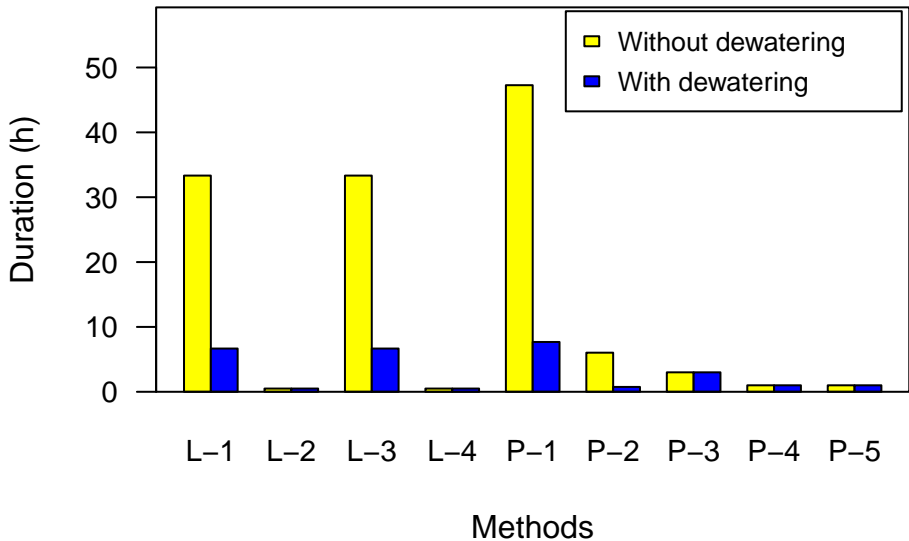
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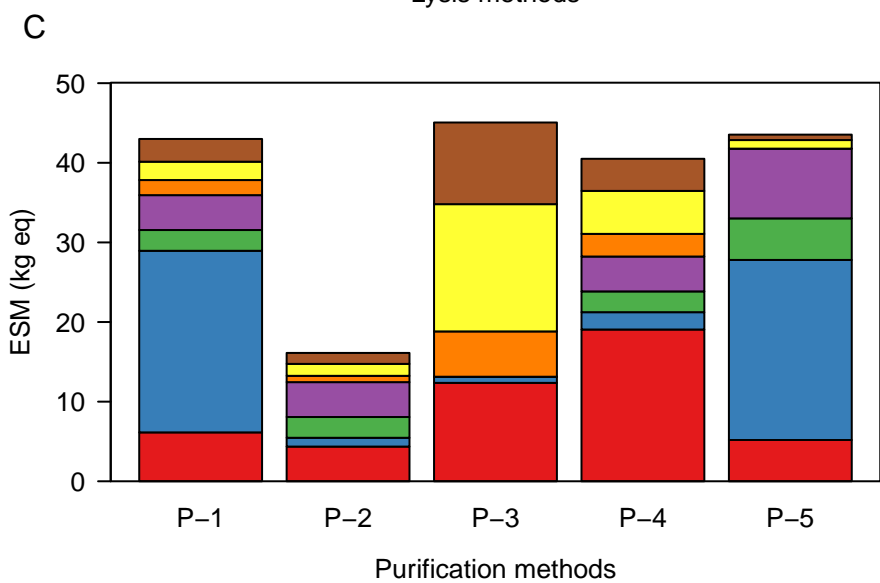
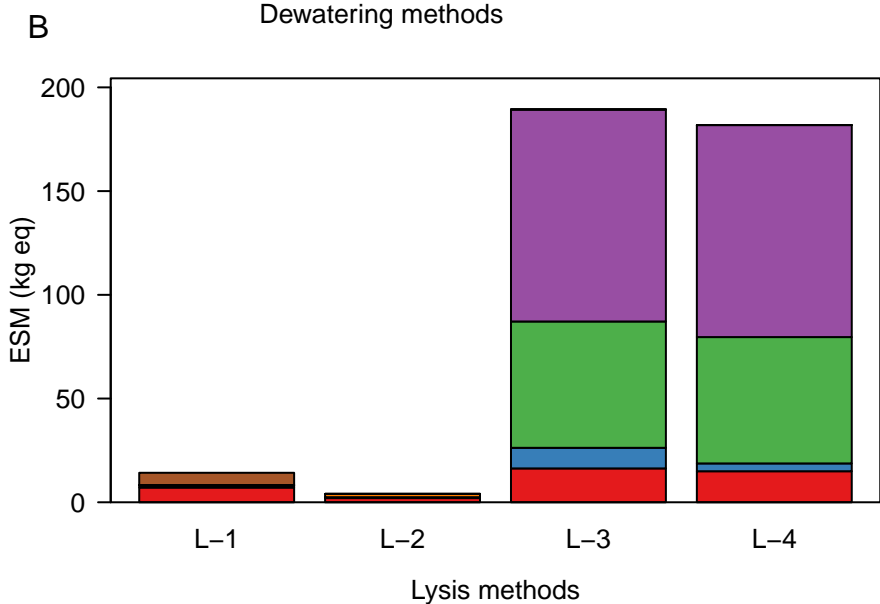
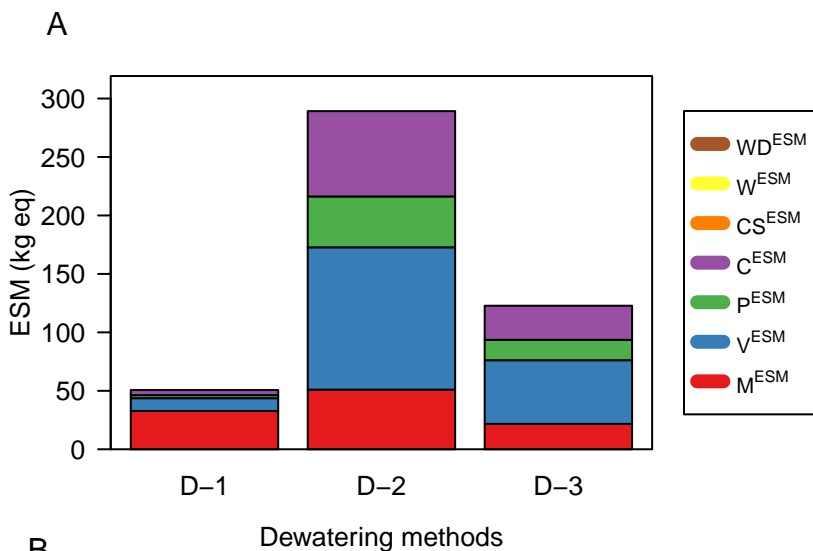
