



Biomni: A General-Purpose Biomedical AI Agent

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1 Abstract

2 **Biomedical research underpins progress in our understanding of human health and disease,**
3 **drug discovery, and clinical care. However, with the growth of complex lab experiments,**
4 **large datasets, many analytical tools, and expansive literature, biomedical research is in-**
5 **creasingly constrained by repetitive and fragmented workflows that slow discovery and limit**
6 **innovation, underscoring the need for a fundamentally new way to scale scientific exper-**
7 **tise. Here, we introduce Biomni, a general-purpose biomedical AI agent designed to au-**
8 **tonomously execute a wide spectrum of research tasks across diverse biomedical subfields.**
9 **To systematically map the biomedical action space, Biomni first employs an action discov-**
10 **ery agent to create the first unified agentic environment – mining essential tools, databases,**
11 **and protocols from tens of thousands of publications across 25 biomedical domains. Built**
12 **on this foundation, Biomni features a generalist agentic architecture that integrates large**
13 **language model (LLM) reasoning with retrieval-augmented planning and code-based execu-**
14 **tion, enabling it to dynamically compose and carry out complex biomedical workflows – en-**
15 **tirely without relying on predefined templates or rigid task flows. Systematic benchmarking**
16 **demonstrates that Biomni achieves strong generalization across heterogeneous biomedical**
17 **tasks – including causal gene prioritization, drug repurposing, rare disease diagnosis, micro-**
18 **biome analysis, and molecular cloning – without any task-specific prompt tuning. Real-world**
19 **case studies further showcase Biomni’s ability to interpret complex, multi-modal biomedical**
20 **datasets and autonomously generate experimentally testable protocols. Biomni envisions a**
21 **future where virtual AI biologists operate alongside and augment human scientists to dra-**
22 **matically enhance research productivity, clinical insight, and healthcare. Biomni is ready to**
23 **use at <https://biomni.stanford.edu>, and we invite scientists to explore its capabilities, stress-**
24 **test its limits, and co-create the next era of biomedical discoveries.**

25 1 Introduction

26 Biomedical research is a key pillar of modern science and medicine, driving discoveries in disease
27 mechanisms, diagnostics, and therapeutics^{1–4}. Yet, with the growth in large-scale experiments,
28 data, tools, and literature, progress is increasingly slowed by fragmented, complex workflows that
29 require specialized tools, exhaustive literature reviews, intricate experimental design, and careful
30 statistical modeling^{5,6}. A vast volume of valuable biomedical data sits underutilized⁷, many so-
31 phisticated analyses are not conducted, and many connections for past knowledge and literature are
32 not made, not for lack of significance, but because the demand for expert researchers far exceeds
33 the supply. This mismatch between data abundance and limited human bandwidth highlights an
34 urgent need for a fundamentally new approach – one that can effectively scale expertise, streamline
35 workflows, and unlock the full potential of biomedical research.

36 Recent advances in Artificial Intelligence (AI) have created a paradigm shift, opening the
37 possibility for fundamentally reshaping biomedical research⁸. AI agents have dramatically re-
38 shaped fields such as software engineering⁹, law¹⁰, material science¹¹ and healthcare¹² by au-
39 tomatizing repetitive tasks, enhancing productivity, and enabling breakthroughs that were previ-
40 ously unimaginable. Given these developments, the question emerges: *Can we build a virtual*
41 *AI biomedical scientist?* Such a virtual scientist would autonomously tackle diverse biomedical
42 research tasks spanning multiple subfields, unlocking extensive capabilities and fostering novel
43 insights through interdisciplinary integration – an achievement that can radically augment human
44 biologists limited by specialized expertise. Capable of efficiently managing thousands of concur-
45 rent tasks, this virtual scientist could dramatically enhance human productivity and accelerate the
46 pace of biomedical discovery.

47 Previous approaches have largely relied on specialist agentic workflows tailored to nar-
48 row biomedical tasks^{13–19}, which restricts their capacity to move fluidly and generalize across
49 the full spectrum of biomedical domains, as needed to answer key research questions. Enabling
50 an AI agent to handle a broad range of biomedical tasks introduces substantial technical chal-
51 lenges – most notably, the need to tightly couple advanced reasoning²⁰ with the ability to exe-
52 cute highly specialized biomedical actions²¹. Although LLM-based reasoning has seen significant
53 advancements²², such LLMs need access to an environment that explicitly defines the biomedical

54 action space, which is inherently diverse, domain-specific, and complex. Moreover, a truly capable
55 system requires an agentic architecture that can natively interact with this biomedical environment
56 – autonomously selecting and composing actions, using its reasoning capabilities to plan and exe-
57 cute diverse tasks without relying on rigid, pre-defined workflows.

58 Here we present Biomni, a generalist biomedical AI agent purpose-built to automate and
59 advance biomedical research across a wide range of subfields. Acting as a virtual AI biologist,
60 Biomni autonomously formulates novel, testable hypotheses, performs complex bioinformatics
61 analyses, and designs rigorous experimental protocols. To enable this capability, we first con-
62 structed a unified and comprehensive biomedical action space by systematically analyzing tens
63 of thousands of biomedical research papers spanning 25 distinct subfields, curated from major
64 bio-literature repositories. From this foundation, we developed an LLM-powered action discovery
65 agent capable of reading papers and extracting key tasks, tools, and databases essential to driving
66 biomedical discoveries. These elements are then selected and implemented into Biomni-E1, the
67 foundational environment that defines the biomedical action space for agentic interaction. Biomni-
68 E1 includes 150 specialized biomedical tools, 105 software packages, and 59 databases. We then
69 designed Biomni-A1, a general-purpose agent architecture capable of flexibly executing a broad
70 spectrum of biomedical tasks by using tools and datasets provided by Biomni E1. Given a user
71 query, the agent first uses a retrieval system to identify the most relevant tools, databases, and soft-
72 ware needed. It then applies LLM-based reasoning and domain expertise to generate a detailed,
73 step-by-step plan. Each step is expressed through executable code, enabling precise and flexible
74 compositions of biomedical actions – an essential feature given the domain’s reliance on highly
75 specialized tools and data resources. Unlike traditional function-calling methods, this approach
76 supports the dynamic and complex nature of biomedical workflows. This integrated system allows
77 Biomni not only to solve challenging, large-scale biomedical problems with efficiency, but also to
78 generalize to novel tasks across previously unseen areas of biomedical research.

79 Rigorous benchmarking demonstrates Biomni’s outstanding performance across established
80 biomedical Q&A benchmarks, and robust generalization performance in eight challenging, realis-
81 tic scenarios never encountered during development. Additionally, we highlight Biomni’s practical
82 capabilities through three impactful case studies: (1) analyzing 458 files of wearable sensor data
83 to generate novel insights; (2) rapidly performing comprehensive bioinformatics analyses on mas-

84 sive raw datasets, such as single-cell RNA-seq and ATAC-seq data, to generate novel insights and
85 hypotheses; (3) autonomously designing laboratory protocols to assist wet-lab researchers. With
86 Biomni, we introduce the first generation of a scalable, general-purpose biomedical AI agent,
87 setting the stage for an era where virtual AI biologists work alongside human researchers to dra-
88 matically accelerate biomedical discovery from basic research to translation.

89 2 Results

90 **Overview of Biomni.** Biomni is a general-purpose biomedical AI agent comprising two main
91 components: Biomni-E1, a foundational biomedical environment with a unified action space, and
92 Biomni-A1, an intelligent agent designed to utilize this environment effectively.

93 Curating a unified biomedical action space is challenging due to its inherent complexity and
94 vastness. We systematically address this by employing an AI-driven approach (Figure 1a). Specif-
95 ically, we leveraged the 25 subject categories defined by bioRxiv, selecting the 100 most recent
96 publications per category. An action discovery LLM agent processed each paper sequentially,
97 extracting essential tasks, tools, databases, and software necessary to replicate or generate the de-
98 scribed research. This comprehensive set of resources constitutes the essential actions required to
99 perform a large set of biological research tasks.

100 We then curated Biomni-E1, an environment for a biomedical AI agent to perform a wide
101 range of actions (Figure 1b). Identified tools were rigorously verified by human experts, along
102 with corresponding test cases. These tools (Supplementary Table 1-Table 18) were specifically
103 chosen for their non-trivial nature, encompassing complex code, domain-specific know-how, or
104 specialized AI models. Recognizing the inherent flexibility required by biological software, which
105 cannot always be simplified into static functions, we constructed an execution environment pre-
106 installed with 105 widely-used biological software packages (Supplementary Table 23-30), sup-
107 porting Python, R, and Bash scripts. For database integration, we categorized resources into two
108 distinct groups. The first group consists of massive relational databases accessible via web APIs
109 (e.g., PDB, OpenTarget, ClinVar) (Supplementary Table 19-20). Rather than creating numerous
110 individual retrieval tools, we implemented a unified function per database. Each function accepts
111 natural language queries and internally employs an LLM to parse database schemas and generate
112 executable queries dynamically. Databases without web interfaces were downloaded into a data

113 lake and preprocessed locally into structured pandas DataFrames for seamless integration with the
114 agent, for a total of 59 databases in Biomni-E1 (Supplementary Table 21-22). In summary, Biomni-
115 E1 is the first environment for biomedical AI agent and includes 150 specialized biomedical tools,
116 105 software, and 59 databases.

