



sciblock

User Manual

A research workbench · an AI assistant that works like a senior labmate

October 2026

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Part 1 · Getting to know sciblock

Chapter 1 · What sciblock is

sciblock is a desktop research workbench for scientists. It keeps your projects, experiments, data, literature, records and outputs (briefs, reports, papers, patents) in one place, and it comes with a built-in AI assistant that understands research: sciAI. Like a senior labmate, sciAI works from the real data you upload to help you analyze results, design the next round of experiments, organize records and write reports.

Keep these basic principles of sciblock in mind before you read the rest of the manual:

- **The AI speaks only from your data.** Every factual statement sciAI makes carries a source marker that you can open to trace back to the original file. When the data is insufficient, it says so plainly instead of making up numbers for you.
- **Everything follows the "Scope".** The Scope Bar at the top of the center column always tells you which project, module or experiment the AI is looking at right now.
- **AI inferences are labeled separately from your measurements.** Any value the AI derived in a draft, board or record is labeled "Inferred" or "To confirm", and it only counts once you confirm it.
- **Outputs are editable.** Briefs, reports, papers and patents can all be revised in the chat, and the final result exports as an editable Word file or PDF.

1.1 Who it is for

You are	What sciblock does for you
Master's / PhD student	Manage experiment records, analyze data, design the next round of experiments, write briefs, research proposals and papers
Advisor / PI	Set up a lab, bring your students in, follow each student's progress at any time, and use AI to see the whole group's situation
Research administrator	Use "Records Organizer" to turn certificates, rosters, notices, contracts and similar materials into searchable, citable records

1.2 How to read this manual

- **First time using it:** start with Chapter 2, "Ten-minute quick start", and walk through the full workflow once.
- **To complete a specific task:** jump to the relevant section from the table of contents. Every section follows the structure "When to use → Steps → What you'll see → If something goes wrong" and can be read on its own.

- **To look up a term or a limit:** go to the final part, "Reference", which contains an index of interface elements, file formats and limits, a glossary, FAQs and troubleshooting.

Text in quotation marks in this manual is the actual wording in the app's interface, so you can match it on screen.

Chapter 2 · Ten-minute quick start

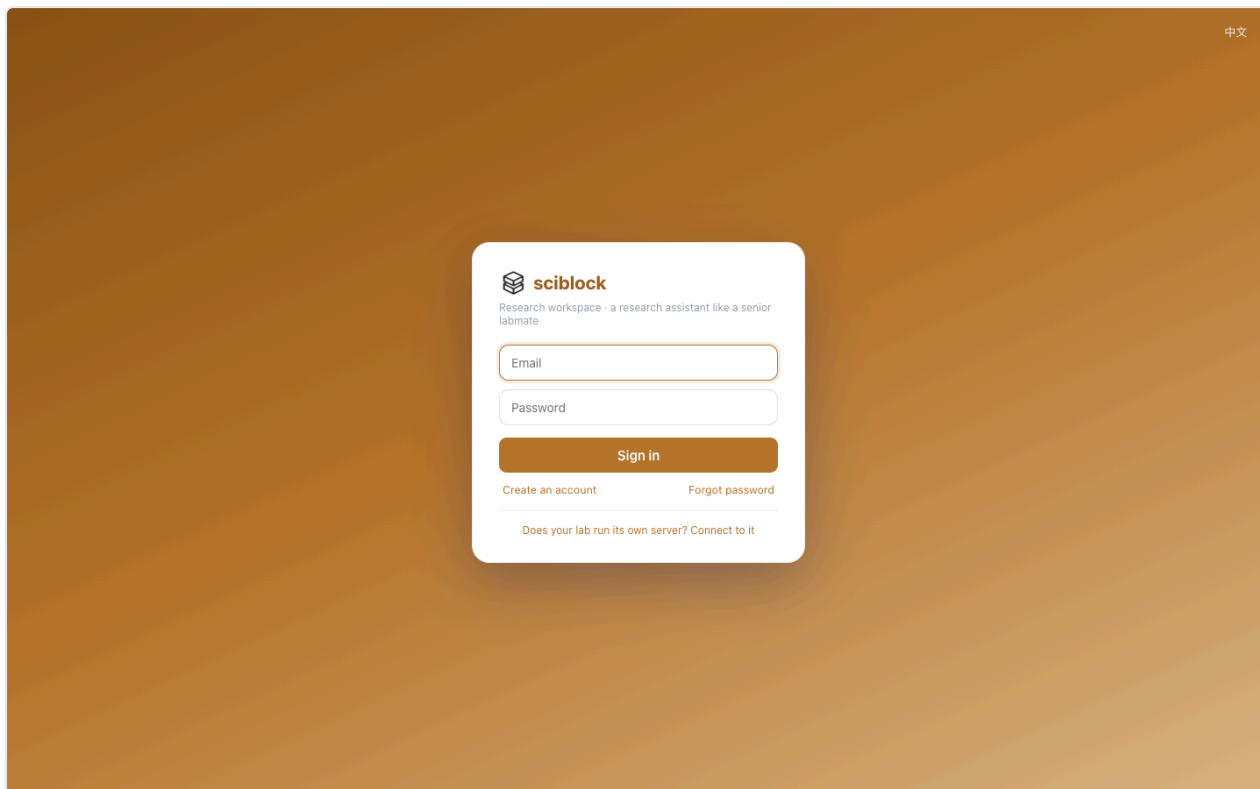
For: researchers using sciblock for the first time. **Estimated time:** 10 to 15 minutes. **You'll need:** an email address that can receive verification codes; a CSV or Excel data file is helpful, but you can also just get familiar with the interface first.

2.1 Installation and first launch

1. Download the installer for your platform (Windows / macOS) from an official channel and double-click to install.
2. On first launch you'll see the "Welcome to sciblock" page, which asks you to choose where to store your data. Click "Choose folder..." to pick a location yourself, or keep the default, then click "Use this location, start →".
3. After that, every launch goes straight to the sign-in page.

Choose an ordinary local folder as the data location. Do not choose a folder synced by a cloud drive such as iCloud, OneDrive or Jianguoyun (a Chinese cloud drive); the sync software will fight sciblock over the files.

2.2 Sign up and sign in



Sign-in page: email + password, with "Create an account" and "Forgot password" at the bottom

Sign up

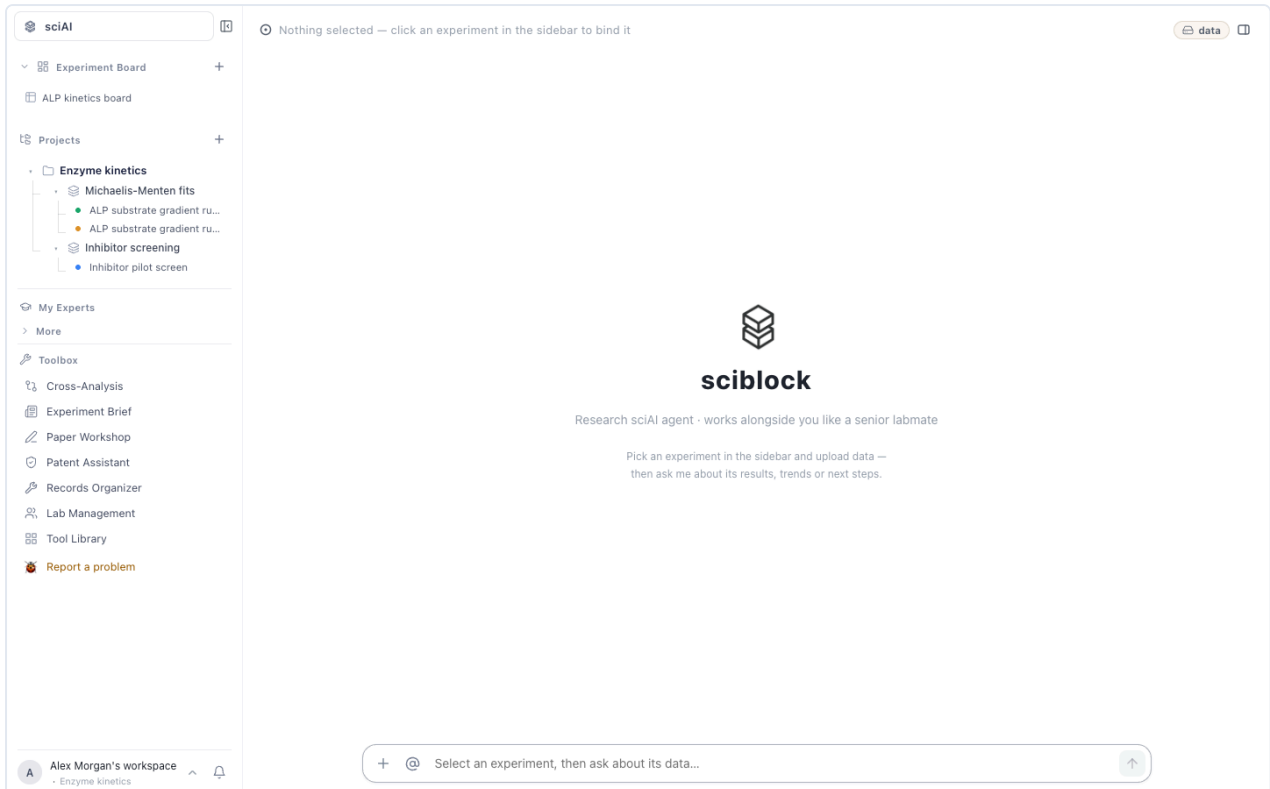
1. At the bottom of the sign-in page, click "Create an account".
2. Enter your email and click "Send code"; the button starts a 60-second countdown. Check your inbox for a 6-digit verification code (look in your spam folder if it isn't in your inbox).
3. Enter the code, set a password (at least 8 characters), enter your name (your real name is recommended, since it is used in experiment records, bylines and collaboration later), and fill in your university, major and research area.
4. If sign-up is currently invitation-only, you also need to enter the invitation code your administrator gave you.
5. Click "Sign up and sign in". Once sign-up succeeds, you go straight into the workbench.

Signing in and resetting your password

From then on, open sciblock, enter your email and password, and click "Sign in". If you forget your password, click "Forgot password" and reset it with an email verification code. After a successful reset, sessions on your other devices are signed out and you need to sign in again with the new password.

Once you have signed in at least once, you can enter the workbench and keep working with your local data even when you are temporarily offline.

2.3 The three-column workbench



Three-column workbench: project tree and toolbox on the left, chat in the center, structured panel on the right

After signing in, you land on sciblock's core interface, which is split into three columns:

Left column: what you're researching and what tools you have

- "❖ sciAI" at the top: the entry to the global research assistant. It isn't tied to an experiment, and you can ask it anything.
- "Experiment Board": put several experiments in one table to compare them side by side.
- The "Projects" tree: a three-level structure of project > module > experiment that expands and collapses like a file manager. Click a row and the AI uses it as the analysis scope.
- The "More" group (collapsible): contains entries such as LabHub and the Literature Library; the row just above it is "My Experts".
- "Toolbox": the tools you've added (Cross-Analysis, Experiment Brief, Paper Workshop, Patent Assistant...) and the entry to the "Tool Library".
- At the bottom: your avatar and name (the Account menu) and the message bell (a red dot means unread messages).

Center column: the main area for chatting with the AI and using tools

- Top: the Scope Bar, which shows the project > module > experiment the AI is currently looking at, plus the experiment status control.
- Middle: the chat messages.
- Bottom: the input box, "Ask something, or type @ to reference an attachment..."

Right column: details of the current experiment

It is controlled by the row of icons on the right side of the center column's header: Draft, Attachments and Record sheet are always shown, and "⋮ More panels" also contains Evidence, Analysis, Assets and Experts.

You can drag the dividers between the side columns and the center column to adjust their widths.