596 **Fig. 6.** Top-level block diagram of the three bioprocessing designs used to calculate SCM. Major
597 components (N) are in boxes. Individual interconnections (I) are diagrammed with arrows
598 indicating the direction of material flow. Dashed arrows indicate outputs of the bioprocessing
599 systems, and red arrows require crew assistance to complete the actions for the
600 interconnection.

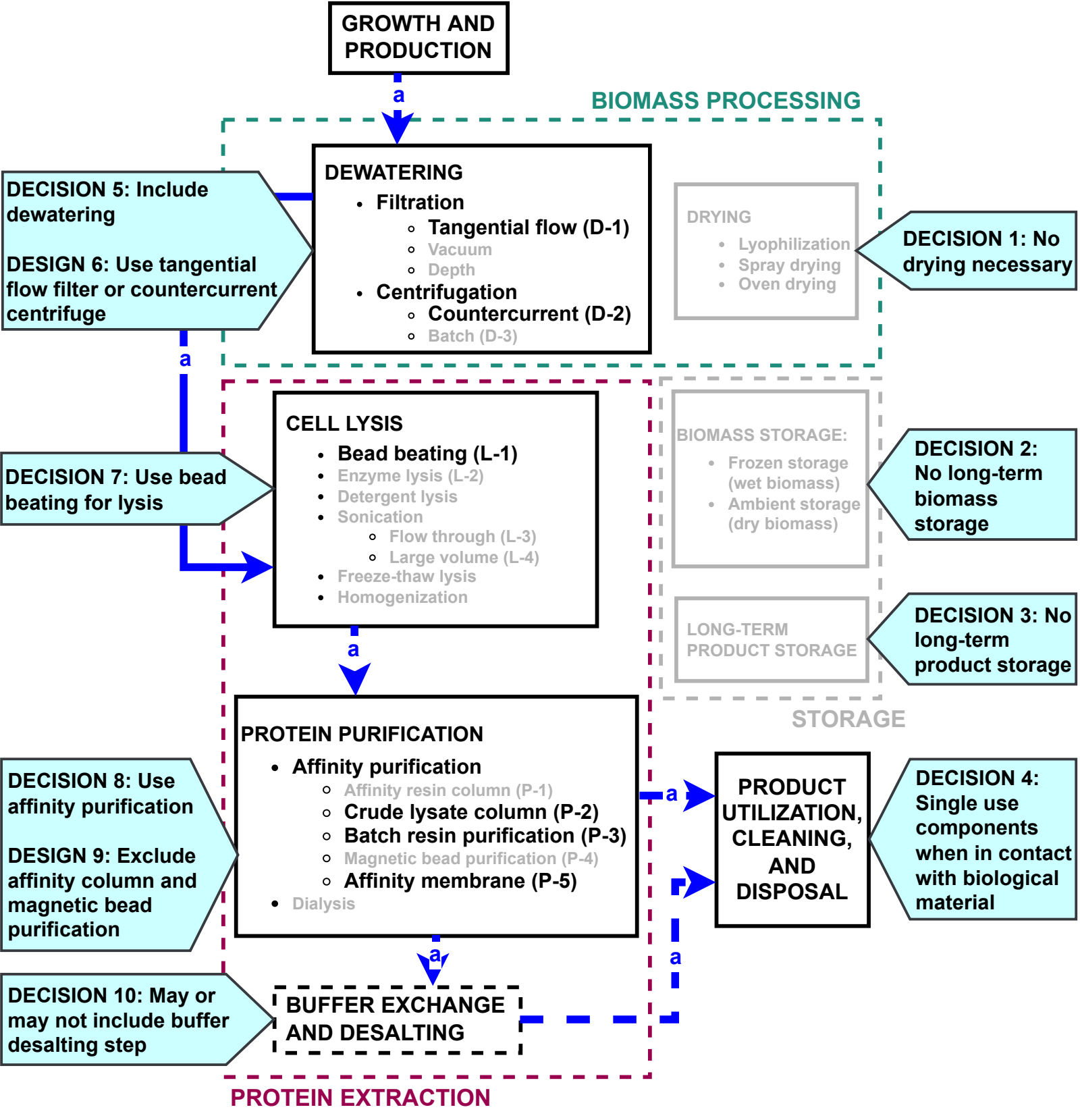