117 To build a general-purpose agent capable of tackling diverse biomedical tasks, we require a
118 specialized agentic architecture – one that avoids hardcoding workflows for each individual task.
119 This led to the development of Biomni-A1, which incorporates several core innovations critical
120 for operating across the biomedical research landscape. First, we introduce an LLM-based tool
121 selection mechanism designed to navigate the complexity and specialization of biomedical tools,
122 dynamically retrieving a tailored subset of resources based on the user’s goal. Second, recognizing
123 that biomedical tasks often require rich procedural logic, Biomni-A1 uses code as a universal
124 action interface – allowing it to compose and execute complex workflows involving loops, par-
125 allelization, and conditional logic. Crucially, this approach also enables the agent to interleave
126 calls to software, tools, databases, and raw data operations that do not conform to predefined func-
127 tion signatures-supporting flexible and dynamic integration of heterogeneous resources. Third, the
128 agent adopts an adaptive planning strategy: it formulates an initial plan grounded in biomedical
129 knowledge and iteratively refines it throughout execution, enabling responsive, context-aware be-
130 havior. Together, these innovations enable Biomni-A1 to generalize to previously unseen tasks and
131 domains, dynamically composing intelligent actions and interfacing with software, data, and tools
132 in a way that embodies generalist biomedical intelligence (Figure 1c).

133 **Biomni excels on general biomedical knowledge and reasoning benchmarks.** We evaluated
134 Biomni on three challenging multiple-choice benchmarks of general biomedical knowledge and
135 reasoning: Humanity’s Last Exam (HLE)²³ and LAB-Bench²⁴, which includes two key subtasks –
136 DbQA (Database Question Answering) and SeqQA (Sequence Question Answering) (Figure 2a).
137 These tasks span tool use, symbolic reasoning, and structured biological information retrieval –
138 core competencies for any robust biomedical AI agent. To isolate the impact of tool access and
139 agent design, we compared Biomni against six strong general-purpose baselines (details in Sup-
140 plementary Notes A). Specialized methods^{25,26} designed for each task is not considered as we aim
141 to compare on generalist performance.

142 For LAB-Bench, a 45-question development set was used to refine tool and database inter-
143 faces, while the final evaluation was conducted on 315 held-out test questions, with performance
144 averaged across three independent runs. We only curated a representative 12.5% subset of the full
145 benchmark due to API cost constraints. In DbQA, which requires structured querying over biolog-
146 ical databases, Biomni achieved 74.4% accuracy – matching expert human performance (74.7%)
147 and outperformed all baselines, including the coding agent (ReAct+Code, 40.8%). In SeqQA,
148 which involves reasoning over DNA and protein sequences, Biomni achieved 81.9% accuracy,
149 again exceeding human-level performance (78.8%).

150 To test true generalization of biomedical knowledge and reasoning *without any development*
151 *set*, we also evaluated Biomni on a 52-question subset of HLE spanning 14 biomedical subfields
152 – from molecular biology to physiology. Biomni achieved 17.3% accuracy, significantly outper-
153 forming the base LLM (6.0%), coding agent (12.8%), and literature agent (12.2%). These re-
154 sults demonstrate Biomni’s ability to generalize across unfamiliar, open-ended biomedical domains
155 without any task-specific adaptation. Additional ablation results are shown in Supplementary Fig-
156 ures 1-2. Performances across each subfield are reported in the Supplementary Figure 3.

157 **Biomni generalizes to new, real-world biomedical tasks across diverse subfields.** To evaluate
158 generalization in realistic research tasks, we curated eight new biomedical benchmarks spanning
159 genetics, genomics, microbiology, pharmacology, and clinical medicine (Figure 2b). Each task
160 was framed to reflect a common, well-defined, but complex real-world biomedical research goal,
161 including: (1) Variant prioritization: Identify the most likely causal variant from a list of poten-
162 tial variants for a trait, requiring reasoning about regulatory functions in non-coding regions. (2)
163 GWAS causal gene detection: Select the most likely causal gene within a locus, demanding fine-
164 grained locus-level inference. (3) CRISPR perturbation screen design: Construct gene panels to
165 maximize post-perturbation effect across a large (~20,000 genes) search space. (4) Rare disease
166 diagnosis: Map patient phenotypes and genetic findings to rare disease diagnosis. (5) Drug repur-
167 posing: Given a rare disease and a list of candidate drugs, select the best therapeutic match. (6)
168 Single-cell RNA-seq annotation: Assign accurate cell-type labels to individual cell profiles across
169 tissues, species, and platforms. (7) Microbiome disease-taxa analysis: Perform statistical associa-
170 tion tests on microbiome datasets to uncover disease-relevant taxa. (8) Patient gene prioritization:

171 Given an individual patient's genetic profile and phenotype description, identify the most plausi-
172 ble causal gene. We benchmarked Biomni without prompt engineering or task-specific fine-tuning
173 against three baselines: (1) a base LLM (Claude Sonnet 3.7) without tool use, (2) a coding agent
174 with direct function calls and code execution (ReAct+Code), and (3) Biomni-ReAct, an ablation
175 of Biomni that replaces code-based planning with ReAct-style chaining. The complete benchmark
176 constructions are described in Methods, with detailed performance comparisons in Supplementary
177 Notes B.

178 Across all tasks, Biomni outperformed the base LLM by an average relative performance
179 gain of 402.3%, the coding agent by 43.0%, and its own ablated variant Biomni-ReAct by 20.4%.
180 These findings highlight the importance of code-centric planning and environment grounding, en-
181 abling Biomni to compose precise, flexible, and context-aware actions. For each benchmark, we
182 further analyzed the execution trajectories, identifying commonly invoked tools, software, and
183 datasets, as detailed in Supplementary Figures 6-16. These trajectories provide insight into the
184 complexity and structure of agent behavior across tasks. On average, Biomni executes between 6
185 and 24 distinct steps per task, involving combinations of 0-4 specialized tools, 1-8 software pack-
186 ages, and 0-3 unique data lake items. The agent interleaves data extraction, search/retrieval, rea-
187 soning, and computational analyses (Supplementary Figure 8) – reflecting a workflow pattern that
188 mirrors how human scientists alternate between retrieving knowledge and generating new insights.
189 Resource usage varies by task type: information synthesis tasks, such as CRISPR perturbation
190 screen design and GWAS causal gene identification, rely heavily on database queries (e.g., KEGG,
191 Reactome) and literature search (e.g., PubMed, Google), whereas bioinformatics analysis tasks
192 like microbiome profiling and single-cell annotation involve minimal database use but extensive
193 code execution with software libraries such as scanpy.

194 **Biomni jointly analyzes 458 wearable sensor files to generate physiological hypotheses.** To
195 evaluate Biomni's performance in real-world biomedical workflows, we invited scientists to ap-
196 ply it directly to their own research questions. In this case study, a researcher used Biomni to
197 analyze 458 Excel files containing months-long wearable sensor data (continuous glucose moni-
198 toring (CGM) and body temperature) from 30 participants. The data were highly heterogeneous:
199 file formats varied, annotations were inconsistent, and participants exhibited substantial variability

200 (Figure 3a). The researcher posed an open-ended question: Can we uncover biologically meaningful
201 thermogenic patterns?

202 Biomni autonomously generated and executed a 10-step analysis pipeline (Figure 3b), inferring
203 meal events from glucose spikes, extracting pre/post meal temperature windows, normalizing
204 across individuals, and synthesizing population-level trends. Crucially, after completing the
205 pipeline, the agent delivered a structured, human-readable report summarizing its key findings
206 (Supplementary Notes D). It identified a consistent postprandial thermogenic response, with an
207 average temperature rise of 2.19°C (median: 1.10°C) and a wide range across individuals (-
208 0.11°C to 15.56°C). Some participants showed rapid, pronounced spikes within 30 minutes of
209 eating, while others had delayed or muted responses – indicating divergent metabolic phenotypes
210 (Figure 3c,d). These insights were not manually curated or extracted by a human; the agent per-
211 formed the entire analysis end-to-end and surfaced the results as a concise narrative highlighting
212 patterns that would otherwise be ignored in raw data.

213 In a parallel workflow, the scientist requested Biomni to analyze 227 nights of wearable-
214 recorded sleep data across 10 participants. Biomni computed averages for duration, efficiency,
215 latency, and sleep stage composition, derived a composite sleep quality score, and conducted
216 chronobiological analyses. The agent delivered a structured summary to the user (Supplemen-
217 tary Notes D, Supplementary Figure 4), including personalized sleep profiles and timing insights,
218 without human post hoc synthesis. Biomni uncovered several novel insights: sleep efficiency
219 consistently peaked mid-week (on Wednesdays) and declined on Sundays, suggesting a potential
220 behavioral pattern tied to pre-Monday stress or weekend-induced disruptions. Another important
221 finding was that consistent sleep timing correlated more strongly with higher sleep quality than
222 total sleep duration, highlighting the critical role of circadian regularity in maintaining restorative
223 sleep.