Someone walks you through it the first time. When a new account enters the workbench for the first time (no projects in the left column yet), a 7-step "Welcome tour" starts automatically: Projects tree → What the AI is looking at → Hand it your data → Right column → sciAI → Toolbox → Where to find help later. The highlighted area is clickable (clicking it counts as "try it" and moves to the next step); "Back / Next / Skip" or Esc leaves the tour at any time; the last step ends with "Start using". The first time you select an experiment and the icon row appears in the upper right, a second short tour walks you through the right column: a sentence each on Draft, Attachments and Record sheet, then a pointer to ⋮.

A "Getting started · N/5" checklist also appears above the chat area: create your first project, create an experiment, upload a file, ask your first question, look at a source or confirm a draft. Each "Do it" button takes you to the right place ("Ask your first question" only fills a starter question into the input box; it never sends for you). Items are ticked automatically from the real state of your data. Once closed, a small "Getting started N/5" pill stays at the bottom of the left column; close that too and it is gone. Later, an occasional in-place hint appears (💡 one sentence + ×), for example "⋮" in the upper right also holds Evidence, Analysis, Assets and Experts"; only one at a time.

All of this is shown to new accounts only. Existing accounts, or anyone who wants to see it again: the account menu's "Help & guide" (shortcut ? or F1) has "Replay tour", "Right panel tour" and "Getting-started checklist", plus a "Feature map" (one sentence per entry in all three columns, with "Go there" jumping straight there) and a "Shortcuts" table.

2.4 Create your first project and experiment

1. In the left column, click "+" to the right of the "Projects" heading, type a project name (for example, "Enzyme kinetics study"), and press Enter.
2. Hover over the project row, click the "+" in the row, type a module name (for example, "Km determination"), and press Enter.
3. On the module row, click the "+" in the row, type an experiment name (for example, "Enzyme activity curve – batch 1"), and press Enter.

The left column should now have a three-level structure. Once you select the experiment node, the Scope Bar at the top of the center column shows "Enzyme kinetics study > Km determination > Enzyme activity curve – batch 1", which means the AI knows which experiment you're working on.

sciAI

Enzyme kinetics › Michaelis-Menten fits › ALP substrate gradient run 1 Succeeded

I read this table as a "condition × response record table": 5 conditions · factors substrate_mM, each record measures rate_uM_per_min. Factors are conditions you set, not measured quantities, so I won't average them, and comparisons will be grouped by level. Click "Open record sheet" below to see the whole table — it comes from your upload "alp_gradient_run1.csv" and is read-only; to change it, edit the original file and upload it again.

Data record sheet [Open record sheet →](#)

5 conditions · factors substrate_mM
Record: rate_uM_per_min

[Review](#) [Like](#) [Share](#)

[Fit Michaelis-Menten to run 1 and report Km and Vmax](#)

Fitting the Michaelis-Menten model to run 1 gives $V_{max} \approx 8.0 \mu\text{M}/\text{min}$ and $K_m \approx 1.6 \text{ mM}$ ^{Source}. The two replicates agree within about 3%, so the fit is stable.

Next steps - click or type a number

1 Verify Repeat run 2 with 3 replicates to confirm the quercetin effect

2 Dig deeper Fit a competitive-inhibition model to runs 1 and 2

Basis [No literature search this round](#) [Based on this experiment's records](#) [Opened 2 original records](#) [Ran 1 code block](#)

[Review](#) [Like](#) [Share](#)

[+ Design the next round from this one](#)

[+ @ Ask something, or type @ to reference an attachment...](#)

After selecting an experiment: the Scope Bar shows the full path, and panels such as Draft can be opened on the right

2.5 Upload your first data file

sciAI

Enzyme kinetics › Michaelis-Menten fits › ALP substrate gradient run 1 Succeeded

I read this table as a "condition × response record table": 5 conditions · factors substrate_mM, each record measures rate_uM_per_min. Factors are conditions you set, not measured quantities, so I won't average them, and comparisons will be grouped by level. Click "Open record sheet" below to see the whole table — it comes from your upload "alp_gradient_run1.csv" and is read-only; to change it, edit the original file and upload it again.

Data record sheet [Open record sheet →](#)

5 conditions · factors substrate_mM
Record: rate_uM_per_min

[Review](#) [Like](#) [Share](#)

[Fit Michaelis-Menten to run 1 and report Km and Vmax](#)

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Next steps - click or type a number

1 Verify Repeat run 2 with 3 replicates to confirm the quercetin effect

2 Dig deeper Fit a competitive-inhibition model to runs 1 and 2

Basis [No literature search this round](#) [Based on this experiment's records](#) [Opened 2 original records](#) [Ran 1 code block](#)

[Review](#) [Like](#) [Share](#)

[+ Design the next round from this one](#)

[+ @ Ask something, or type @ to reference an attachment...](#)

Attachments

[Handoff package 1/6](#) [5 items missing](#)

Drop files here or click to upload (Excel / CSV / Images / PDF / Word / video)

CSV alp_gradient_ru... [Parsed](#) [Refresh](#) [Delete](#)

133 B · 2026-10-09 18:47 · 10 rows × 3 columns

[+ Add a note \(the AI will use it\)](#)

condition × response record sheet · 5 conditions · factors substrate_mM=0.5/1/2/4/8 · measures rate_uM_per_min — factors are set conditions and are not analyzed statistically.

Right-hand Attachments panel: drop files in to upload and parse them; each file shows its parse status

1. In the left column, select the experiment you just created.

2. Click the attachments icon at the top of the center column to open the "Attachments" panel on the right.
3. Drag a CSV or Excel file onto the "Drop files here or click to upload (Excel / CSV / images / PDF / Word / video)" area, or click the area to choose a file.
4. Wait for the status to change from "Pending parse" to "Parsed".

Expand the file entry to see a table preview, "Previewing the first 12 rows of N". This shows the data has been parsed into structured evidence the AI can read.

When you upload a single image, a card with three choices pops up above the input box: "Analyze this file only", "Compare with the whole experiment", and "Pick attachment files on the right to compare together". If you upload several images at once, they go into a gallery first; write a note for each one, then click "Analyze together".

2.6 Your first AI analysis

1. Make sure the Scope Bar shows the target experiment.
2. Type a question in the input box, for example "Analyze the relationship between substrate concentration and reaction rate, and calculate K_m and V_{max} ".
3. Press Enter to send (pressing Enter while an input method is composing characters only confirms the candidate and won't send the message by accident).

What you'll see:

- The AI starts streaming its answer. The activity line at the top shows "Analyzing · N s" and the current step, such as "Gathering materials", "Reading images", "Analyzing" or "Searching literature".
- The answer text carries source markers that you can open to jump to the corresponding attachment.
- At the top of the answer is a "Grounding" bar, for example "Checked 5/5 experiments", "Viewed 3 images", "Grounded in your data", showing which data this answer covered.

If the AI says there isn't enough data, it will quietly suggest that you add real data. Once you've added it, come back and ask again.

2.7 Save the experiment record (generate a draft)

1. When the conversation is done, click the draft icon at the top of the center column to open the "Draft" panel on the right.
2. Click "Generate experiment record draft". Generation runs in the background, and the interface shows "Organizing... (you can switch away; it keeps running)".
3. Once it's generated, review the entries one by one: each one is labeled with its source (Measured / Inferred / sciAI (AI suggestion) / Missing). You can edit or delete entries, and finally click "Confirm".

The confirmed draft is the official record of this experiment, and tools such as the brief and paper tools will cite it.

2.8 Chapter summary

You've now completed sciblock's basic loop: sign up and sign in → learn the three columns → create a project, module and experiment → upload data → AI analysis → generate a draft. Next, you can:

- Write a progress brief → "Experiment Brief" in the Toolbox (Chapter 8)
 - Compare across experiments → "Cross-Analysis" in the Toolbox (Chapter 8)
 - Have the AI help design your next round of experiments → start a research thread in one click with " " on the project row (Chapter 9)
 - Let your advisor see your progress → join a lab (Chapter 11)
-

Part 2 · Projects, experiments and data

Chapter 3 · Managing projects and experiments

3.1 Build the "project → module → experiment" structure

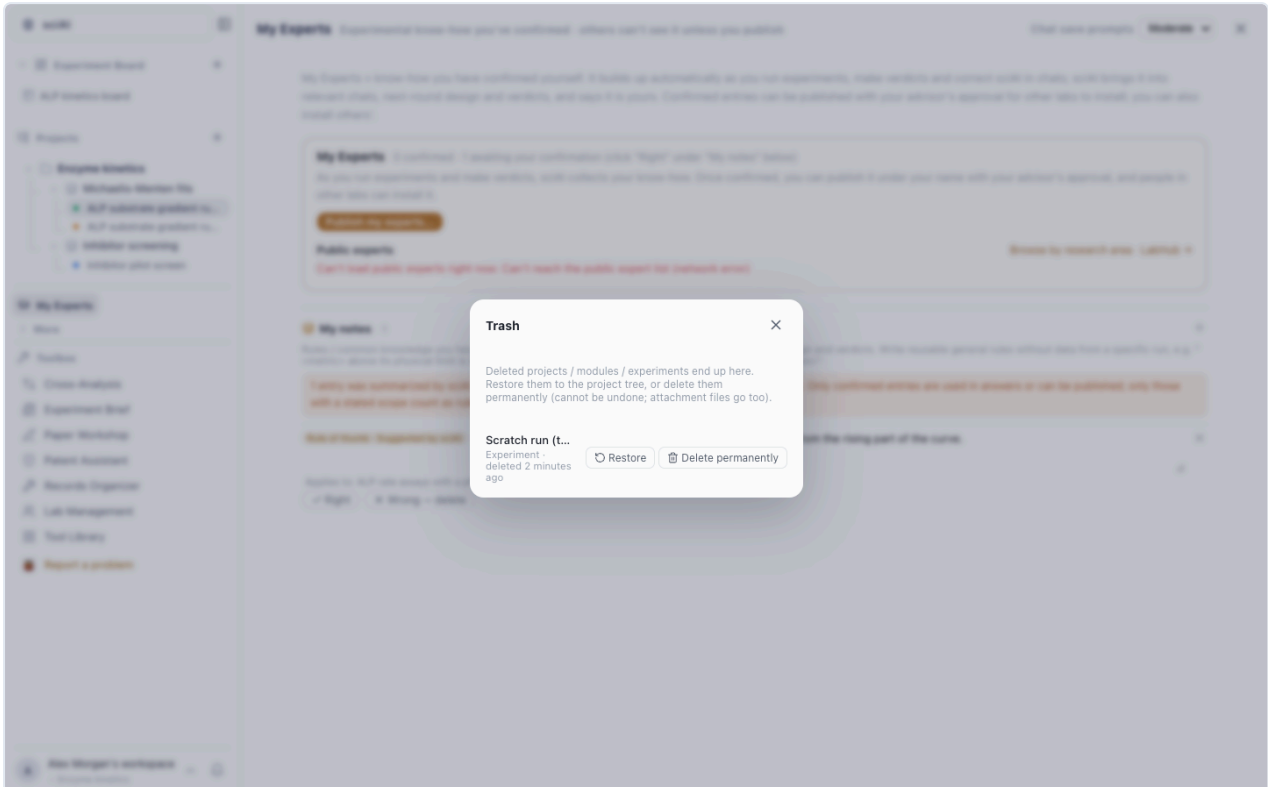
When to use: you're just starting with sciblock, or you're opening up space for a new research direction.

1. In the left column, click "+" to the right of the "Projects" heading, type a project name, and press Enter.
2. On the project row, click the "+" in the row, type a module name, and press Enter.
3. On the module row, click the "+" in the row, type an experiment name, and press Enter.
4. Click any node to make it the AI's analysis scope.

What the three levels mean: a **project** is a research direction; a **module** is a sub-question or a category of experiments within the project; an **experiment** is one specific experiment record, and data, attachments and drafts all belong to an experiment.

When the tree is empty, it reads "No projects yet. Click + at the top right to create your first one."