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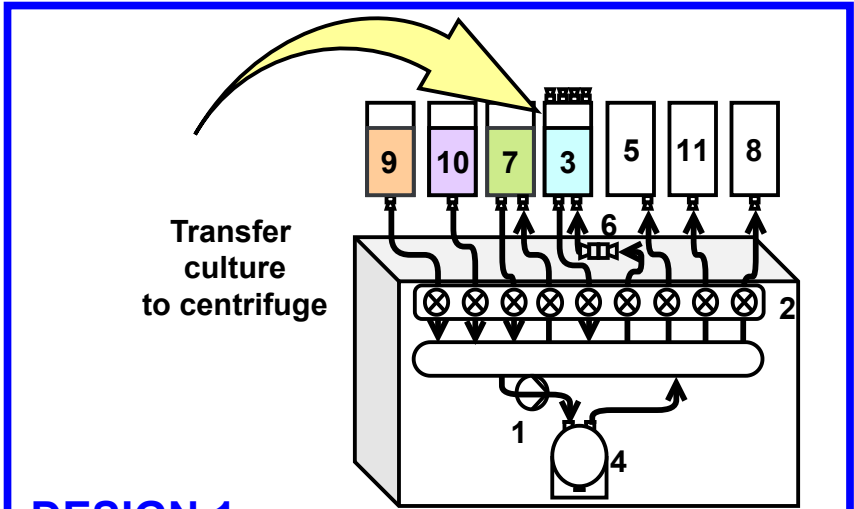
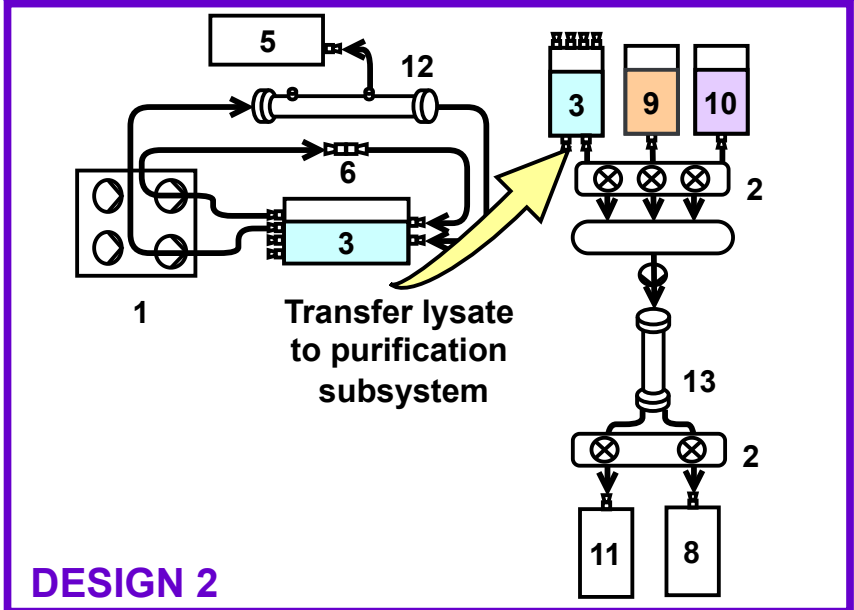
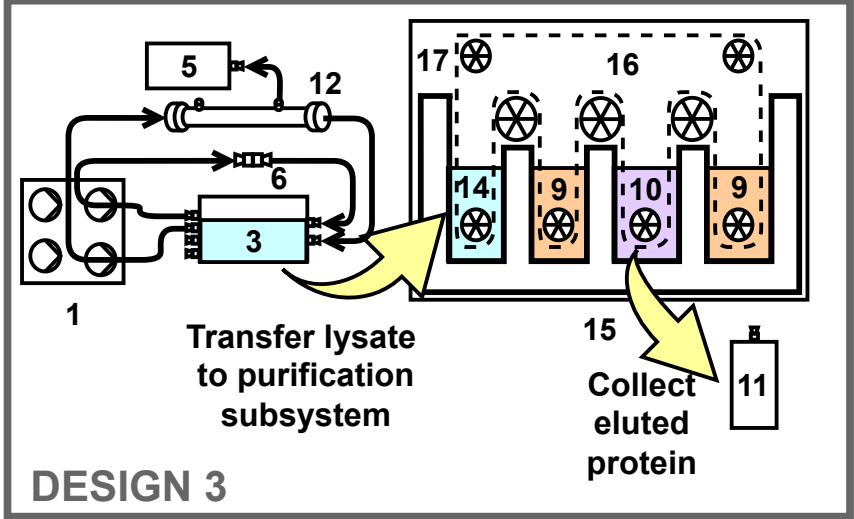
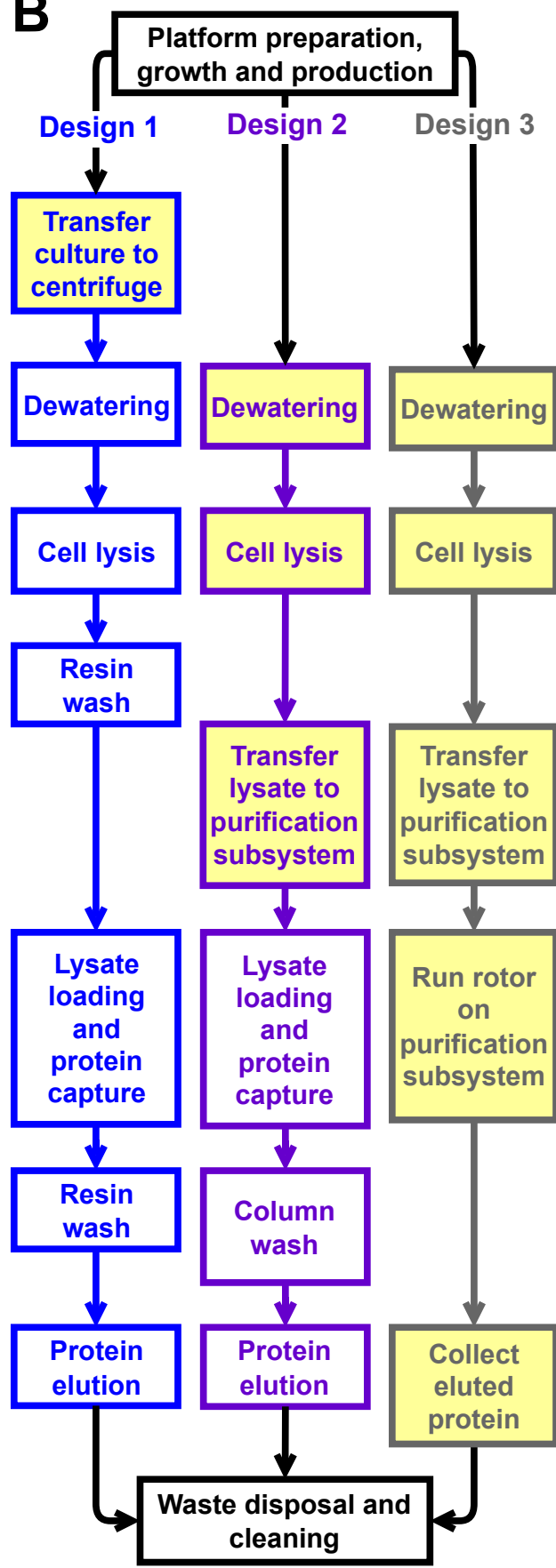