224 The scientist then tasked Biomni with analyzing multi-omics data (652 lipidomic, 731 metabolomic,
225 and 1,470 proteomic features), jointly with the CGM data. Biomni conducted cross-omics correla-
226 tion analysis, applied hierarchical clustering to uncover biologically coherent feature groups, and
227 performed unsupervised PCA to link CGM signals to molecular pathways. It automatically gener-
228 ated interpretable outputs – trajectory plots, heatmaps, boxplots, PCA biplots, and cluster maps –
229 empowering rapid insight generation from complex multimodal datasets (Supplementary Notes D,

230 Supplementary Figure 5). Significant correlations among lipids, metabolites, and proteins revealed
231 tightly interlinked regulatory pathways, underscoring the systems-level nature of metabolic regula-
232 tion. Notably, several identified biomarkers showed consistent patterns across samples and exhib-
233 ited high connectivity within correlation networks. Across all cases, the scientist noted that Biomni
234 accelerated the path from messy real-world data to testable hypotheses, supporting applications in
235 sleep optimization, metabolic research, and precision health.

236 **Biomni automates complex multi-omics analysis to decipher transcriptional regulation of**
237 **skeletal lineages.** To test whether Biomni could generalize to complex omics workflows, a sci-
238 entist used it to analyze a recently published multi-omics dataset of the developing human skeleton ²⁷.
239 This dataset comprises 336,162 single-nucleus RNA-Seq (snRNA) and ATAC-seq (snATAC-Seq),
240 paired with spatial transcriptomics data collected from human embryos between 5-11 weeks post-
241 conception (Figure 3e). While the original study emphasized developmental trajectories and dis-
242 ease mechanisms, the scientist was interested in exploring gene regulatory mechanisms across
243 emerging skeletal cell types – a technically demanding task typically requiring extensive bioinfor-
244 matics support.

245 The scientist asked Biomni to investigate transcriptional regulation across skeletal lineages
246 using a detailed instruction (Supplementary Notes E). The system autonomously planned and exe-
247 cuted a ten-stage analysis pipeline: (1) loading and exploring all datasets, (2) preparing RNA-seq
248 data for analysis, (3) configuring pySCENIC to retrieve motifs, (4) running GRNBoost2 to infer
249 gene regulatory networks, (5) pruning networks using cisTarget, (6) calculating regulon activity
250 with AUCell, (7) extracting accessibility data from ATAC-seq, (8) filtering predicted targets us-
251 ing ATAC-seq accessibility, (9) analyzing activity patterns across cell types, developmental stages,
252 and anatomical regions, and (10) summarizing findings and preparing a report to the scientist. It
253 enabled Biomni to predict transcription factor-target gene links and filter regulons based on mo-
254 tif enrichment and chromatin accessibility correlations (Figure 3f). The full run, completed in
255 just over five hours, handled real-time execution issues (e.g., variable name mismatches) by sub-
256 sampling and debugging locally. Throughout, Biomni maintained all intermediate outputs – code,
257 figures, and logs – organized in a reproducible folder structure for validation and inspection. The
258 agent summarized all the analysis and generated a report describing the analysis and key findings

259 (Supplementary Notes E).

260 In its final gene regulatory network (GRN) analysis (Figure 3h), Biomni re-capitulated known
261 regulatory relationships between key osteogenic transcription factors such as RUNX2 and HHIP,
262 confirming how they are regulated by a shared set of anti-osteogenic transcription factors including
263 TWIST1, LMX1B, and ALX4 ²⁷. These findings align with author's report ²⁷ about the balanced
264 regulation needed for proper bone formation and suture patency. Furthermore, Biomni also uncov-
265 ered several unreported TFs, including AUTS2, ZFHX3, and PBX1, showed unexpectedly high
266 regulatory activity across multiple skeletal cell types. Although PBX1 is a well-established skele-
267 tal regulator ²⁸ and ZFHX3/AUTS2 have only limited or indirect skeletal reports (in mouse ²⁹
268 or zebrafish ³⁰), their broad activity here suggests under-appreciated roles across diverse skele-
269 tal lineages. Biomni reported that these novel regulators were particularly active in osteoblasts,
270 preosteoblasts, and various chondrocyte populations, suggesting they play important but previ-
271 ously unrecognized roles in the transcriptional control of skeletal cell fate determination during
272 human embryonic development. Finally, Figure 3g-h reveals how Biomni's visualizations effec-
273 tively captured both temporal dynamics of regulator activity and cell-type-specific variations in key
274 regulons like RUNX2. This demonstrates how Biomni enables researchers to autonomously per-
275 form complex multi-omics analysis and rapidly generate testable hypotheses without specialized
276 programming expertise.

277 **Biomni designs wet-lab validated experimental protocol for cloning.** To evaluate Biomni's
278 ability to support real-world experimental design, we focused on a core task in molecular biology:
279 cloning. This process is central to countless workflows in research and biotechnology and requires
280 complex reasoning, from designing high-fidelity primers to choosing the right assembly method
281 and validating constructs. While general-purpose LLMs have struggled to perform such tasks due
282 to limited domain knowledge and tool access ²⁴, Biomni integrates LLM reasoning with dynamic
283 tool execution, enabling expert-level performance in molecular biology tasks.

284 To rigorously evaluate this task, we first collaborated with an expert group of gene-editing
285 researchers to design an open-ended cloning benchmark and expert user study (Figure 4a). Our
286 benchmark consisted of 10 realistic, representative cloning tasks covering Golden Gate, Gibson,
287 Gateway, and restriction cloning – each with options including single-fragment vs. pooled assem-

288 bly. The benchmark also included essential validation steps, such as designing Sanger sequencing
289 primers and analyzing restriction digests. We posed these tasks to four entities: an LLM (Claude
290 3.7), Biomni, a human trainee (Stanford Biology Master with previous experience in cloning),
291 and a senior human expert (Stanford Genetics PostDoc with 5+ years of cloning experience).
292 Each was asked to generate a complete, end-to-end protocol along with the final cloned plas-
293 mid map. Blinded expert reviewers assessed the outputs. Biomni produced protocols and designs
294 that matched the human expert in accuracy and completeness – often providing comparable lev-
295 els of detail and anticipating the same edge cases. In contrast, the human trainee’s submissions
296 were frequently incomplete or suboptimal, reflecting the experience gap typical in early-stage re-
297 searchers. Remarkably, Biomni completed all tasks autonomously in a fraction of the time taken
298 by the expert.

299 To further validate Biomni in a real-world setting, a scientist assigned it a practical cloning
300 task: cloning a guide RNA targeting the human B2M gene into the lentiCRISPR v2 Blast construct
301 (Figure 4b). Biomni successfully executed the task through a comprehensive workflow (Figure 4c).
302 First, it analyzed the plasmid structure using annotation and pattern search tools to identify key fea-
303 tures necessary for cloning. It then designed three Cas9 sgRNAs targeting B2M using specialized
304 knockout sgRNA design tools. For the cloning process, Biomni generated forward and reverse
305 oligos with BsmBI overhangs to enable directional insertion of the sgRNA sequence. It produced
306 detailed protocols (Figure 4d) for oligo annealing, double-stranded DNA formation, and Golden
307 Gate cloning into the target vector. Biomni also provided complete bacterial transformation in-
308 structions, including heat-shock steps and antibiotic selection. For quality control, it designed a
309 U6 promoter sequencing primer to verify sgRNA insertion and simulated the Golden Gate assem-
310 bly to produce the final plasmid map.

311 The scientist followed Biomni’s protocol exactly to perform the wet-lab experiment (Fig-
312 ure 4e). Colonies appeared on the plate the next day; two were cultured, miniprepped, and se-
313 quenced using the Biomni-designed primers – both showing perfect alignment. This case illustrates
314 how scientists can rely on Biomni to autonomously design complex molecular biology experiments
315 with accuracy comparable to human experts, but in a fraction of the time.

316 **User-friendly interface to empower scientists to generate biomedical discoveries.** To bring the

317 power of Biomni into the hands of every scientist, we built an intuitive graphical interface – avail-
318 able at <https://biomni.stanford.edu> – to help transform the way researchers interact with biomedical
319 data and tools. This seamless platform enables users to submit natural language queries and receive
320 results powered by the full capabilities of Biomni’s agentic system. Whether designing complex
321 cloning experiments, querying multi-omics databases, or generating hypotheses from wearable
322 data, scientists can now access the intelligence of a general-purpose biomedical AI agent without
323 writing a single line of code. The interface is designed for rapid iteration, real-time feedback, and
324 visual traceability, allowing users to explore intermediate steps, inspect tool usage, and validate
325 results interactively. By closing the gap between biomedical intent and execution, Biomni opens a
326 new era of accessible, automated, and scalable scientific discovery. An example of this interface is
327 shown in Supplementary Figure 17.

328 3 Discussion

329 Biomni marks a major step forward in biomedical research, demonstrating robust generalization
330 across diverse subfields and laying the groundwork for AI agents as integral collaborators in sci-
331 entific discovery. Its zero-shot performance across complex tasks – including those in genetics, ge-
332 nomics, microbiology, immunology, pharmacology, and clinical medicine – underscores its poten-
333 tial to boost research productivity, accelerate discovery, and broaden access to advanced biomedical
334 analyses.

335 By automating complex, labor-intensive workflows, which normally require both expert
336 knowledge and coding skills, Biomni enables researchers to redirect their efforts toward creative
337 hypothesis generation, experimental innovation, and cross-disciplinary collaboration. This shift
338 holds profound implications. In the context of target and drug discovery for biopharma, Biomni
339 can autonomously prioritize targets, design perturbation screens, or repurpose drugs – offering a
340 path to faster, more cost-effective research. In clinical application settings, its capabilities in gene
341 prioritization and rare disease diagnosis point to more accurate, personalized insights and stream-
342 lined diagnostics. For consumer health, Biomni’s integration of wearable data and multi-omics
343 analyses envisions real-time, individualized health monitoring and intervention.