3.2 Rename, delete and the Trash



Trash: deleted projects / modules / experiments can be restored or permanently deleted

- **Rename:** hover over a node, click the "✎" in the row, change the name and confirm.
- **Delete:** click the "X" in the row. The confirmation dialog explains what will be affected, for example "Delete project "X" and everything in it?", "Delete module "X" and all its experiments?" or "Delete experiment "X"?". After you confirm, the node goes to the Trash rather than disappearing immediately.
- **Restore:** click your name at the bottom of the left column to open the Account menu → "Trash" → click "Restore" next to the node, and it returns to its original position.
- **Permanently remove:** in the Trash, click "Delete permanently". Its attachments are deleted too, and this cannot be undone.

3.3 Manage experiment status and record why an experiment failed

When to use: to see progress at a glance when several experiments run in parallel, and to leave a failure attribution when an experiment doesn't go well.

1. In the left column, select the target experiment.
2. Find the status control on the right side of the Scope Bar at the top of the center column, and open the dropdown.
3. Choose one of "In progress / Needs refinement / Succeeded / Failed / Discarded".

4. When you choose "Failed", you're prompted with "Record a failure · pick a type first (optional)". Write one line in the input box and click "Save".

The status label updates immediately, the colored dot on the node in the left column changes color to match, and the change is automatically recorded in the progress log.

3.4 View the progress log and generate a stage summary

When to use: writing a monthly report, briefing your advisor on progress, or reviewing "what has happened in this project recently".

1. In the left column, select a **project** or **module** node (not an experiment).
2. The right column shows the "Project progress log" or "Module progress log", listing events in reverse chronological order: new experiments, data parsing, analyses, drafts, research thread designs and verdicts, notes and so on.
3. Click "🌟 Generate stage summary" in the upper right. The AI summarizes what was accomplished during this period, the key conclusions, sticking points and suggested next steps, and shows the summary at the top of the log.

When the log is empty, it shows "No progress records yet. Adding experiments, uploading data, running analyses and DOE are logged here automatically."

Chapter 4 · Uploading and parsing data

4.1 Upload files to an experiment

Prerequisite: you've selected an experiment in the left column; otherwise you'll see "Please select an experiment on the left first".

Use any of three methods:

- **Button:** click "Add files" (📎 / +) to the left of the center column's input box and choose files in the file dialog; you can select several.
- **Drag and drop:** drag files from your system's file manager into the center column's input area, and release when you see "Drop to add files to this experiment".
- **Paste:** copy a screenshot and paste it directly into the input area.

You can also drag files onto the "Drop files here or click to upload" area in the "Attachments" panel on the right.

Files are parsed automatically after upload. **When you upload a single image**, a card asking how to analyze it pops up above the input box: "1. Analyze this file only", "2. Compare with the whole experiment", "3. Pick attachment files on the right to compare together"; type the number or click a button. **When you upload several images at once**, they go into a gallery first ("Added N images · write a note for each, then analyze them together"). You can keep adding images, and finally click "Analyze together".

Writing a one-line note for an image is very useful. The note box prompt is "What is this image? (the AI will take this as given instead of guessing)"; you can describe the chart type, axes and units, legend colors, sample conditions and so on.

4.2 Supported file formats

Format	Parsing behavior
CSV (.csv)	Parsed into a structured data table; must be UTF-8 encoded
Excel (.xlsx / .xls)	Parsed into a structured data table; every worksheet is parsed
PDF (.pdf)	Text is extracted; OCR is attempted automatically for scanned PDFs; encrypted PDFs can't be parsed
Word (.docx, legacy .doc)	Text is extracted; the original layout is not kept
PPT (.ppt / .pptx)	Text only; legacy .ppt files also have their speaker notes read
Images (png / jpg / webp / bmp, etc.)	Visual recognition; charts can be digitized
Video (mp4 / webm, etc.)	Stored as an attachment only; not used in AI analysis
Other formats	Stored as attachments; not parsed for now

4.3 View parse results and re-parse

1. Open the "Attachments" panel on the right and find the target file.
2. Click the entry to expand it: you'll see the worksheet name, a summary and the "Previewing the first 12 rows of N" preview. Check that the column names and format are correct.
3. If parsing failed or is incomplete, click "Re-parse".
4. Click "Delete" for files you don't need. For PDF papers you can click "Add to Literature Library" to put them on your shelf; papers already in the library show  In library".

Every attachment shows a status: "Parsed / Parse failed / Pending parse".

View the original: click the eye icon "Original preview" on an attachment entry. PDF, Word, Excel and PowerPoint files are shown as they are (not as extracted text) in a dialog, with "Maximize", "Restore size", "Open in new window" and "Download original file". Types that can't be previewed fall back to "Text / table".

view" and suggest downloading the original. The 👁 "View original" in Records Organizer (Chapter 13) uses the same preview dialog.

What to do if parsing keeps failing: check that the format is in the supported list and the file isn't encrypted or corrupted; save CSVs with UTF-8 encoding; very old **.xls** files (Excel 95 or earlier) can be saved as **.xlsx** and uploaded again.

The screenshot shows the sciAI interface. On the left is a sidebar with navigation options: Experiment Board, Projects, My Experts, and Toolbox. The main panel displays a 'Data record sheet' for 'Enzyme kinetics > Michaelis-Menten fits > ALP substrate gradient run 1'. It shows a table with 5 conditions and factors, including substrate_mM and rate_uM_per_min. A 'Fit Michaelis-Menten to run 1 and report Km and Vmax' button is present. The 'Evidence' panel on the right shows parsed data grouped into Facts, Metrics, and Images, each with its source file noted.

Evidence panel: parsed data grouped into Facts / Metric / Image, each item noting its source file

Under "More panels" → "Evidence" you can see all the structured data that was parsed: facts, metrics (with min ~ max and mean), images, literature and so on, each noting its source file. The AI only cites what is here.

4.4 Digitize the data in a chart

When to use: you only have an image of a curve, no raw data table, and you want to turn it into numbers you can analyze and fit.

Method 1: one-click estimate (fast, when high precision isn't required)

1. Below the image message, click "⚡ Estimate values".
2. Wait through "Reading axes, picking points, fitting..."
3. The result panel is labeled "Estimated · not calibrated": the shape of the curve and the relative relationships are reliable, but the absolute values are only estimates. Click "Send the estimate back to

the chat" to let the AI continue the analysis.

Method 2: precise reading editor (calibrate → trace points → import and fit)

1. Below the image message, click " Precise reading".
2. **Calibrate the axes:** drag the four markers X①, X②, Y①, Y② onto known tick marks on the axes and enter their real values.
3. **Trace and name curves:** choose the curve type (such as "Standard curve (linear → sensitivity / LOD)" or "Other"), trace points along the curve with at least 3 points per curve, and name the curve. You can "+ Add a curve", and fix misplaced points with "Delete selected point".
4. The AI has usually prefilled the axes, points and curve identities (the hint reads "✨ The AI prefilled the axes, points and labels — you just fix mistakes"). If the markings get messy, click "Clear and redo".
5. Click "Import and fit". The generated data table CSV goes into the attachments, and the fit result corresponds to the curve type you chose.

If something goes wrong: if calibration doesn't take effect, check that all four markers sit on axis tick marks and have values entered; a failed fit is most often due to too few points—each curve needs at least 3.

4.5 Correct how the AI reads a chart (reading conventions)

When to use: the AI misread a chart, for example getting the axis units wrong, treating a log axis as linear, or swapping the legend.

1. Next to the image evidence, click "Read it wrong? Correct the reading".
2. In the input box, write how this chart should be read, for example "use a log scale for the frequency on the x-axis".
3. Click "Generate rule" and preview the reading rule the AI generates.
4. Choose "Apply to this image now, and save as a "X" reading convention" and click "Apply".

The interface shows "✓ Applied — this image's readings now follow your ruling". Conventions are matched by the axis text, so similar charts follow them automatically from then on; a chart with different axis text needs another rule.

Chapter 5 • Other parts of the experiment record

5.1 Experiment assets: materials, sample locations, SOPs and handoff

When to use: record an experiment's reagents and consumables, where its samples are stored, its operating procedure and who to hand it over to, for the next cohort of students and your advisor.

1. Select the experiment and click ": More panels" → "Assets" at the top of the center column.
2. **Reuse the previous experiment:** click "Carry over from previous" to automatically copy the materials, instruments, SOP and contacts of the previous experiment in the same module; samples are not copied.
3. **Material catalog:** click "New category" to create a category (reagents / instruments / electrodes...), then fill in each item's name, batch no. / model, supplier / source, spec / purity, amount and notes.
4. **Samples · physical location:** fill in the location, batch, type (Product / Intermediate / Aliquot), status (In stock / Used up / Discarded) and remaining amount.
5. **Standard operating procedure (SOP):** write, step by step, what each step does, its key parameters and cautions.
6. **Handoff · who to ask:** fill in the operator, contact details and handoff notes.

If "Carry over from previous" brings in nothing, no experiment in the same module has assets filled in (assets are not carried over across modules).

5.2 Record sheet: factors prefilled, responses filled in cell by cell

When to use: the raw record for one round of a research thread. Fill in each experiment's conditions (factors) and results (responses) cell by cell, and the AI reads the sheet directly when judging the round.

1. In the research thread chat, find the  "Data record sheet" card and click "Open record sheet →"; the editor opens in the right column.
2. Factor columns are prefilled according to the design (you can change them), and response columns are marked "to fill"; enter the values cell by cell.
3. If needed, click "+ Column" to add a column or "Add a row" to add a row; the X at the end of a row or column deletes it.
4. When you're done, click "Save to attachments"; you'll see "Saved as the attachment "record-sheet.csv"". You can also "Download CSV" to save a copy on your computer first.

Always click "Save to attachments" before closing the editor; otherwise what you entered won't be kept.

5.3 Decisions and notes: the AI collects, you confirm

When to use: write down the "why" behind an experiment (decisions, failures, tips, anomalies) to pass on to future students, and to help the AI understand you better.

1. In the "Draft" panel on the right, find the "Decisions and notes" section.

2. **Let the AI distill them:** first chat with sciAI for a bit about this experiment's decisions and failure causes, then click "Re-collect". The AI organizes them into entries labeled "Distilled by sciAI · to confirm".
3. **Review each entry:** click ✓ "Confirm" to endorse it as know-how (the label changes to "Confirmed"); if you disagree, click X to delete it, or edit the text directly.
4. **Add entries manually:** click "+" next to any of the four categories "Decision / Failed / Tip / Anomaly" and type.
5. When you see "💡 No reason given — add one:", adding the reason makes the entry more complete.

Unconfirmed entries show "N to confirm"; only after you confirm them are they kept and passed on as your know-how.

5.4 Experiment Board: put several experiments in one table

When to use: compare batch conditions and results across experiments, and maintain a master table with "one experiment per row".

The screenshot displays the 'ALP kinetics board' interface. On the left, a sidebar shows a hierarchical project tree under 'Enzyme kinetics'. The main workspace is a table view titled 'ALP kinetics board' with columns for Experiment, Status, Modules, and Results. It lists three experiments: 'ALP substrate gradient run 1' (Succeeded), 'ALP substrate gradient run 2 (q...)' (Needs refinement), and 'Inhibitor pilot screen' (In progress). To the right of the table, there's a panel for materials and reagents, including buffer (Tris-HCl, pH 9.0), substrate (p-nitrophenyl pl), MgCl2 (9.5), pNPP (3), and Tris base (121.1).

Experiment Board: a tree-linked table, one experiment per row, with the status column synced to the project tree

Create a board page

1. In the left column, "Experiment Board" → "+ New board page".
2. Choose a page type: - **Tree-linked table:** check modules (rows = the experiments in those modules, so you can compare batches across modules), then click "Create table (single module)" or "Create

comparison table (N modules)". - **Free table**: not linked to the project tree; you maintain the rows yourself. - **Doc**: a block-editor page. Type "/" to insert text, headings, tables, equations, images, @ references to experiments and more.