602 **Fig. 7.** Design metrics for the three integrated bioprocessing designs. See Table 2 for total ESM
603 values and Supplementary data 2 for detailed ESM calculations.



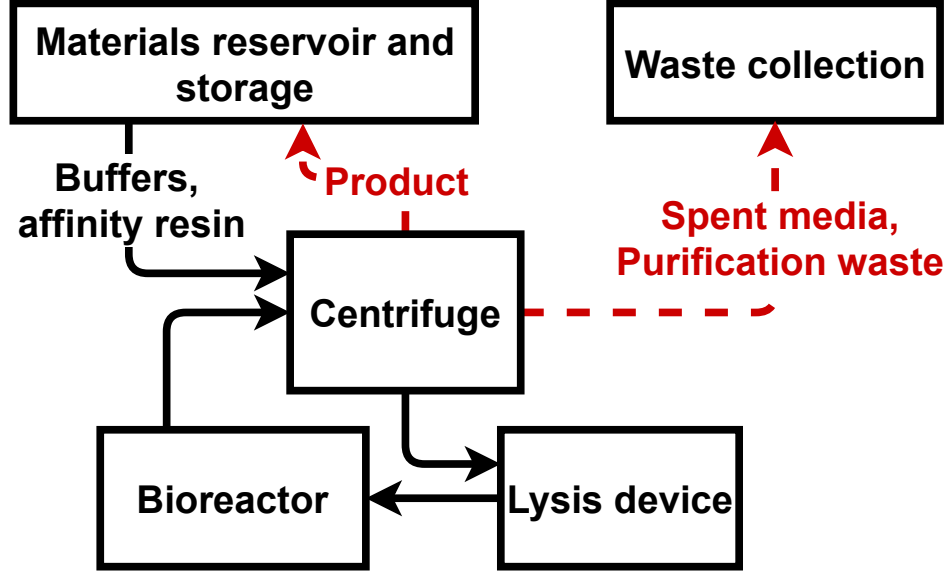