344 Nonetheless, several limitations remain. While Biomni’s unified environment spans a wide
345 range of biomedical tools and databases, the evaluated tasks represent only a subset of the field,

346 and key domains remain unexplored. In addition, in the action discovery agent, our decision to pri-
347 oritize the most recent literature makes the agent appear timely, but risks overlooking foundational
348 concepts and techniques that have faded from current discourse despite their enduring relevance.
349 The future versions should encapsulate a larger coverage of publications when defining the envi-
350 ronment. Moreover, although Biomni approaches human-level performance in tasks like database
351 querying, sequence analysis, and molecular cloning, it still struggles in areas requiring nuanced
352 clinical judgment, novel experimental reasoning, analytical inventions, or deep biological thinking
353 and synthesis. No system yet captures the full scope of human biomedical expertise. As reflected
354 in our benchmarks, Biomni has not achieved expert-level performance across all task categories.
355 We expect continued improvements as foundation models evolve and the agentic environment ex-
356 pands, as well as thanks to human experts and trainees deploying Biomni to facilitate or augment
357 their work.

358 These limitations open promising directions for future development. Training biomedical
359 reasoning agents with reinforcement learning could enable continuous self-improvement in plan-
360 ning and execution. Integrating multimodal data – text, images, and structured inputs – may further
361 deepen reasoning capabilities. Equipping Biomni to autonomously discover and incorporate new
362 tools and databases, as well as incorporate more historical methods (which may have high utility
363 but can be easily forgotten by human users), would ensure adaptability and long-term relevance.

364 Looking ahead, Biomni and its successors could become foundational infrastructure in an AI-
365 powered biomedical ecosystem, working seamlessly with human experts to unlock novel insights
366 into health and disease. This hybrid partnership may radically reshape biomedical research –
367 automating hypothesis generation, scaling discovery pipelines, and enabling medical innovation
368 to proceed at unprecedented speed and scope. General-purpose agents like Biomni could not only
369 accelerate breakthroughs but redefine the future of scientific inquiry itself.

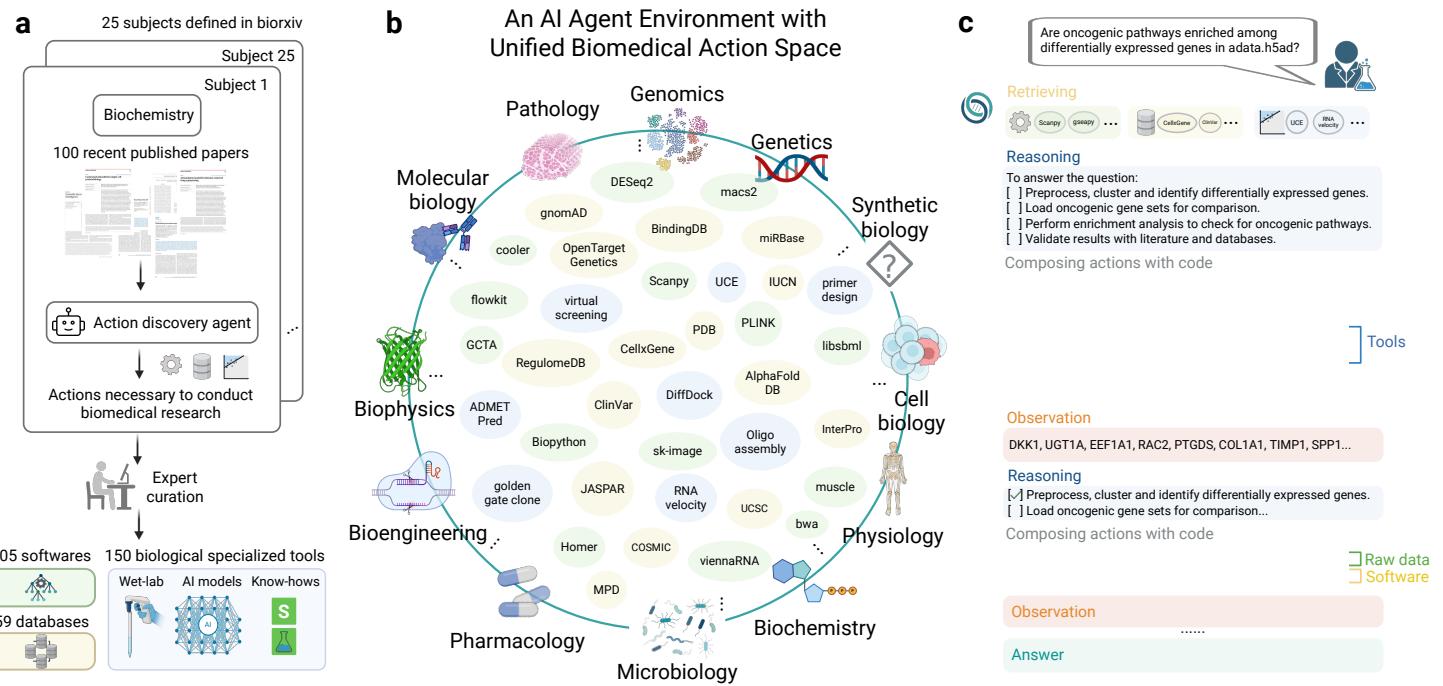


Figure 1: Overview of the unified biomedical action space and agent environment in Biomni. (a) Workflow for systematically curating the unified biomedical action space. Actions necessary to conduct biomedical research were extracted from 2,500 recent bioRxiv publications across 25 biomedical subfields using an AI-driven discovery agent. Extracted actions were rigorously validated and curated by human experts, resulting in the integration of 105 biomedical software tools, 150 specialized biological tools (including wet-lab protocols, AI-driven predictive models, and domain-specific know-how), and 59 comprehensive biomedical databases. (b) Illustration of the unified biomedical action space spanning diverse biomedical subfields such as genetics, genomics, synthetic biology, cell biology, physiology, microbiology, pharmacology, bioengineering, biophysics, molecular biology, and pathology. Representative tools and databases integrated into Biomni’s environment are shown, highlighting its general-purpose capabilities. (c) Example workflow demonstrating Biomni’s reasoning and action composition process to autonomously answer a complex biological question. Biomni retrieves relevant tools based on the user’s query, formulates a structured reasoning plan, and composes executable code to perform comprehensive bioinformatics analyses, iteratively refining its reasoning based on observations until converging on a final, precise answer.