Columns and cells

- "New column" in the toolbar: enter the column name, type and unit. Types include Text, Number, Single select, Multi-select, Person, Link, Date, Formula, Status and others.
- Column header menu: "Rename", "Insert column to the right", "Move into category...", "Property type", "Delete column"; double-click a column name to rename it, and drag a column edge to adjust its width.
- **Category containers**: group several columns into one category (such as "Materials"). They are shown as a pouch of "Name | Value" pills; click a pill to edit its value in place, and use "+ Add sub-column" to keep extending it.
- **AI estimates**: on an empty cell, choose "Have the AI estimate this cell from the experiment's evidence". You'll see "AI inference, to confirm" (an amber dot + the basis + a confidence level), with three choices: "Confirm as measured", "Change the value", "Ignore and clear". Until you confirm it, AI analysis won't treat it as a measurement.

Views and export

- Switch with "Table / Kanban" in the toolbar: the Kanban view arranges columns by the status column (or the first single-select column), and cards show condition pills.
- "Group": group by a column; group headers can be collapsed.
- Row hover: "↗ Open experiment record" jumps to the right column, or "Analyze this experiment in the chat".
- "Export Excel" downloads the whole table; "Add columns from experiments" reads the materials, conditions, methods and key results directly from each experiment's draft and inserts them as a group.

If something goes wrong: if "Add columns from experiments" says there are no drafts to organize yet, generate one under "Draft" on the right first; if the Kanban view is grayed out with "This table has no single-select column to group by", add a single-select column or use the status column of a tree-linked table instead; if you see "The AI didn't estimate this cell: insufficient evidence", fill in the value manually or add more evidence first.

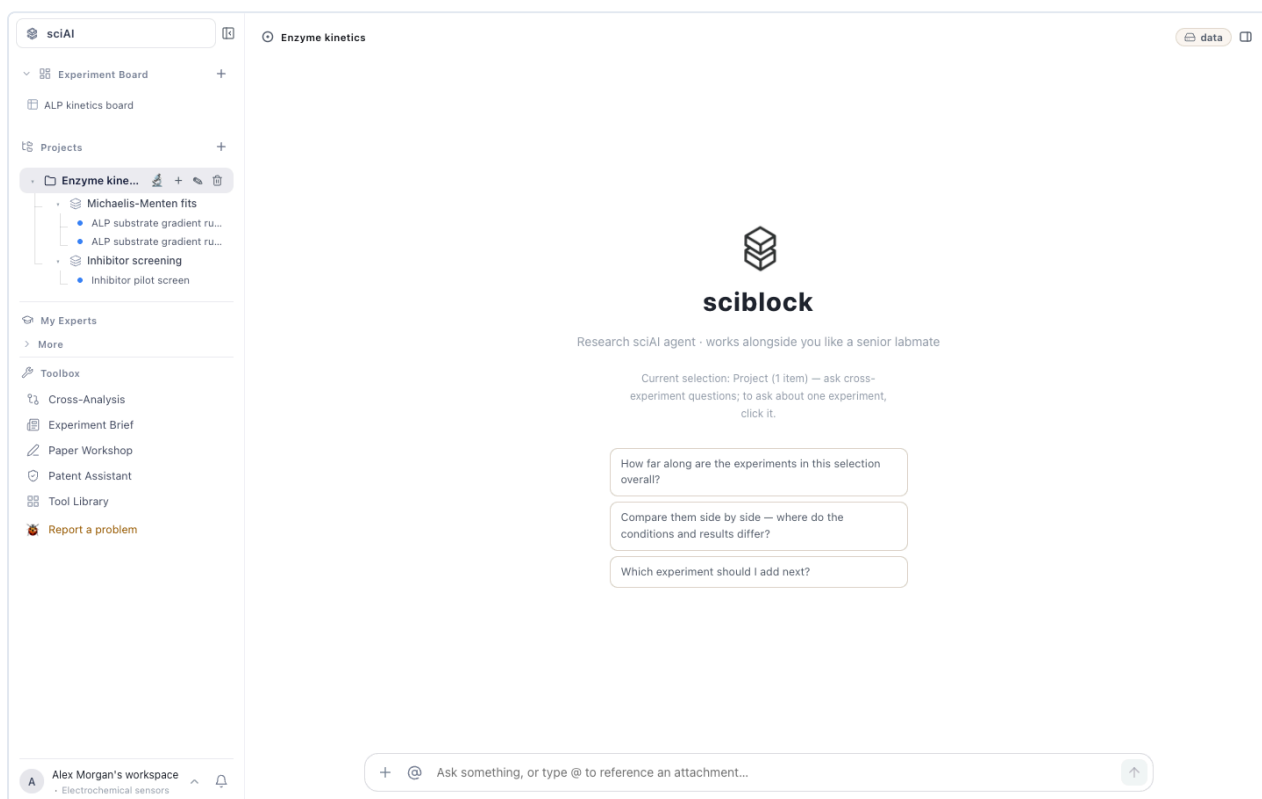
Part 3 · Doing research with AI

Chapter 6 · AI chat basics

6.1 Choose the analysis scope and @-mention items to compare

The **Scope** determines what the AI looks at:

- Click an **experiment** in the left column: the AI looks only at that experiment and analyzes it data point by data point.
- Click a **module** or **project**: the scope expands to all the experiments under it. When there are many experiments, the AI gives a high-level overview; for details, narrow the scope to a single experiment.
- The Scope Bar always shows the current scope and is the single source of truth for "what the AI is looking at". Each scope has its own independent chat history, and switching scopes switches the chat as well.



After selecting a project: the scope expands to the whole project, and the starter questions also become cross-experiment questions

@-mention to compare

1. Click the "@" button next to the input box and type keywords in the "Pick an experiment / board / paper to compare or check against this one" search box.
2. Each selection becomes a "Compare:" tag (remove it with X; up to 12).

3. Send your message as usual; the AI reads these items directly into its context. If you select 2 or more experiments, it automatically does a comparative analysis.
4. To reference an attachment: type @ and choose "@filename" from the dropdown.

When the "Grounding" bar at the top of the reply shows "Checked N/M experiments", the AI really did read those experiments.

6.2 Asking and controlling

- The input box prompt is "Ask something, or type @ to reference an attachment...". Press Enter or click ▲ to send, and click ■ at any time during generation to stop.
- Generation is a background task; if you switch away and come back, it picks up automatically.
- After uploading a file, choose from the analysis card that pops up: "1. Analyze this file only / 2. Compare with the whole experiment / 3. Pick attachment files on the right to compare together".
- A "Next steps · click or type a number" card occasionally appears in the message area; click an option to continue.
- "New chat" starts a clean thread. The old thread is kept, and you can switch back to it in "History".

Tips for asking: specific beats vague. "Based on the data table I uploaded, list the crystallinity for each temperature and cite the source" works much better than "take a look at my data".

6.3 Understanding the AI's replies

- **Source markers:** [1][2] or "Source" superscripts in the text. Open one to see the original (image, table, PDF, paper, related experiment) in the "Source" drawer on the right. Each card in the drawer says which paper, which experiment, or whose entry it is; other people's know-how you installed appears as a "Peer know-how" card marked "A peer's know-how you installed — not your own"; a figure drawn by code in this turn is tagged "AI-generated", and its number is only for tracing, not experimental data of yours.
- **Check citation:** under a literature source in the drawer there is "Check citation". Nothing runs until you click it: the system re-reads the paper and checks every claim in the answer that cites it against the text ("Checking... (about half a minute)"), marking each one "Match / Weak / Not found in the original" with its basis (full-text chunks in the library, or only the abstract). When only the abstract was available it says so plainly.
- **Grounding bar:** the tags at the top of the answer show the evidence boundary of this answer: "Checked N/M experiments", "Read N raw records in depth", "Viewed N images", "Grounded in your data", "General knowledge · not your data", "Citations verified · N fake removed" and so on. Hover to see an explanation.
- **Activity line:** during generation it shows "Analyzing · N s" and the steps "Gathering materials / Reading images N/M / Analyzing / Searching literature".
- **Code steps:** when calculation is needed, the AI runs a Python code card (" Code 1", "Running...", "Done"), so what you see are real calculation results. Numbers typed into the code by hand are flagged

on the card as "hand-written / estimated from a figure / carried over" and don't count as this turn's sources. Figures and files produced by code survive a page refresh; to keep one, click " Save to experiment" next to it and it becomes an attachment of this experiment (recording where the numbers came from). If the output has been cleaned up, the card says "This output no longer exists".

- **Grounding gap hints:** after the AI answers on weak or missing data, it suggests that you add real data. Click to jump to the board or draft to fill it in, then come back and tell it.

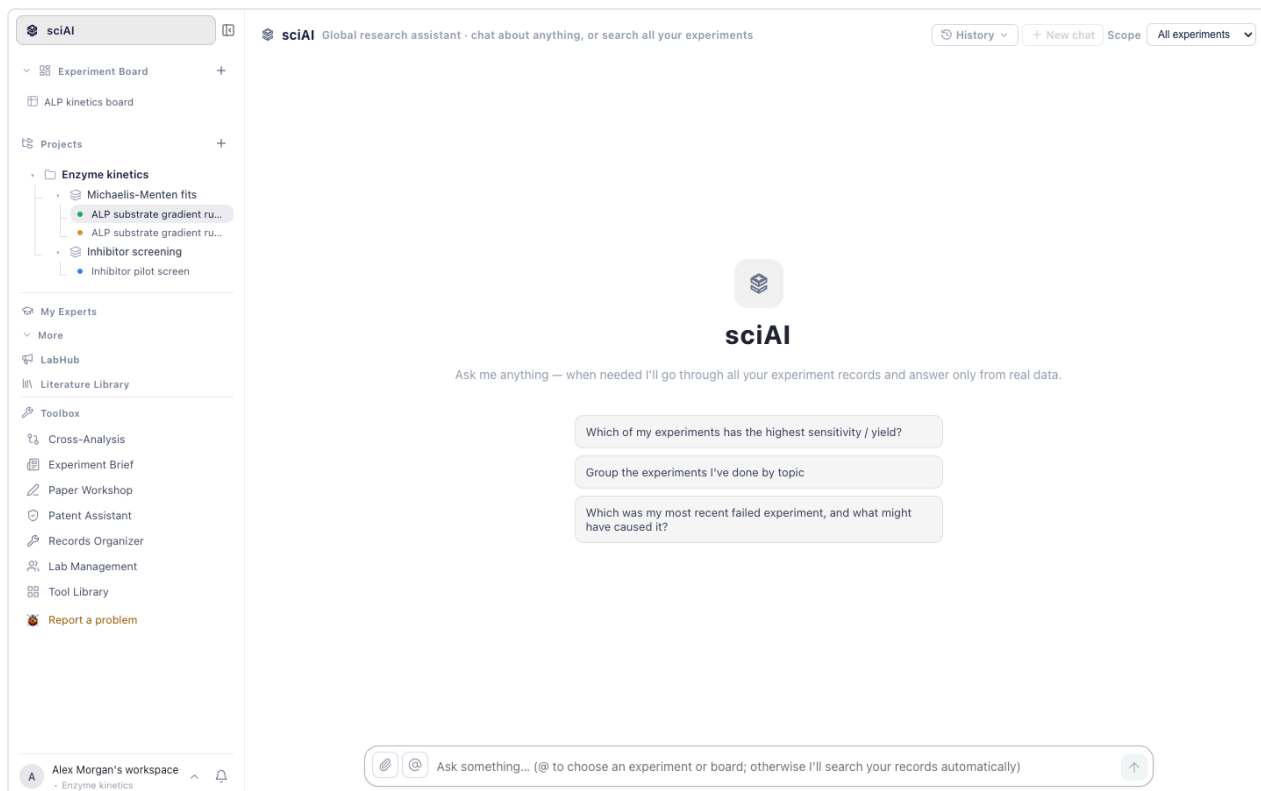
Factual numbers without source markers most likely come from the AI's general knowledge rather than your data; use the Grounding bar to tell them apart.