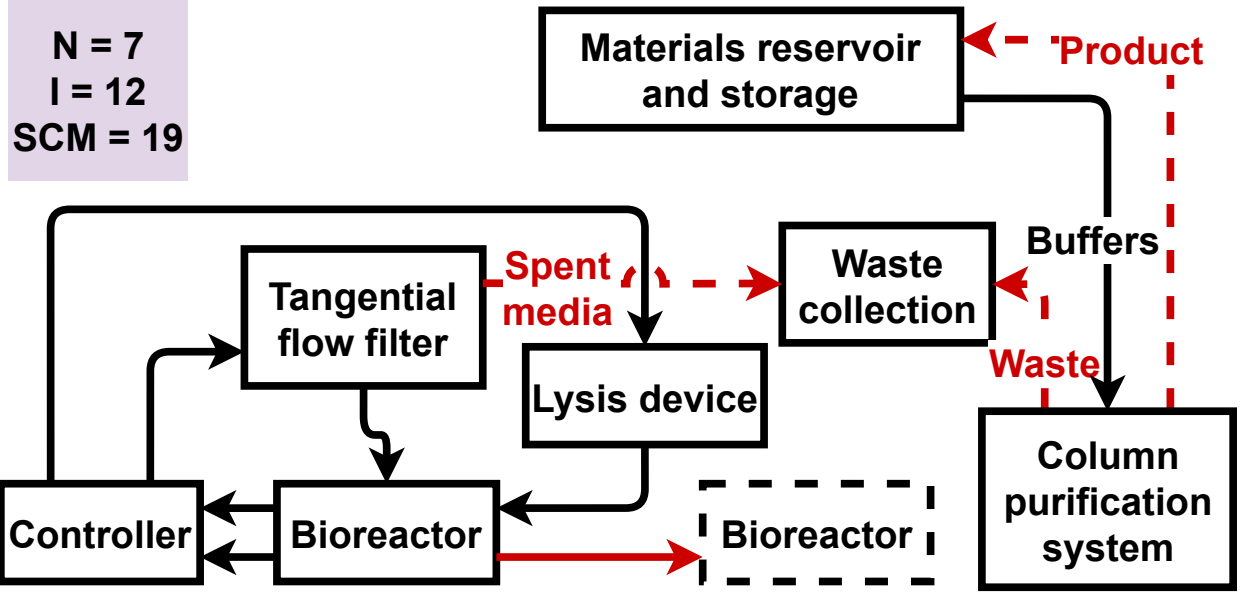
A**DESIGN 1****DESIGN 2****DESIGN 3****B**

N = 5
I = 6
SCM = 11



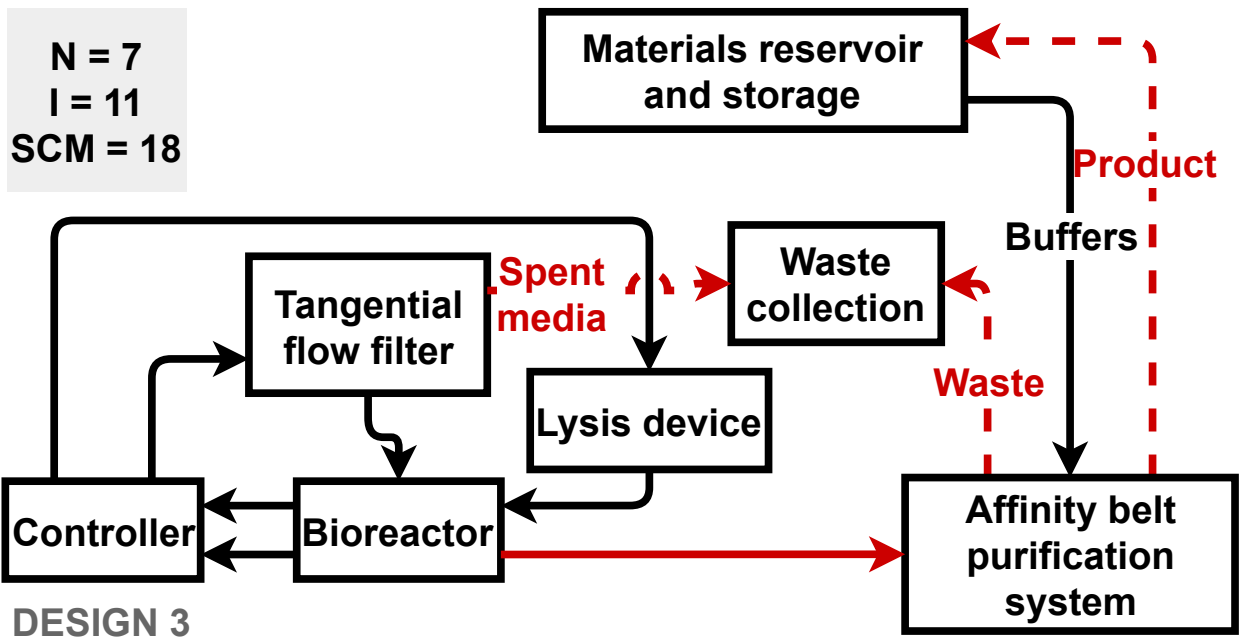
DESIGN 1

N = 7
I = 12
SCM = 19



DESIGN 2

N = 7
I = 11
SCM = 18



DESIGN 3