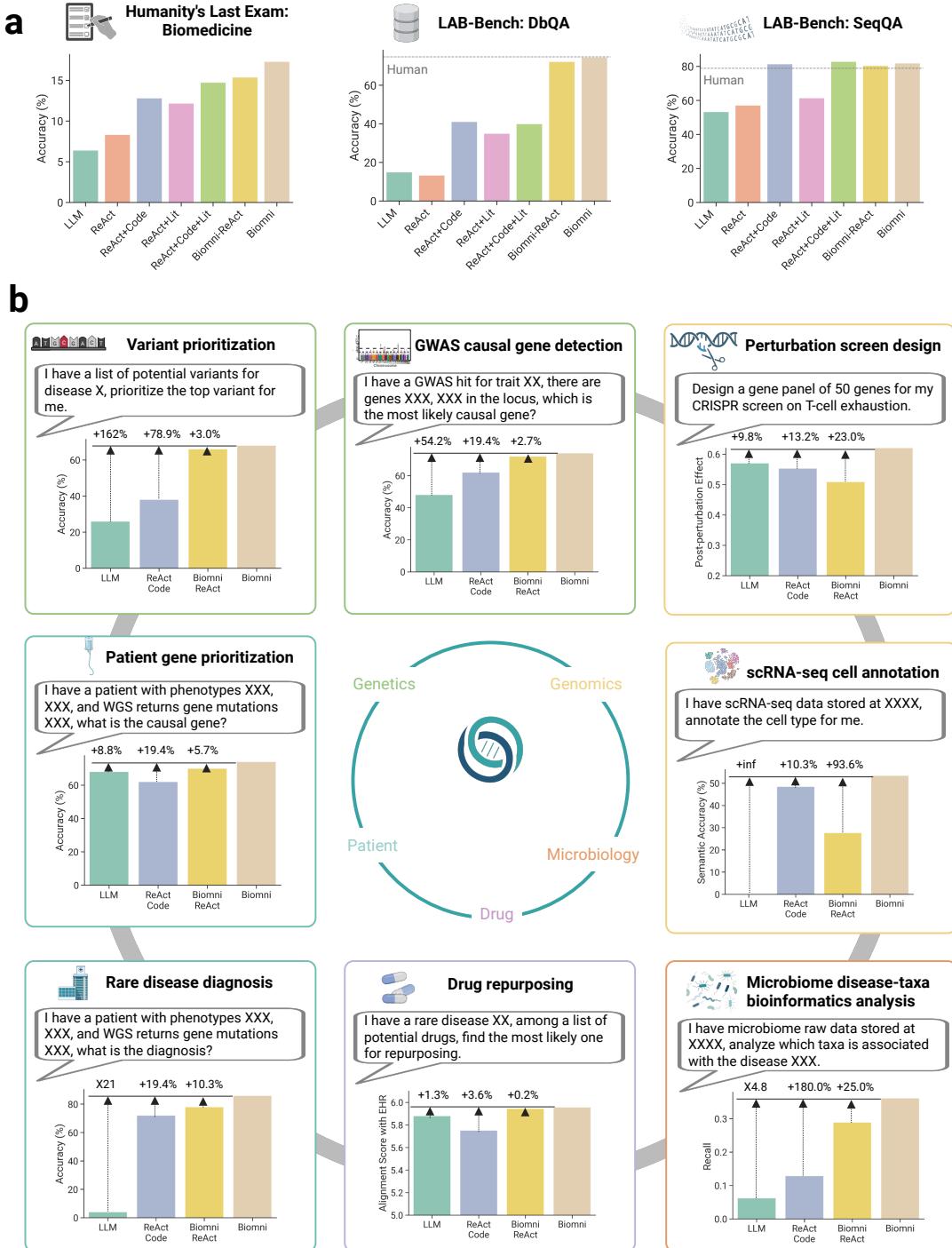


Figure 2: Zero-shot generalization of Biomni across diverse realistic biomedical tasks. (a) Biomni is superior to 6 baselines in Q&A multiple choice benchmarks that broadly evaluate the model's capability across biomedical fields. (b) Biomni demonstrates robust zero-shot performance across eight previously unseen, real-world biomedical scenarios spanning multiple biomedical sub-fields, without any task-specific fine-tuning or prompt engineering. Evaluated tasks include variant prioritization and GWAS causal gene detection (genetics and genomics), perturbation screen design (functional genomics, immunology), patient gene prioritization, rare disease diagnosis (clinical genomics), drug repurposing (pharmacology), microbiome disease-taxa bioinformatics analysis (microbiology), and single-cell RNA-seq cell annotation (single-cell biology). Across these diverse scenarios, Biomni consistently outperformed baseline models (Base LLM, ReAct+Code) and specialized environments (Biomni ReAct), highlighting its general-purpose biomedical capabilities and ability to autonomously adapt to new and complex biomedical tasks.

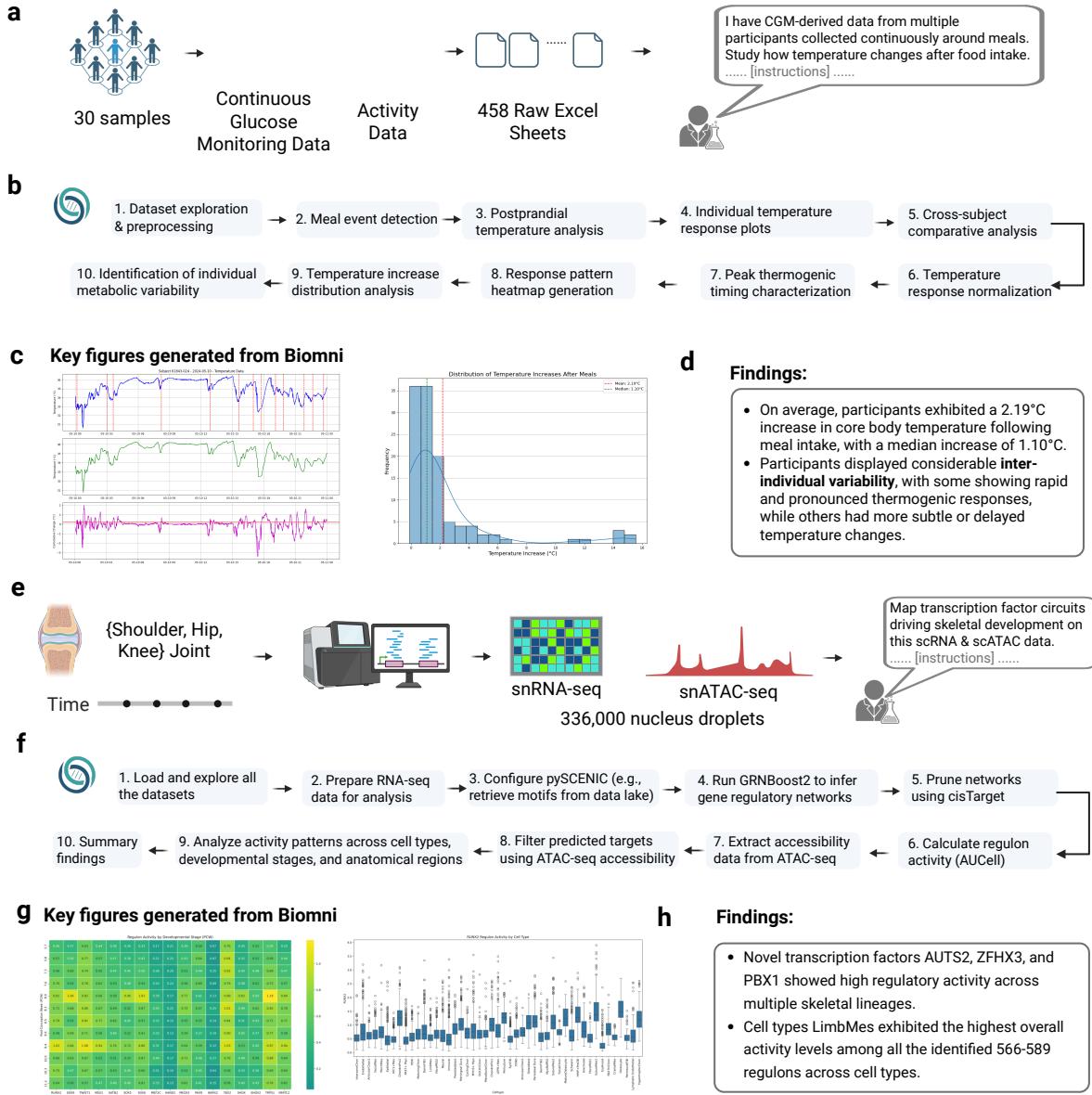


Figure 3: Biomni autonomously executes complex multi-modal biomedical analyses to generate hypothesis. (a-d) Biomni rapidly analyzed CGM-derived thermogenic responses data and activity data from 30 individuals, comprising 458 raw Excel sheets. (b) Workflow demonstrating Biomni's autonomous execution of data preprocessing, meal event detection, postprandial temperature analysis, and thermogenic response characterization. (c) Representative individual temperature-response plots and temperature increase distribution following meals, automatically generated by Biomni. (d) Summary of unique biological findings identified by Biomni, including significant increases in core body temperature post-meal intake (average 2.19°C , median 1.10°C), and notable inter-individual variability in thermogenic responses. (e-h) Biomni autonomously analyzed single-cell multiomics data from approximately 336,000 nucleus droplets, combining single-nucleus RNA (snRNA-seq) and single-nucleus ATAC sequencing (snATAC-seq) across human embryonic joint development (shoulder, hip, knee). (f) A detailed workflow diagram showing Biomni's 10-step analysis pipeline for gene regulatory networks with multiomics. (g) Two key figures generated from Biomni: Left panel shows a heatmap of regulator activity by developmental stage, with color intensity indicating activity levels. Right panel displays a boxplot of RUNX2 regulon activity by cell type, showing variation in expression across different cell populations. (h) Key findings from the GRN analysis: 1) Novel transcription factors (AUTS2, ZFHX3, and PBX1) showing high regulatory activity across multiple skeletal lineages despite no previous association with skeletal development, and 2) Across the 566-589 regulons recovered, limb mesenchyme cells display the highest mean regulon activity score, underscoring their prominent role in skeletal transcriptional control.