6.4 Review a reply and send feedback

1. Below the answer, click " Review" to run a fresh audit in the background ("Reviewing...").
2. When it finishes, the reply gets an overall confidence label (High / Medium / Low) and a claim-by-claim audit result (Supported / Weak / Unsupported).
3. You can "Review again".
4. If you think the answer is wrong, click  to give feedback; you can also submit it through "Report a problem" in the Toolbox (a screenshot is taken automatically, and you can choose a category and severity).

Be wary of "Unsupported" claims and rely on the original data; if needed, add data and have the AI answer again.

6.5 sciAI, the global research assistant



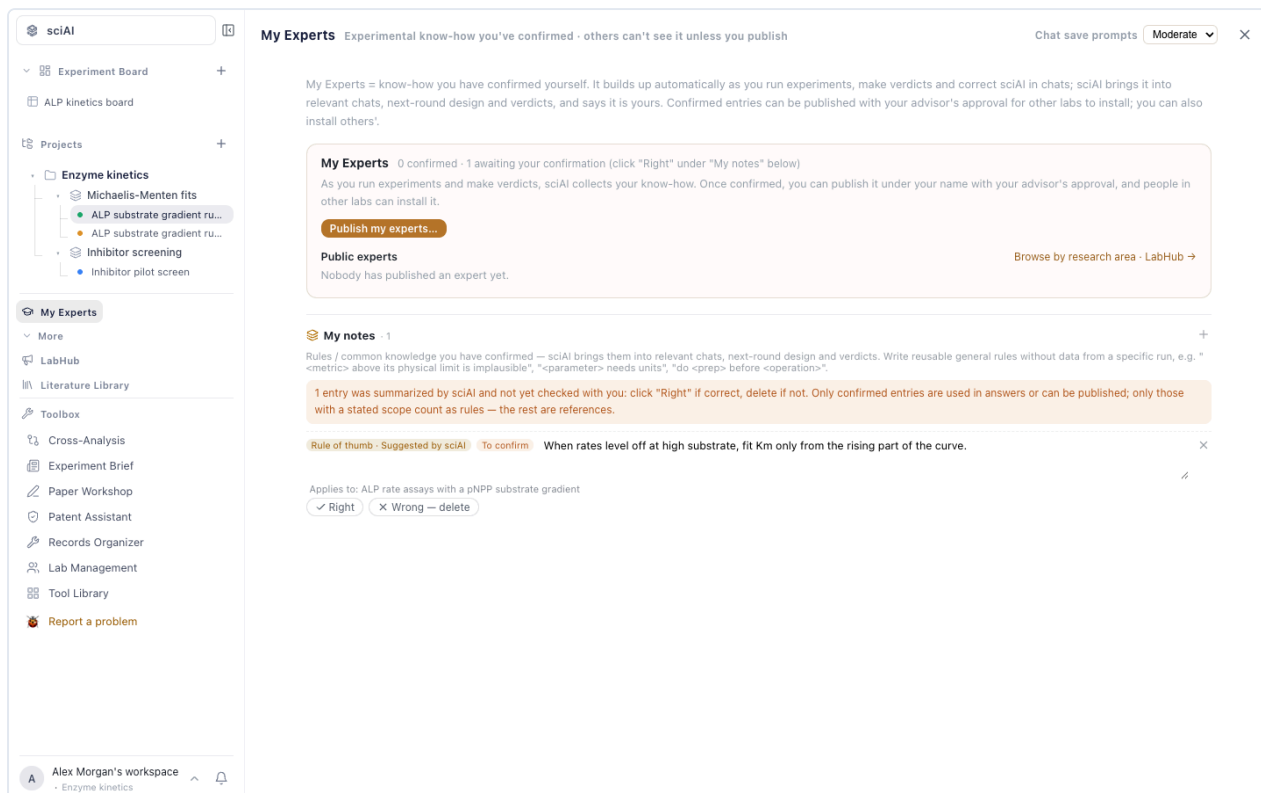
sciAI, the global research assistant: not tied to one experiment; it goes through all your experiment records when needed

When to use: asking questions across all your experiments, or asking general questions.

1. Click "◆ sciAI" at the top of the left column.
2. The "Scope" dropdown at the top defaults to "All experiments"; you can narrow it to one project.
3. Ask directly, for example "Which of my experiments has the highest sensitivity / yield?", "Group the experiments I've done by topic", "Which was my most recent failed experiment, and what might have caused it?". When needed, the AI goes through your experiment records and answers only from real data.
4. To have it keep an eye on certain experiments: click "@" and choose experiments or boards to create "Watching:" tags (they persist across pages; up to 12).
5. Use "History" to switch back to an old chat, and "New chat" to start a new thread.
6. When you type a clear intent such as "write a research proposal", a hand-off card "📄 Open the Research Proposal tool" appears; click it to enter the tool with the current project scope.

Chapter 7 · My Experts: let the AI bring your know-how

7.1 How know-how accumulates



"My Experts" page: confirmed know-how, public experts, my notes

As you run experiments, make verdicts and correct sciAI, it gathers your know-how and keeps it under "My Experts" in the left column. **Only know-how you have confirmed is used in answers.**

- When you correct sciAI in a chat, or add a general rule, it pops up "Save this to your experts?" → "Save / Edit / Ignore".
- In the annotations of the "Experts" panel on the right, you can "+Save" checkpoints that are not normal.
- Under "My Experts" → "My notes", click "+" to write one by hand: the kinds are Rule of thumb / Methodology / Terminology, and you can fill in the source and the scope it applies to.
- "Chat save prompts" in the upper right of the page can be set to Off / Moderate / Active, controlling how often the AI proactively suggests saving.
- "Growth history" shows which experiment and which conversation each entry grew out of. Click "Check now" and sciAI immediately distills once more from your latest experiment records, under the same rules as the automatic pass; anything new is still labeled "To confirm" for you to review.

7.2 Know-how awaiting confirmation

Know-how that sciAI summarized automatically and hasn't checked with you yet is labeled "To confirm", and it isn't used to answer questions until you confirm it.

- When you ask about something related in an experiment chat, the reply ends by asking "...does it still hold?": reply "confirm" to keep it; if it's wrong, just correct it; reply that it doesn't hold to delete it. A reply of just "ok" or "thanks" doesn't count as confirmation.
- When there is new know-how awaiting confirmation, the bell brings at most one notice per day: "N newly summarized knowledge entries are waiting for your confirmation".
- The top of the "My Experts" page shows how many entries are confirmed and how many await confirmation, so you can go through them together when you have time.

7.3 The "Experts" panel on the right

After selecting an experiment, open ": More panels" → "Experts" to see:

- "Your know-how used for this experiment"
- "Others' know-how" (public experts from other people that you have installed)
- "Expert reviews": two general checks—whether the record states the number of replicates / sample size, and whether there is a control / baseline. They look only at the record text, and only remind you without passing judgment.

7.4 Publish my experts, install other people's experts

Publishing as a student (requires approval from the advisor of the lab you belong to)

1. "My Experts" → "Publish my experts...".
2. First go through the know-how awaiting confirmation and choose "Right / Edit / Delete" for each; you can submit without checking them, but those entries won't be published this time.
3. Know-how without a "scope" is listed separately: know-how without a scope won't be published. sciAI drafts a sentence based on where the know-how came from and puts it in the input box; if it's fine, click "Use it", otherwise edit it.
4. Use "See which" to check what will be published this time.
5. Choose which lab to publish under, enter the expert name and a note to your advisor, and click "Submit for advisor approval".
6. After the advisor approves, a "Publish" button appears, and **it only actually goes out once you click it**. If it's returned, the reason is shown; make your changes and click "Edit and resubmit".

Only the know-how itself (including its scope) is published, under your name and attached to the lab. When you republish a new version, the old version is taken down automatically. A published expert has "Withdraw" below it.

Publishing as an advisor: it is attached to your own lab and needs no approval. "Publish my experts..." → review the know-how awaiting confirmation → choose your own lab → "Confirm this version" → "Publish".

Advisor approval: after a student submits, a "wants to publish their experiment knowledge" card appears in your inbox, listing each entry of know-how and its scope. After reading it, click "Approve publishing", or "Return..." and write a reason. After the student publishes, the card has "Withdraw", which lets you take it

down from the public feed.

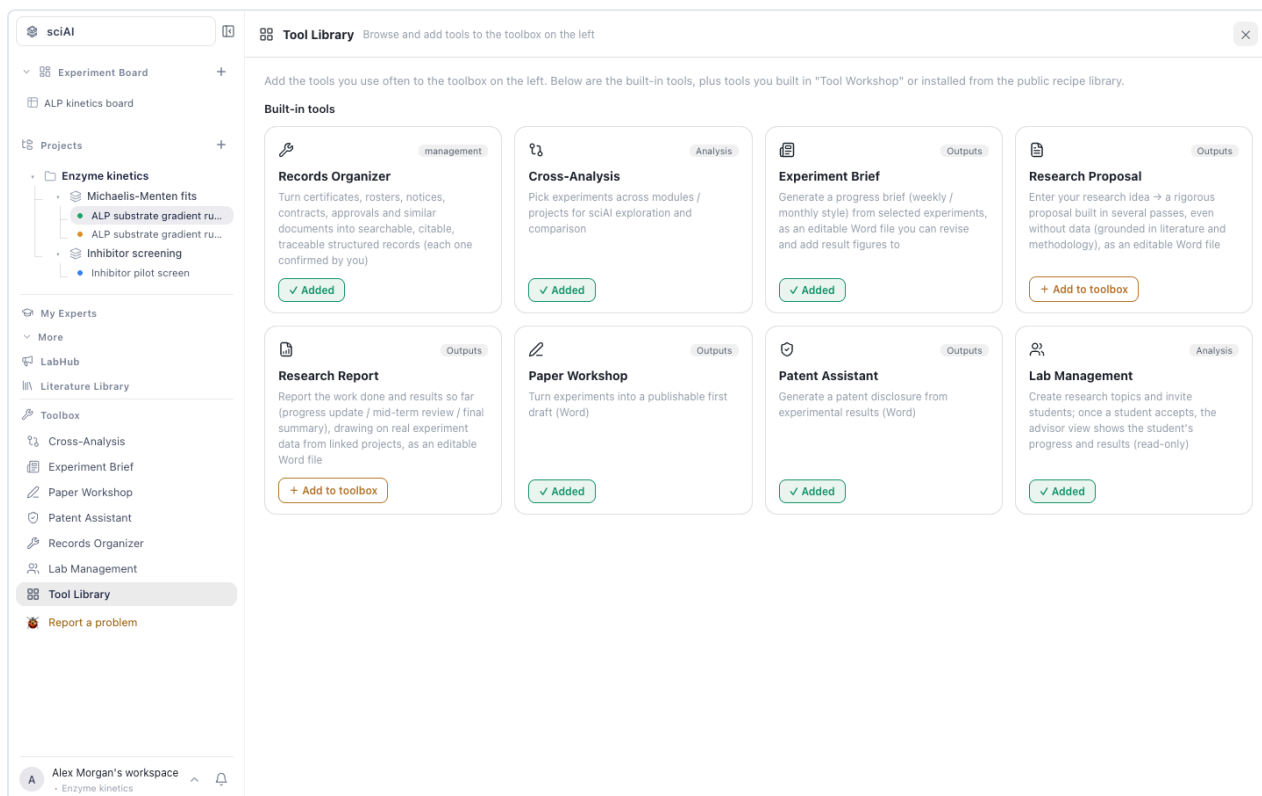
Install other people's experts

1. In the left column, "LabHub" → the "Experts" tab; you can filter by "Relevant to me" or by research area. The "Public experts" list on the "My Experts" page shows the same set.
 2. Click "View entries" to expand each entry of know-how and its scope, and click "Install" if it looks suitable.
 3. From then on, in related chats sciAI refers to this author's know-how and says whose judgment it is. When it says the same thing as your own know-how, the two are shown side by side (yours first) rather than merged into one. Judging a round refers only to know-how you have confirmed yourself; other people's know-how doesn't reach conclusions for you.
 4. Under "Experts I installed" you can "Uninstall", or mark just one entry as "Doesn't apply to me" (you can leave a reason, which the author receives anonymously); "Restore" undoes it.
-

Part 4 · Producing Documents

Chapter 8 · Drafts, Briefs, Reports, Papers and Patents

By default, the toolbox already contains Cross-Analysis, Experiment Brief, Paper Workshop and Patent Assistant. Research Proposal, Research Report, Lab Management and Records Organizer are in the "Tool Library"; click "+ Add to toolbox" to add them to the left column.