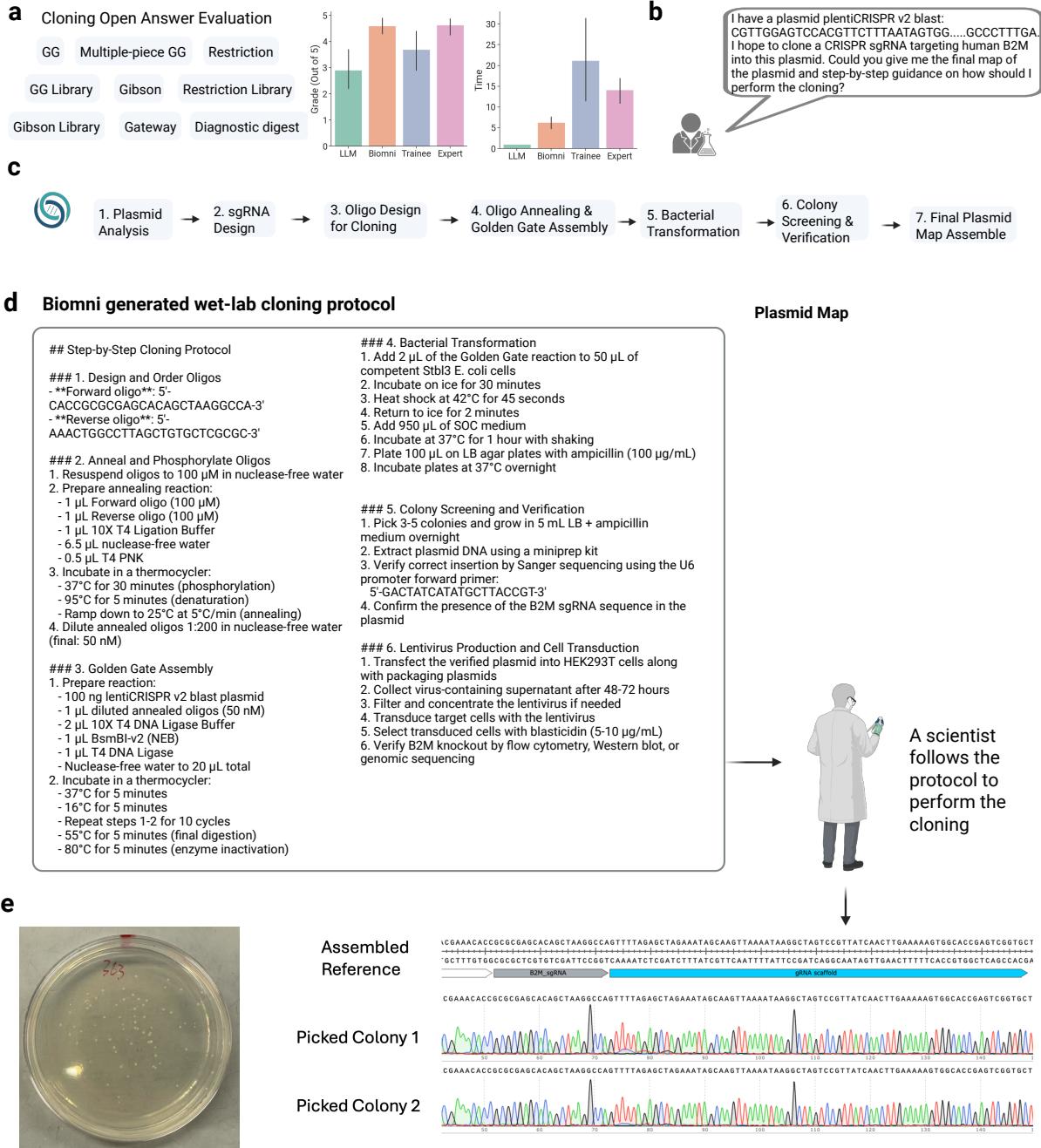


Figure 4: Biomni designs wet-lab experimental protocol. (a) Open-ended cloning benchmark on 10 real cloning scenarios. We compared against base LLM, trainee-level human, and expert-level human scientists. We found that Biomni has similar accuracy as the expert level scientist, and significantly higher accuracy than trainee level, while using much less time. (b) Example of a user request to Biomni for cloning an sgRNA targeting the human B2M gene into the lentiCRISPR v2 Blast plasmid. (c) Biomni's automated stepwise workflow, including plasmid analysis, sgRNA design, oligo synthesis, Golden Gate assembly, bacterial transformation, colony screening, and final plasmid mapping. (d) Biomni-generated detailed cloning protocol with step-by-step instructions and comprehensive plasmid map, enabling laboratory scientists to execute the experiment autonomously. (e) Validation of Biomni's cloning protocol through successful colony growth on selection plates, followed by Sanger sequencing confirming perfect alignment of sgRNA insertion in picked colonies, demonstrating Biomni's robust capability for precise and reliable experimental design.

370 4 Methods

371 **Action Discovery from Literature.** 100 recent publications from the year 2024 at biorxiv Were
372 collected and analyzed by extracting and parsing their PDF contents. Each paper was processed
373 in chunks, and a specialized prompt guided an LLM through each chunk to explicitly identify
374 and extract three categories of actionable insights: tasks, software, and databases. Specifically for
375 tasks, the LLM was instructed to highlight recurrent tasks requiring specialized implementations
376 within biomedical research workflows.

377 **Implementing the Biomni Environment.** In the initial iteration of environment construction, a
378 conservative and focused approach was adopted for tool curation. Initially, tasks were filtered
379 based on relevance to the primary research interests-drug discovery and clinical biomedicine-
380 retaining fields such as biochemistry, bioengineering, biophysics, cancer biology, cell biology, de-
381 velopmental biology, genetics, genomics, immunology, microbiology, molecular biology, pathol-
382 ogy, pharmacology, physiology, synthetic biology, and systems biology. Subsequently, these were
383 narrowed down to approximately 1,900 commonly recurring tasks. These tasks were further man-
384 ually reviewed to eliminate redundancy and exclude tasks that were trivial or easily implementable
385 through simple code. Selecting highly specialized tasks that require significant domain expertise
386 was emphasized, such as wet-lab protocols and advanced AI models.

387 Human scientists then collaborated with software engineering agents equipped with web
388 search capabilities to implement each specialized tool. Every tool underwent rigorous validation,
389 requiring a clearly defined test case that it successfully passed. This stringent process culminated in
390 a curated collection of 150 specialized tools. Additionally, essential literature retrieval tools were
391 included, such as PubMed and Google Scholar, with provisions for future iterative expansions.

392 Each tool was strictly defined using a comprehensive checklist that mandated: (1) a clear
393 and descriptive name, (2) detailed documentation, (3) outputs formatted as detailed research logs
394 optimized for LLM interpretation, (4) the inclusion and successful passing of a specific test case,
395 and (5) specialization criteria-if a task could easily be implemented via brief LLM-generated code
396 (e.g., simple database queries), no specialized tool was created.

397 Databases were categorized and extensive relational databases accessible via web APIs (e.g.,
398 PDB, OpenTargets, ClinVar) were integrated using a unified querying function. This function
399 accepts natural language inputs and leverages an LLM to dynamically parse database schemas
400 and execute corresponding queries. Databases lacking web APIs were downloaded and locally
401 preprocessed into structured pandas DataFrames for seamless accessibility by the agent.

402 For software integration, recognizing the frequent necessity of concurrently utilizing multiple

403 software tools, a unified containerized environment was constructed, which was pre-installed with
404 a comprehensive suite of relevant software. Additionally, this environment supports the execution
405 of R packages and command-line interface (CLI) tools.

406 **Biomni-A1.** The Biomni agent is a general-purpose biomedical AI agent built upon the CodeAct³¹
407 framework, designed to systematically solve biomedical tasks by combining LLMs with an inter-
408 active coding environment. Given a user query, Biomni begins by prompting the LLM to generate
409 a clear, numbered bullet-list plan detailing the steps needed to tackle the given problem, keeping
410 careful track of progress and adjustments along the way. As the tool, software, and database space
411 is vast, the query task may only use a small set of these resources. To avoid long context, a prompt-
412 based retriever is utilized, powered by a separate LLM, where the agent dynamically selects the
413 most relevant functions, datasets, and software libraries from available resources. During execu-
414 tion, the LLM generates code, executes it in a coding environment (Python, R, or Bash), and returns
415 the resulting observations to inform subsequent reasoning. This iterative approach continues until
416 the agent converges on an accurate, validated solution.

417 **Q&A Benchmarks.** Development and testing sets were created by sampling the LAB-Bench
418 Database Question-Answering and Sequence Question-Answering benchmarks²⁴. Due to resource
419 constraints, each set comprises 12.5% of the complete reference, proportionally distributed across
420 benchmark subtasks, providing a cost-effective and representative assessment of model perfor-
421 mance. The development set informed iterative refinements to Biomni’s database integrations and
422 tool implementations, while the test set provided an independent evaluation of generalization ca-
423 pabilities. Accuracy was evaluated by following the LAB-Bench protocol, using multiple-choice
424 answer options with an option for abstention due to insufficient information. Results represent
425 averages across three independent evaluation runs.

426 For Humanity’s Last Exam (HLE)²³, a representative sample of questions was selected, span-
427 ning fourteen subdisciplines of Biology/Medicine: Genetics, Biology, Ecology, Neuroscience,
428 Biochemistry, Microbiology, Immunology, Molecular Biology, Computational Biology, Biophysics,
429 Bioinformatics, Genomics, and Physiology. From each subdiscipline, up to five questions were
430 sampled (or the maximum number available if fewer than five existed in the category). This
431 sampling approach yielded a final evaluation set of 52 questions that comprehensively assessed
432 Biomni’s performance across the biological sciences. The evaluation was conducted directly with-
433 out the use of a development set.

434 **Curating real-world benchmarks.** The variant prioritization benchmark was curated from Open
435 Target Genetics³² ground truth set, and processed such that given a variant, a negative set of vari-

436 ants is found. The prompt was as follows: "Your task is to identify the most promising variant
437 associated with a given GWAS phenotype for futher examination. From the list, prioritize the
438 top associated variant (matching one of the given variant). GWAS phenotype: {trait} Variants:
439 {variant_list}". Accuracy was used as the metric. The GWAS causal gene detection benchmark
440 utilized a dataset curated from Shringarpure et al³³, using the original prompt: "Your task is to
441 identify likely causal genes within a locus for a given GWAS phenotype. From the list, provide
442 only the likely causal gene (matching one of the given genes). Identify the causal gene. GWAS
443 phenotype: {trait} Genes in locus: {gene_str}". Accuracy was used as the metric. The pertur-
444 bation screen design benchmark was curated from Schmidt et al.³⁴. The prompt is "Task: Plan
445 a CRISPR screen to{task_description}. There are 18,939 possible genes to perturb and only per-
446 turb {num_genes} genes. For each perturbation, you can measure out {measurement} which will
447 be referred to as the score. Generate {num_genes} genes that maximize the perturbation effect.
448 Output format: a list of genes 1. XXX 2.XXX 3.XXX ...". The evaluation metric was the average
449 post-perturbed effect. As the scale differs for the post-perturbed effect, one screen (IL-2) was used.
450 The scRNA-seq annotation benchmark ensured flexibility across diverse data formats (e.g., Cel-
451 lxGene, author-hosted portals), encompassing multiple tissues, species, sequencing technologies,
452 and experimental conditions. Datasets with author-provided annotations (Tier 1 or Tier 2, typically
453 ≥ 10 cell types) were prioritized, and 20k-50k cells were subsampled proportionally to their cell
454 type distributions. Automatic evaluation was conducted at the single-cell level using LLMs via
455 *semantic match*, accounting for both naming variations (e.g., fibroblast vs. Fibroblast cells) and
456 hierarchical relations (e.g., CD8+ T cells vs. T cells), judged on-the-fly by LLM agents and later
457 verified by humans. In the microbiome benchmark, both Biomni and human experts independently
458 performed differential abundance analysis on five diverse microbiome datasets, selected to reflect
459 different data types, biological contexts, and analytical challenges. Dataset 1 comes from the MGM
460 2.0 platform³⁵ and includes relative microbial abundance across samples and another with sample
461 labels, ideal for classification tasks³⁵. Dataset 2 curated from a well-known Nature study, offers
462 microbial abundance data in mice alongside metadata such as diet and sex, making it valuable for
463 modeling host-microbiome interactions³⁶. Dataset 3, developed by Pasolli et al.³⁷, combines eight
464 human metagenomic studies with species-level features processed using MetaPhlAn2³⁷. Dataset 4
465 explores microbial communities in drinking water systems, providing an OTU matrix with abun-
466 dances represented as relative sequence counts. This environmental dataset allows models to be
467 tested beyond host-associated microbiomes³⁸. Finally, Dataset 5 is an in-house resource derived
468 from the Human Microbiome Project³⁹. Together, these datasets provide a comprehensive foun-
469 dation for benchmarking AI agents in microbiome analysis across both clinical and environmental

470 domains. Biomni results were compared against those generated by human experts for consistency,
471 accuracy, and efficiency. The drug repurposing benchmark used a dataset from Huang et al.⁴⁰, for
472 the task of identifying the most likely drug from a pre-defined list of drugs for repurposing in a
473 given indication. Evaluation was based on the alignment score with off-label prescription patterns
474 of clinicians from an EHR system. The prompt was "Your task is to identify top 5 drugs that can
475 be potentially repurposed to treat the given disease. From the list, prioritize the drug list with
476 the highest potential (matching the given DrugBank IDs). Disease: {disease} Drugs: {drug_list}
477 Output format: a list of drugs with their DrugBank IDs, no drug name, just the IDs: 1. DB00001
478 2. DB00002 3. DB00003 ..". The rare disease diagnosis benchmark used the MyGene2 dataset,
479 curated by Alsentzer et al.⁴¹. The ground truth was expert annotated diagnosis. The prompt was
480 "Task: given a patient's phenotypes and a list of candidate genes, diagnose the rare disease that
481 the patient has. Phenotypes: {phenotype_list} Candidate genes: {candidate_genes} Output format:
482 {{'disease_name': XXX, 'OMIM_ID': XXX}}". The patient gene prioritization benchmark used
483 a dataset curated by Alsentzer et al.⁴¹. The ground truth was a truly causal gene. The prompt was
484 "Task: Given a patient's phenotypes and a list of candidate genes, identify the causal gene. Phe-
485 notypes: {phenotype_list} Candidate genes: {candidate_genes} Output format: {{'causal_gene':
486 [gene1]}}".

487 **Wearable analysis case study.** A wearable case study integrated CGM-derived body temperature
488 data, sleep metrics, and multi-omics datasets from human participants⁴², as follows: CGM Body
489 Temperature Data: For each participant, continuous glucose monitors (CGMs) equipped with tem-
490 perature sensors recorded skin temperature in high resolution. A total of 485 temperature files were
491 collected, each centered on a presumed meal event. The time window for each file spanned 6 hours
492 total, comprising 2 hours pre-meal and 4 hours post-meal. Sleep Data: Sleep metrics were derived
493 from wrist-worn wearable devices for a subset of 10 participants, covering 227 nights of sleep. Pa-
494 rameters collected included sleep duration, sleep efficiency, sleep latency, sleep stage composition
495 (light, deep, REM), and number of wake episodes. Omics Data: Blood samples were analyzed to
496 generate the following: Lipidomics: 652 lipid features across 147 samples; Metabolomics: 731
497 metabolite features across 147 samples; Proteomics: 1,470 protein features across 20 samples.

498 **Multiome analysis case study.** The authors' dataset was directly downloaded and used with no
499 modifications²⁷. The authors' study generated a multi-omic dataset of human embryonic skeletal
500 development from 5-11 weeks post-conception. The dataset includes snRNA-seq and snATAC-seq
501 data from approximately 336,000 nuclei across five anatomical regions (hip, knee, shoulder joints,
502 calvaria, and skull base). The dataset covers both appendicular (limb) and cranial regions. No

503 additional tools or manual preprocessing were added. As the analytical traces are extensive, more
504 guidance was included in the prompt instruction and two use cases were tested:

505 *Comparative Analysis.* This analysis focused on how cellular processes differ across anatomical
506 locations and developmental timepoints. Biomni was instructed to characterize the cellular
507 composition across anatomical regions (calvaria, skull base, shoulder, hip, knee) and developmen-
508 tal stages. We prompted Biomni with detailed instructions (Supplementary Section E), including
509 cell type proportion estimates, region-specific population labels, UMAP embeddings, stacked bar
510 plots, a comparison of intramembranous versus endochondral ossification, key transcription factor
511 highlights, and developmental trajectory tracing.

512 *Gene Regulatory Network Analysis* We asked Biomni to identify transcriptional programs underly-
513 ing skeletal development. Following a systematic 10-step process, Biomni inferred gene regulatory
514 networks by: (1) loading and exploring all datasets, (2) preparing RNA-seq data for analysis, (3)
515 configuring pySCENIC to retrieve motifs, (4) running GRNBoost2 to infer gene regulatory net-
516 works, (5) pruning networks using cisTarget, (6) calculating regulon activity with AUCell, (7)
517 extracting accessibility data from ATAC-seq, (8) filtering predicted targets using ATAC-seq ac-
518 cessibility, (9) analyzing activity patterns across cell types, developmental stages, and anatomical
519 regions, and (10) summarizing findings.

520 *Manual verification* To evaluate whether the aggregated findings are truly reflected by the data or
521 merely simulated or hallucinated by the LLM, manual (human) verification was conducted follow-
522 ing the traces and codes generate by Biomni.

523 **Wetlab Benchmark Development and Evaluation.** A comprehensive benchmark was developed
524 consisting of 20 open-ended cloning questions curated from real-world applications to represent
525 the diversity and complexity of molecular cloning tasks across four major categories: Golden
526 Gate assembly, Gibson assembly, restriction enzyme cloning, and Gateway cloning. Each cate-
527 gory included both single-construct and pooled cloning scenarios. Additionally, the benchmark
528 incorporated common validation methods, including diagnostic restriction digestion, Sanger se-
529 quencing primer design, and sequence alignment analysis. For establishing baseline performance,
530 three human experts with extensive experience in molecular cloning were recruited. These experts
531 were instructed to complete each task without utilizing language models but were permitted to use
532 standard molecular biology tools, search engines, and publicly available online resources such as
533 plasmid repositories and primer design platforms. The time required for each expert to complete
534 each task was recorded, from initial task understanding to the final protocol and plasmid map gen-
535 eration. In parallel, Biomni and general LLM models were evaluated on identical tasks. Each
536 system was provided with the same task descriptions and required to generate detailed end-to-end

537 experimental protocols and final cloned plasmid maps. For general LLMs, Claude 3.7 was used as
538 one of the most capable publicly-available models at the time of testing, providing it with the same
539 information but without access to specialized molecular biology tools. For evaluation, an indepen-
540 dent senior researcher with experience in molecular cloning technologies was recruited and blinded
541 to the source of each protocol (human expert, Biomni, or general LLM). The evaluator assessed
542 each protocol and plasmid map based on two primary criteria: (1) Accuracy: The correctness of
543 the proposed methodology, including appropriate enzyme selection, reaction conditions, primer
544 design parameters, and plasmid construction strategy. (2) Completeness: The thoroughness of the
545 protocol, including all necessary steps, reagents, concentrations, incubation times, and verification
546 methods. Each criterion was scored on a scale of 1-5 according to a detailed rubric (Supplementary
547 Table S31-32). The average scores across all 20 tasks were calculated for each system and human
548 expert to enable direct comparison.

549 **Wetlab Validation.** A practical cloning task was selected for validation: the insertion of a guide
550 RNA targeting the human B2M gene into the lentiCRISPR v2 Blast construct. This task was
551 chosen for its relevance to CRISPR-based gene editing applications and its moderate complexity,
552 involving multiple molecular biology techniques. The experiment was conducted in a standard
553 molecular biology laboratory setting using commercially available reagents and materials. The
554 lentiCRISPR v2 Blast plasmid was obtained from Addgene. All protocols for the experiment were
555 generated entirely by Biomni without modification (Supplementary Notes F), including plasmid
556 analysis, sgRNA design, oligo design with appropriate overhangs, detailed Golden Gate assembly
557 conditions, bacterial transformation parameters, and verification strategies. For validation of the
558 cloning results, standard molecular biology practices were followed, selecting colonies for cul-
559 ture and miniprep, followed by Sanger sequencing using the Biomni-designed primers. Sequence
560 alignment analysis was performed to verify the correct insertion of the sgRNA sequence. The
561 success of the cloning process was determined by the presence of bacterial colonies on selective
562 media and subsequent sequence verification confirming the accurate incorporation of the designed
563 sgRNA construct into the lentiCRISPR v2 Blast backbone.