Tool Library: browse tools and add them to the toolbox in the left column

8.1 Generate an experiment record draft

Prerequisite: An experiment is selected and has at least one successfully parsed attachment.

1. Open the "Draft" panel in the right column and click "Generate experiment record draft". The task runs in the background, so you can switch away in the meantime.
2. Once it is generated, check each entry. Every entry is labeled with its source: "Measured" (real values from your files), "Inferred" and "Suggested by sciAI" (you need to verify these), and "Missing" (you need to fill these in yourself).
3. Edit the content directly, or add and delete entries. Changes are saved automatically ("Autosaved ✓").
4. To reuse the settings of the previous experiment, click "Inherit settings" in the top bar (the previous experiment by default; you can also pick an experiment from another module). Materials / conditions /

methods are appended as entries marked "inherited · to confirm".

5. When you have checked everything, click "Confirm" to endorse the whole draft. If any entries are still unconfirmed, the button flashes as a reminder.

The "📦 Handoff package" completeness bar at the top of the right column changes as your drafts, attachments and assets fill in ("Complete · ready for the next cohort" or "N items missing").

What the draft labels mean: Measured (green) > User (blue) > Inferred (yellow) > Suggested by sciAI (orange) > Missing (gray), in decreasing order of reliability. When reviewing, focus on the yellow and orange entries. Inferred content in a confirmed draft is never treated as hard fact in comparative analysis.

8.2 Experiment Brief

The screenshot displays the 'Experiment Brief' interface within the sciAI workspace. On the left, a sidebar lists various tools and projects, with 'Experiment Brief' highlighted. The main panel shows a 'Choose the experiments to include in the brief' section. It includes a search bar with the placeholder 'Search experiment / module / project names... (3 experiments)', buttons for 'Expand all' and 'Collapse all', and a selection status '0/50 selected'. Below this, a list of experiments is shown, with 'Enzyme kinetics' selected. At the bottom right, a 'Selected: 0' indicator and a 'Create experiment brief' button are visible.

Experiment Brief: select experiments and generate a progress brief

When to use it: To roll several experiments up into a weekly or monthly progress report. We recommend first filling in the brief byline (student name / advisor name / advisor email) under "Settings → Profile".

1. In the toolbox, open "Experiment Brief" → "+ New brief", select the experiments to include, and click "Create experiment brief". The brief automatically pulls together each experiment's board results, draft settings and actual system status.
2. In the "Ask about progress / make a request..." box, describe a change in one sentence, such as "Make the conclusion section more detailed", then click "📄 Generate brief preview". Revised passages are highlighted ("✓ Updated ...").

3. When you are satisfied, click "Confirm brief". The content is locked and the status changes to "Confirmed".
4. Click "Download Word" or "Download PDF" to export. After you deliver it, you can mark it as "Sent".

If something goes wrong: If a revision reports "No changes made", your instruction was too vague; say which section to change and how. A note like "(N not located, skipped)" is normal; rephrase and try again.

Write in your own format: Does your advisor or department have a fixed weekly report form or experiment record sheet? Upload it once and every later brief follows it; when you download, the content is filled straight into your template with the header, borders, merged cells and signature rows untouched.

1. On the "My report format" row at the top of the "Experiment Brief" page, click "+ Upload my format" and drop in the template file (.docx / .xlsx / .doc / .pdf / .txt; an old, already filled-in report works too), or just paste the section names, one per line.
2. Click "Read format". The system lists the blank slots in the template (the body area under each heading, table cells, the value after labels such as "Name:", the grid of a registration sheet); the AI only decides which slot each section and header field maps to.
3. Check the confirmation table: each section's type and "maps to" decide how the AI writes it, and "Where in the template this goes" can be changed; give the format a name and click "Save and use".
4. From then on, new briefs follow it and the page shows a "Brief format" badge; "Download Word" or the Excel download fills your template directly. Cells left for others (advisor comments, signatures, numbering columns) are not touched.
5. To switch formats, pick another one under "My report format"; earlier formats are kept so you can always go back, and "sciblock default (progress brief)" restores the built-in layout. A brief that has already been generated remembers the format it used and is unaffected by later switches.

If no slots can be recognized (a free-flowing prose report, for example), the brief is written with the detected sections in sciblock's own layout, and the page tells you so.

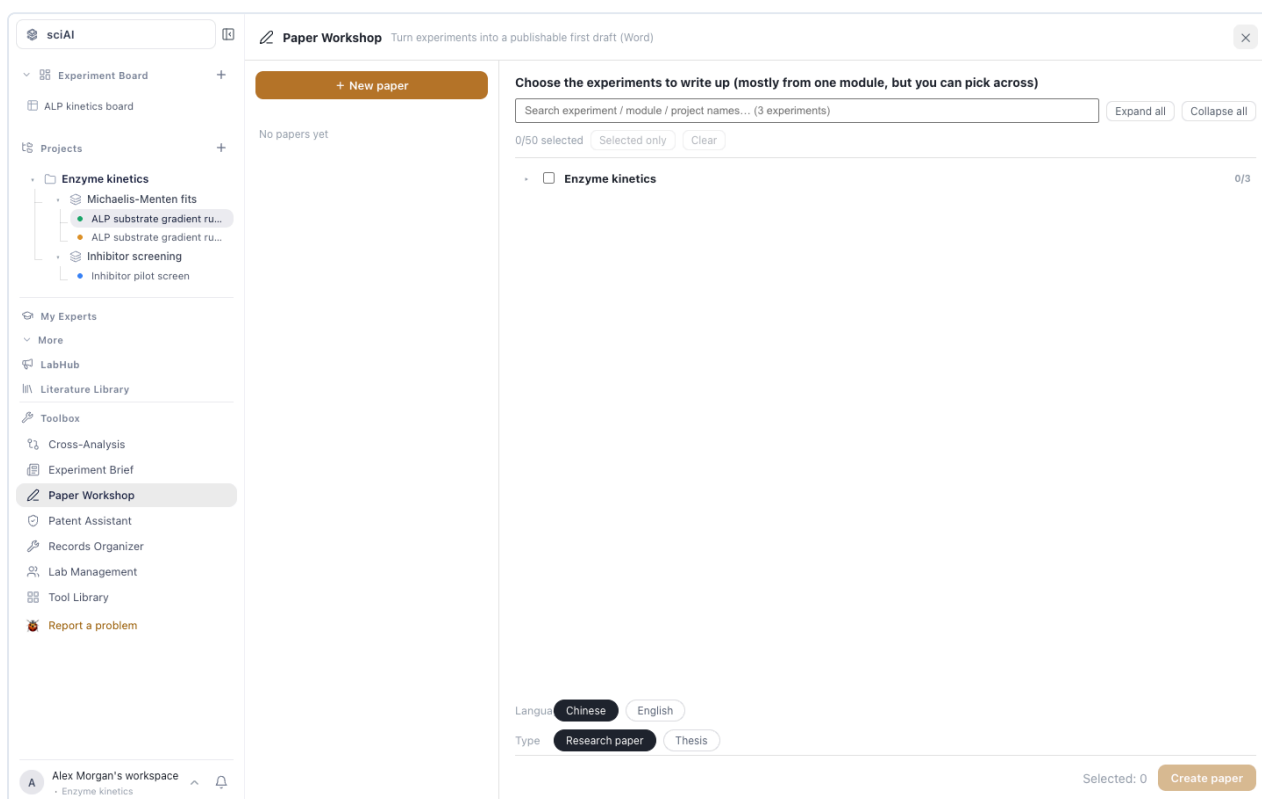
8.3 Research Proposal and Research Report

Research Proposal: Written before the research starts. You can write it without any data; it is built on a literature review and the methodology of the field. **Research Report:** For progress updates, mid-term reviews and final summaries; it automatically includes real experimental data from the linked project.

1. In the toolbox, open "Research Proposal" or "Research Report" (add them from the Tool Library).
2. Fill in the research information. For a Research Proposal, fill in the "Research idea" (required) and, optionally, the project title, research direction, advisor, major and degree level. For a Research Report, fill in the "Research summary" (what you did / what to report).
3. Click "Create and draft outline" and the AI drafts an outline. You can click "+ Add section", edit headings, or click "Redraft outline".

- The first time you generate a Research Proposal, you are asked whether to search the web for literature ("Yes, search the web"). If you agree, the AI searches online and compiles the references. You can also decline and use your local Literature Library instead.
- Click "Generate Research Proposal / Generate Research Report". The AI writes section by section in multiple passes, checks its own work and compiles the references. This takes a dozen minutes or more and runs in the background; you are notified when it finishes. Meanwhile, the drawer on the right shows a live preview.
- After previewing, revise through the chat (changes are highlighted). When you are satisfied, click "Download Word".

8.4 Paper Workshop

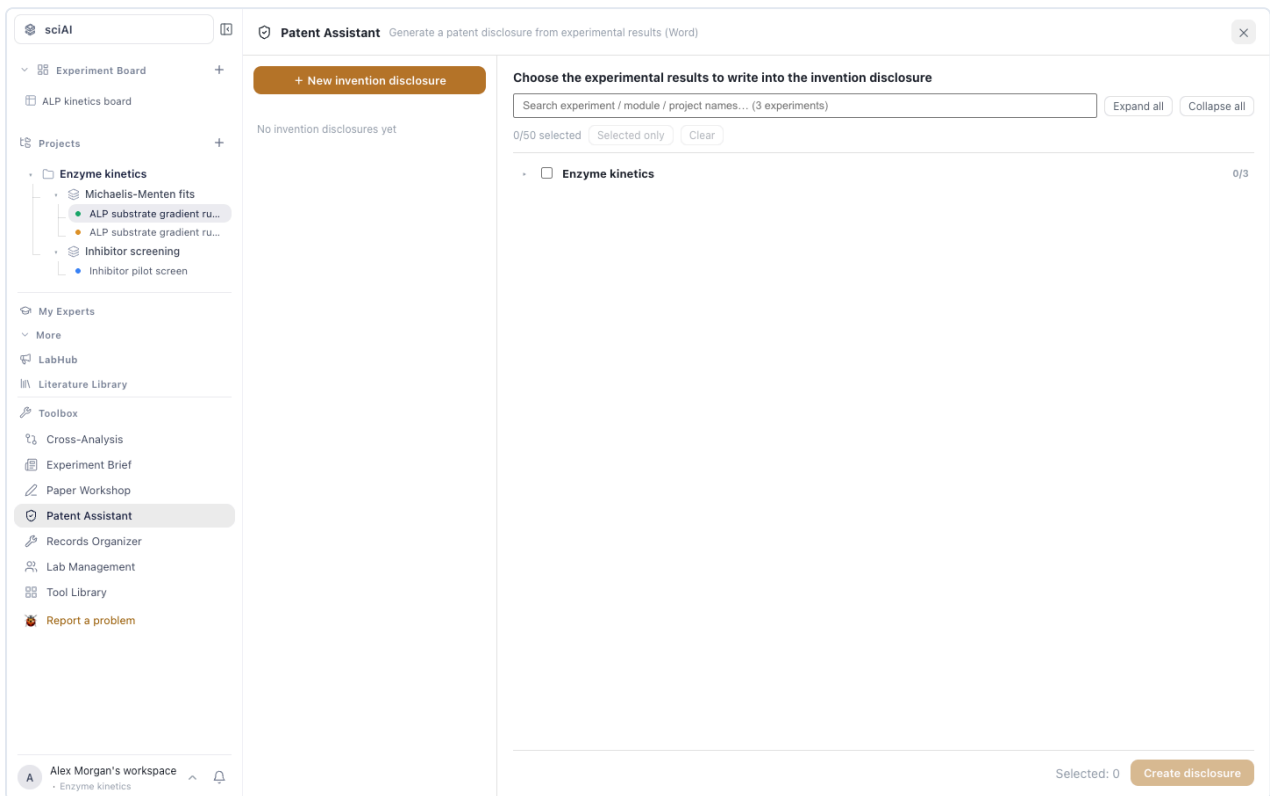


Paper Workshop: choose experiments, language and type, then create the paper

- In the toolbox, open "Paper Workshop" → "+ New paper" → select experiments (mostly from one module, but you can select across modules) → language (Chinese / English) → type (academic paper / thesis) → "Create paper".
- Go through three stages in order: - "① Outline (editable)": The AI drafts a structure; you can edit the chapter headings. - "② Your key statements": Write your own core arguments. This is something the AI cannot supply. - "③ Claim list": Check the claims one by one. Only the claims you check go into the paper; unchecked ones are not stated as conclusions.
- Click "Generate body". The paper is generated section by section in the background from your real data, and you are notified when it is done.

- Click "Open preview" and describe a change in one sentence in the input box. Changes are highlighted, and the view scrolls automatically to the first one.
- Click "Download Word". Layout: centered title, automatically numbered sections, figures and tables with "Figure N / Table N" captions, centered equations, and clickable numbered references. Where a figure is missing, a "Suggested: insert a figure here" placeholder is left; after downloading, replace it with your own experiment figure.

8.5 Patent Assistant

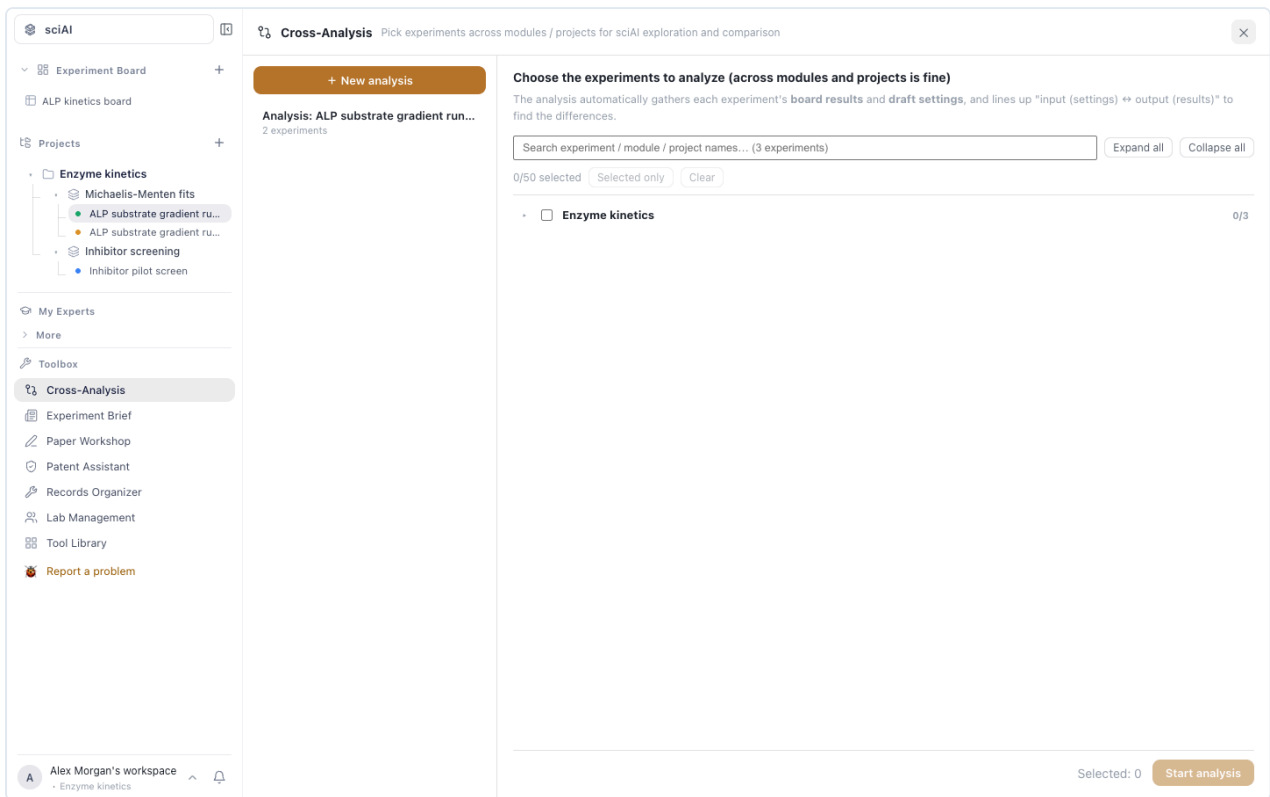


Patent Assistant: generate an invention disclosure from experimental results

- In the toolbox, open "Patent Assistant" → "+ New invention disclosure" → select experimental results → "Create disclosure".
- Fill in "① Your key statements": the technical problem to solve, the technical solution and the innovations.
- Choose the "Prior-art source for the background section": Local literature library / External patent search / No prior art. An unfiled patent is confidential, so assess the risk yourself before choosing "External patent search".
- Click "Generate disclosure" (runs in the background).
- "Open preview" → revise through the chat → "Download Word". The layout follows the invention disclosure format: fixed sections, body paragraphs numbered consecutively as [0001], and claims numbered one by one.

The claims section carries the note "(Claims to be completed; we recommend a patent attorney finalize them)". This is part of the normal process.

8.6 Cross-Analysis



Cross-Analysis: select several experiments to compare

When to use it: Comparing across experiments (even across modules and projects).

1. In the toolbox, open "Cross-Analysis" → "+ New analysis", select the experiments to compare → "Start analysis". The analysis automatically pulls together each experiment's board results and draft settings, and lines up inputs (settings) ↔ outputs (results) to find differences.
2. Once the roll-up is done ("🇮🇹 Boards & drafts included"), ask comparison questions in the chat, such as "Which formulation has the highest yield?" or "Group the three batches by temperature and compare their yields."
3. Click "📄 Generate analysis report preview" → revise through the chat → download Word.
4. The history list on the left lets you look back at every analysis; each entry is labeled "N experiments".

Part 5 · In-Depth Research

Chapter 9 · Research Threads: Let the AI Guide You Through Iterative Experiment Design (DOE)

9.1 Why iterate

"Design every condition up front and run one big experiment" often fails in complex systems, because you don't know what you don't know. A research thread uses data-driven iteration: the first round probes the direction and magnitude of the key factors' effects → you adjust based on the data (confirm supported hypotheses, look for alternatives to refuted ones) → each round picks the conditions that best distinguish the competing hypotheses → once the hypothesis is consistently supported over several rounds and statistically significant, the thread converges. You run the experiments; the AI makes the design decisions. After several rounds, the AI combines all rounds to give you the big picture.

9.2 Start a research thread in one click

1. In the left column, hover over a project row and click " " on the right.
2. Enter your research question, that is, the "factor → response" relationship you want to test round by round, for example "How do annealing temperature and time affect the crystallinity of perovskite films?"
3. After you confirm, the interface shows " Starting a research thread... (the AI drafts a hypothesis and designs round 1 — one moment)". The AI automatically drafts a hypothesis, designs the first round and creates the Round 1 experiment.
4. Wait for the design to produce 2 to 3 candidate option cards, then choose: - "Create the round with this →": Adopt that option as is. - " Edit this one": Edit the condition values in place, then create the round. - "Try a different approach": Have the AI redesign. - "None fit": Dismiss this set of options. Later you can say "design it differently".
5. When creating a round, confirmation cards such as " Create this experiment?" or " Start a research thread?" may appear; click "✓ Create experiment" or "✓ Start research thread". Creating a round is a background task; when it is done, the experiment appears in the tree in the left column.

9.3 Run, judge, next round

1. Run the experiment in the lab, then come back and upload the results to that round's experiment node (CSV / Excel / images all work), or fill in the " Data record sheet" cell by cell and click "Save to attachments".
2. Once the results are parsed, click "Judge this round" on the research thread status rail at the top of the chat. If this round has no results uploaded yet, the button is disabled with the hint "Upload results to

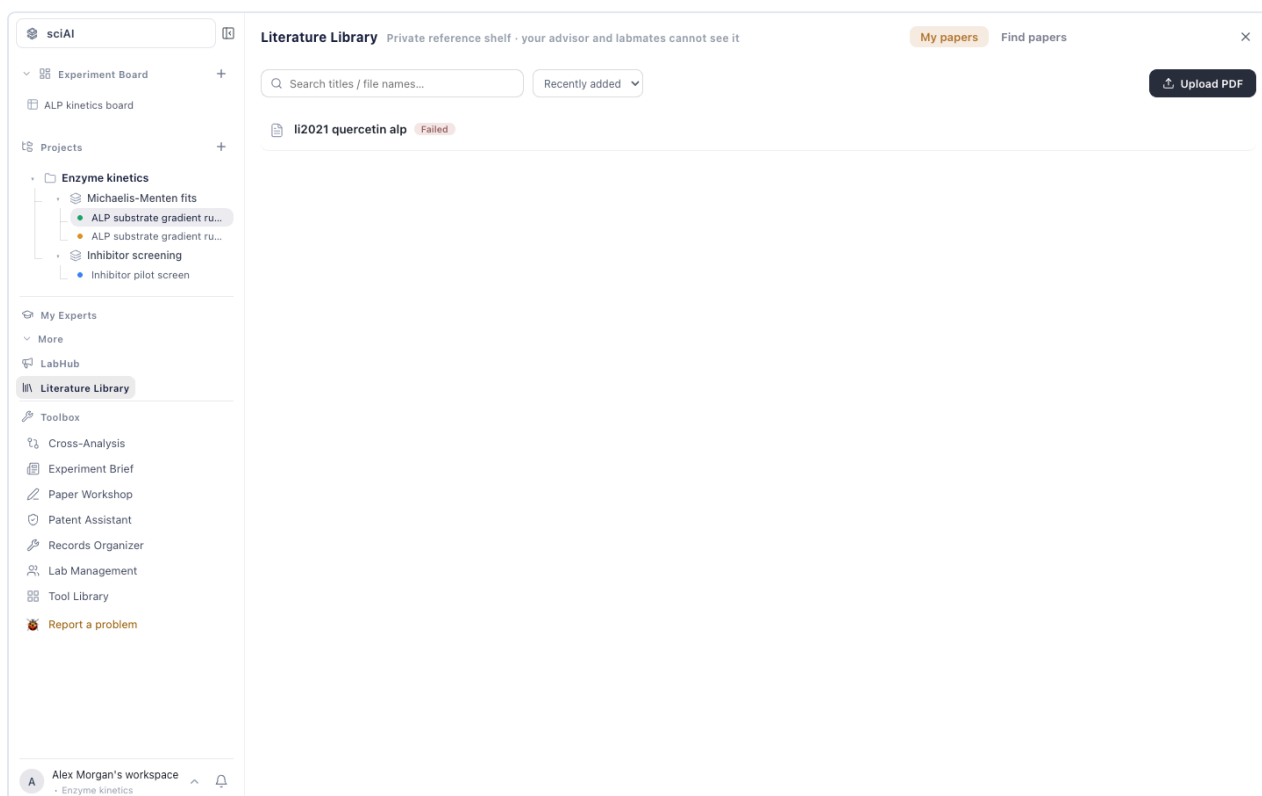
this experiment first, then judge". When results arrive, you are prompted automatically: "Round N results are in — shall I judge them against the hypothesis...?"

3. The judgment returns "supported / refuted / inconclusive" along with statistical test results (p-values, effect sizes, etc.), with superscript citations to this round's evidence.
4. Click "Design the next round" to get candidate options for the next round; "Judge vs last round →" compares against the previous round's judgment.
5. SOP cards that appear in the chat can be saved with "Save to draft ↓", which appends the procedure to the "Methods" section of the draft.