564 **Data availability.** All data used in Biomni are publicly available at Harvard Dataverse under
565 <https://doi.org/10.7910/DVN/CE4ZYG>.

566 **Code availability.** Biomni is open-sourced at <https://github.com/snap-stanford/biomni>. A web-
567 based user interface is available at <https://biomni.stanford.edu>. Note that the public tool is not for
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579 **Authors contribution.** K.H., Y.R., J.L. conceived the study. K.H. and J.L. supervised the project.
580 K.H. designed and developed the framework. K.H., S.Z., H.W., Y.Q., Y.L. implemented tools
581 and databases. K.H. designed and implemented the generalist agent architecture. K.H. and R.L.
582 designed the action discovery agent. S.Z. performed benchmarks on Q&A tasks. K.H., H.W., Y.L.
583 collected and implemented benchmarks on realistic tasks. X.Z. provided advice on microbiome
584 benchmark. H.W., J.Z., P.H., K.H. performed multi-omics integration case study. Y.L., K.H.
585 performed wearable data analysis case study. Y.Q., J.Z., D.Y., S.Z., Y.L., K.H. performed wet-
586 lab case study. K.H., S.M., J.C., M.W., J.B. performed rare disease diagnosis case study. R.L.
587 performed qualitative trace analysis. R.L., L.Q., G.L., provided support for software. K.H., S.Z.,
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589 the final manuscript.

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592 References

- 593 1. Cong, L. *et al.* Multiplex genome engineering using crispr/cas systems. *Science* **339**, 819–823
594 (2013).
- 595 2. Jumper, J. *et al.* Highly accurate protein structure prediction with alphafold. *nature* **596**,
596 583–589 (2021).
- 597 3. Van Dyck, C. H. *et al.* Lecanemab in early alzheimers disease. *New England Journal of
598 Medicine* **388**, 9–21 (2023).
- 599 4. López-Otín, C., Blasco, M. A., Partridge, L., Serrano, M. & Kroemer, G. Hallmarks of aging:
600 An expanding universe. *Cell* **186**, 243–278 (2023).
- 601 5. Botvinik-Nezer, R. *et al.* Variability in the analysis of a single neuroimaging dataset by many
602 teams. *Nature* **582**, 84–88 (2020).
- 603 6. Thiele, I. & Palsson, B. Ø. A protocol for generating a high-quality genome-scale metabolic
604 reconstruction. *Nature protocols* **5**, 93–121 (2010).
- 605 7. Gibney, E. & Van Noorden, R. Scientists losing data at a rapid rate. *Nature* **10** (2013).
- 606 8. Wang, H. *et al.* Scientific discovery in the age of artificial intelligence. *Nature* **620**, 47–60
607 (2023).
- 608 9. Ridnik, T., Kredo, D. & Friedman, I. Code generation with alphacodium: From prompt engi-
609 neering to flow engineering. *arXiv preprint arXiv:2401.08500* (2024).
- 610 10. Cui, J., Li, Z., Yan, Y., Chen, B. & Yuan, L. Chatlaw: Open-source legal large language model
611 with integrated external knowledge bases. *CoRR* (2023).
- 612 11. Tom, G. *et al.* Self-driving laboratories for chemistry and materials science. *Chemical Reviews*
613 **124**, 9633–9732 (2024).
- 614 12. Peng, C. *et al.* A study of generative large language model for medical research and healthcare.
615 *NPJ digital medicine* **6**, 210 (2023).
- 616 13. Qu, Y. *et al.* Crispr-gpt: An llm agent for automated design of gene-editing experiments.
617 *bioRxiv* 2024–04 (2024).
- 618 14. Swanson, K., Wu, W., Bulaong, N. L., Pak, J. E. & Zou, J. The virtual lab: Ai agents design
619 new sars-cov-2 nanobodies with experimental validation. *bioRxiv* 2024–11 (2024).
- 620 15. Roohani, Y. *et al.* Biodiscoveryagent: An ai agent for designing genetic perturbation experi-
621 ments. *International Conference on Learning Representations* (2025).
- 622 16. Wang, E. *et al.* Txgemma: Efficient and agentic llms for therapeutics. *arXiv preprint
623 arXiv:2504.06196* (2025).
- 624 17. Xiao, Y. *et al.* Cellagent: An llm-driven multi-agent framework for automated single-cell data
625 analysis. *BioRxiv* 2024–05 (2024).
- 626 18. Youngblut, N. D. *et al.* scbasecamp: an ai agent-curated, uniformly processed, and continually
627 expanding single cell data repository. *bioRxiv* 2025–02 (2025).

629 19. Hu, M. *et al.* Evaluation of large language models for discovery of gene set function. *Nature methods* 1–10 (2024).

630

631 20. Wei, J. *et al.* Chain-of-thought prompting elicits reasoning in large language models. *Advances in neural information processing systems* **35**, 24824–24837 (2022).

632

633 21. Yao, S. *et al.* React: Synergizing reasoning and acting in language models. In *International Conference on Learning Representations (ICLR)* (2023).

634

635 22. Guo, D. *et al.* Deepseek-r1: Incentivizing reasoning capability in llms via reinforcement learning. *arXiv preprint arXiv:2501.12948* (2025).

636

637 23. Phan, L. *et al.* Humanity’s last exam. *arXiv preprint arXiv:2501.14249* (2025).

638 24. Laurent, J. M. *et al.* Lab-bench: Measuring capabilities of language models for biology research. *arXiv preprint arXiv:2407.10362* (2024).

639

640 25. Narayanan, S. *et al.* Aviary: training language agents on challenging scientific tasks. *arXiv preprint arXiv:2412.21154* (2024).

641

642 26. Ghareeb, A. E. *et al.* Robin: A multi-agent system for automating scientific discovery. *arXiv preprint arXiv:2505.13400* (2025).

643

644 27. To, K. *et al.* A multi-omic atlas of human embryonic skeletal development. *Nature* **635**, 657–667 (2024).

645

646 28. Gordon, J. A. *et al.* Pbx1 represses osteoblastogenesis by blocking hoxa10-mediated recruitment of chromatin remodeling factors. *Molecular and cellular biology* (2010).

647

648 29. Gomez, G. A. *et al.* Evaluation of potential roles of zinc finger homeobox 3 (zfhx3) expressed in chondrocytes and osteoblasts on skeletal growth in mice. *Calcified Tissue International* **115**, 445–454 (2024).

649

650

651 30. Geng, Z., Tai, Y. T., Wang, Q. & Gao, Z. Auts2 disruption causes neuronal differentiation defects in human cerebral organoids through hyperactivation of the wnt/β-catenin pathway. *Scientific reports* **14**, 19522 (2024).

652

653

654 31. Wang, X. *et al.* Executable code actions elicit better llm agents. In *Forty-first International Conference on Machine Learning* (2024).

655

656 32. Ghoussaini, M. *et al.* Open targets genetics: systematic identification of trait-associated genes using large-scale genetics and functional genomics. *Nucleic acids research* **49**, D1311–D1320 (2021).

657

658

659 33. Shringarpure, S. S. *et al.* Large language models identify causal genes in complex trait gwas. *medRxiv* 2024–05 (2024).

660

661 34. Schmidt, R. *et al.* Crispr activation and interference screens decode stimulation responses in primary human t cells. *Science* **375**, eabj4008 (2022).

662

663 35. Zhang, H., Kang, Z., Zhang, Y., Yang, R. & Ning, K. Towards a generative paradigm for large-scale microbiome analysis by generative language model. *bioRxiv* 2025–01 (2025).

664

665 36. Turnbaugh, P. J. *et al.* A core gut microbiome in obese and lean twins. *nature* **457**, 480–484 (2009).

666

667 37. Pasolli, E., Truong, D. T., Malik, F., Waldron, L. & Segata, N. Machine learning meta-analysis
668 of large metagenomic datasets: tools and biological insights. *PLoS computational biology* **12**,
669 e1004977 (2016).

670 38. Gomez-Alvarez, V. & Revetta, R. P. Monitoring of nitrification in chloraminated drinking
671 water distribution systems with microbiome bioindicators using supervised machine learning.
672 *Frontiers in Microbiology* **11**, 571009 (2020).

673 39. Turnbaugh, P. J. *et al.* The human microbiome project. *Nature* **449**, 804–810 (2007).

674 40. Huang, K. *et al.* A foundation model for clinician-centered drug repurposing. *Nature Medicine*
675 **30**, 3601–3613 (2024).

676 41. Alsentzer, E. *et al.* Few shot learning for phenotype-driven diagnosis of patients with rare
677 genetic diseases. *medRxiv* 2022–12 (2022).

678 42. Metwally, A. A. *et al.* Prediction of metabolic subphenotypes of type 2 diabetes via continuous
679 glucose monitoring and machine learning. *Nature Biomedical Engineering* 1–18 (2024).

680 43. Katz, D. *et al.* The multi-omic, multi-tissue response to acute endurance and resistance exercise:
681 Results from the molecular transducers of physical activity consortium. *Circulation* **150**,
682 A4143199–A4143199 (2024).