To dig deeper into an existing experiment: In that experiment's chat, click "🔍 Dig deeper into this experiment". It is adopted as Round 1 and Round 2 is designed.

If something goes wrong: If "Judge this round" is grayed out, make sure all experiments in this round have been uploaded and parsed. If you don't like the options, describe in the chat which factors and levels you would prefer.

Chapter 10 • Literature Library



Literature Library: your private reference shelf

10.1 Upload and add to the library

- **Upload a PDF:** In the left column, go to "More" → "Literature Library" → "Upload PDF" → choose where it belongs (project + module; optional) → "Upload". After upload it is indexed automatically, and

OCR is attempted automatically for scanned PDFs.

- **Add from an attachment:** For a parsed PDF paper under "Attachments" in the right column, click "Add to Literature Library". The system copies it into the Literature Library and carries over its three-level location automatically. Once added, the paper exists independently of the experiment and is not deleted along with it.
- **Cite from LabHub:** When you find a useful work on LabHub, click "Cite" → "Add to my library". It goes onto your shelf as a literature entry, labeled "LabHub work · version N".

Paper status: "Indexing → Ready", showing "N chunks". If it shows "Metadata only" or "Failed", upload it again.

10.2 Links and reading notes

Click a row in the paper list to open the detail drawer:

- Change the "Discipline tag" (sciAI assigns it automatically; you can change it or define your own).
- Under "Linked to", add or remove links to projects, modules and experiments. Once linked, when you chat, design the next round or judge a round on that experiment (and on experiments in the same module or project), sciAI searches these papers for passages relevant to your question and uses them as citable sources, marking them in the answer with a "Literature Library: <title>" superscript. Unlinked papers are not pulled in automatically; to name one on the fly, use @ in the input box.
- Write "Reading notes"; use "Original preview" to view the PDF directly.

10.3 Find papers

1. In the Literature Library, open the "Find papers" tab → enter a topic (optional; the search is grounded in your discipline and the current experiment) → "Search". Or click  Find papers related to my library" to expand by citations.
2. Candidate cards show "OA full text", "Cited by N" and "Why it's relevant".
3. Click "Select all" or check individual papers, then "Import selected (N)" to add them to the library in one step and link them to the current node.

Papers the AI finds during a chat also appear as candidate cards, where you can click  View original" or "Add to library".

The first time you use literature search, you can download the local search model (about 1 to 2 GB) in "Settings". With it downloaded, search is faster and also works offline. If it is not downloaded, search automatically runs in a fallback mode, so you can still use it.

Part 6 · Collaboration and Community

Chapter 11 · Lab Collaboration

11.1 Advisors: create a lab and invite students

1. In the Tool Library, add "Lab Management" to your toolbox (it is added automatically for users who have been invited or have joined a lab).
2. " + New lab" → "New research topic" (you can add a one-sentence goal) → "Invite a student to "X"", and enter the email the student registered with.
3. After the student accepts, click "↻" (Sync student data) in the top bar to pull members' data. You will see "Synced N members: M experiments, K attachments updated" or "No changes". If it shows "N to sync", some experiments have not reached this computer yet and the AI can't read them for now; click ↻ again.
4. Click "👤" in the top bar to open the "Lab info" drawer, which has three levels of navigation: lab → research topic (goal, members and the projects they share; you can "Remove" members or "Invite students") → member (read-only; "Projects shared with this group", "Ask only about this student ↗"). A research topic has "Open project group" (11.6). With a student selected, "Discuss" in the top bar opens a direct chat with them (11.5).

Advisors see a read-only view of what students have shared and cannot modify students' data.

11.2 Advisors: follow the whole group's progress with LabAI

Once you open "Lab Management", the center area is the LabAI chat. Just ask:

- "What's the current situation? Who is making progress and who is stalled?"
- "What did everyone do in the past week?"
- "Whose experimental design has variables that aren't cleanly separated?"

The breadcrumb in the top bar, "Lab › Research topic › Ask about", is the single source of truth for scope: switch research topics and the AI looks only at members of that topic; then pick a specific student and it looks only at that person. Each scope change leaves a divider in the chat: " — — Scope switched to X — — ". When an answer names a person, you can click "Only X" to narrow the scope; the X next to the "Asking only about X" pill takes you back to everyone.

A few things worth knowing:

- "Can't see it" and "didn't do it" are two different things. For projects that aren't shared or data that hasn't synced down yet, the AI says "not shared / not on this computer"; it never says "they didn't do it".

- If the group has members with the same name, the AI won't guess for you; it asks you to include the project name.
- Below an answer there is occasionally a "System correction" block. It is a reminder the system appends after its own automatic check, and it is worth a look.

Pull up a student's original experiment images: Just say "Pull up that impedance spectrum." The images are not squeezed into the chat; they open in the image drawer on the right in a grid, and you can click any one to enlarge it. The chat keeps a one-line receipt ("X and N more · View images") that you can click at any time. When the AI says "This experiment has no original images stored", there really are none, so you don't need to ask the student to resend them.

11.3 Students: accept invitations and share projects

1. An invitation arrives in the bell at the bottom of the left column; open it to see the details. Before you click "Accept", it lists what your advisor will be able to see once you join. Check it, then accept, or click "Decline".
2. In the toolbox, open "Lab Management" → "Labs I belong to" → "Projects shared with this group": switch each project on or off. As soon as you switch one off, your advisor can no longer see it.
3. Sharing depends on cloud sync. If you see "You haven't synced any projects to the cloud yet", first turn on sync as described in Chapter 15 and click "Sync now".
4. If your research group's lab has its own server, first connect to that server as described in Chapter 17; after that, both sync and Lab Management go through it.

If something goes wrong: If you see "Can't reach the cloud, so your labs can't be loaded right now.", click "Retry" once your network is back. If you see "The previous sync is still running", wait for it to finish. If you see "This invitation came from an older version and is no longer valid", ask your advisor to invite you again.

11.4 Messages: notifications, chats, contacts

- The red number on the bell at the bottom of the left column = unread notifications + chats with unread messages. It is not a count of messages.
- Click the bell to open the message drawer. It has three tabs:
- **Notifications:** lab invitations, contact invitations, group chat invitations, membership changes, expert publishing requests and approval results, reminders about know-how awaiting confirmation, notices that a work has been taken down, and more. Items that need your decision stay pinned at the top, are never pushed out by other notifications, and are not marked read just because you opened the panel.
- **Chats:** every direct chat, research topic group and group chat, with the last message on the second line. "+ New group chat" is at the top.
- **Contacts:** everyone you can talk to, on one page (see 11.6). When contact invitations are waiting for you, the tab shows how many.
- The inbox lives in the cloud. When you are offline, you'll see "Can't reach the cloud, so messages can't be loaded right now."; click "Retry" once you are back online.

11.5 Discussions: talk about one experiment or attachment, and the conclusion lands in the student's record

When to use: an advisor wants to ask about one of a student's experiments or attachments; a student is unsure about one of their own results and wants the advisor to take a look. A discussion is simply a chat message with that experiment or attachment attached. Any judgment worth keeping is saved by the student into their own experiment record.

Advisor starts it: Lab Management → pick a student → pick an experiment to open the experiment drawer (tabs "Draft", "Attachments" and "Notes"). "Discuss" in the drawer header opens your direct chat with this student, with this experiment already attached above the input box; "Discuss" on an attachment row attaches that attachment instead. To just talk, select the student and click "Discuss" in the top bar.

Student starts it: hover over an attachment row in the right column and click "Discuss this attachment with your advisor". This opens your direct chat with your advisor with the attachment attached. If you are in several labs, you are asked which advisor; if the project containing this experiment isn't shared with any lab yet, you are told so. Inside the chat you can also use the experiment chip "Experiment ▼" at the bottom of the input box to choose an experiment yourself, then reference it or one of its attachments, without going back to the left column.

Reference cards store only a pointer and copy no data. People with permission open the original: "View" on an attachment card opens a preview of the original file, and "Open in experiment" jumps to that experiment. Everyone else sees only "A member referenced experiment content that has not been shared with you.", without even the experiment name.

Saving it to a record: a message with a reference card has saving buttons underneath. Which ones you see depends on whose experiment it is:

- **Experiment owner (the student):** "Save to experiment notes" (category "Decision" by default; you can switch to "Anomaly / Tip / Failed") and "Add to next steps" (appended to the draft's next-step plan). The box starts empty and the other person's words are only shown above for reference; you write what gets saved.
- **Advisor:** "Save as my expertise". Write one general rule without this experiment's specific numbers; it goes into your own "My Experts" (Chapter 7). Advisors never write a single word into a student's record.
- After saving, a reply to that message is posted in the chat automatically, telling the other person what was saved. The button changes to "Saved to experiment notes", "Added to next steps" or "Saved to My Experts", so reopening the chat never saves it twice.
- In the student's right column, notes and next steps saved this way are labelled "From a discussion"; "View discussion" goes back to that message.

Earlier co-research exchanges are now called "Discussion record" and kept read-only; open them from the notification with "Open discussion record". New discussions all happen in chats.

11.6 Contacts, chats and group chats: talk to people, without opening your data

When to use: talking directly with your advisor, labmates, collaborators at other universities or an instrument engineer, to set a time, add a sentence of context or discuss a question with several people. **Being able to chat is not being able to see experiments:** joining a chat grants no access to any project, experiment, attachment or advisor mirror.

The Contacts page: everyone in one place (Messages → Contacts)

- **Waiting for you:** contact invitations from other people. Choose "Accept", "Decline" or "Decline and block"; the invitation shows the other person's school and masked email.
- **My students / My advisor:** taken from the lab roster. You can "Message" them without adding each other as contacts.
- **Labmates:** people who have joined the same lab. Those who are already contacts have "Message"; for the rest, click "Add as contact". You don't need their email, and you can chat once they accept.
- **Contacts:** people who have accepted each other's invitation, usually collaborators outside your lab. "Message" or "Delete".
- **Recent direct chats:** people you have chatted with who aren't listed above.
- "Chats not turned on yet" means that person has never opened Messages → Chats in the desktop app. Opening it once is enough.
- "Invitations I sent" at the bottom of the page shows their status and lets you revoke them. If the other person declined or hasn't registered, it only ever says "Waiting for a reply" until the invitation expires.

" + Add": the one way to add people

- Enter the other person's **complete email** → "Invite as contact". You can add a note; once they accept, it becomes the first message of your chat. People who haven't registered can be invited too: send them the invitation link, or the invite code if the link won't open.
- If you are an advisor, you also get "Invite to my lab" (pick a research topic). This is the same as inviting a student in Lab Management.
- Received an invitation link or code from someone? Paste it in and click "Open this invitation".
- There is no site-wide name search.
- When you are connected to a lab's own server, you need to "Verify email" once before inviting or accepting contacts, because the site never hands your sign-in email to the official relay. Messaging your own advisor or students doesn't need this step.

Three kinds of chat

- **Direct chat:** there is only one between two people. An advisor and their own students can chat directly; anyone else must first become contacts.
- **Research topic group:** one group per research topic; membership follows the lab roster. Use "Project group" in the Lab Management top bar, or "Open project group" on the research topic in the Lab info

drawer.

- **Group chat:** created by you. It can mix your students or advisor, contacts and people from other labs. Click "+ New group chat" at the top of the Chats tab. The people picker lists, in one place: people in the original chat, My students / My advisor, Labmates, Contacts and Recent direct chats, and you can also invite by email. Invitees join only after they accept, and they can't see messages from before they joined. For email invitations, you get each person's invitation link and invite code once the group is created.
- **"Add people" in the chat header:** in a direct chat or a research topic group, it starts a separate group chat with the people here; the earlier history isn't copied over. In a group chat, it invites new members; owners and admins can use it.
- **"Members":** see members and roles, and rename the group. The owner can appoint admins, transfer ownership, remove members and archive the group (after archiving, other members can no longer enter; the owner keeps a read-only history). Everyone else can leave the group chat.

What you can do in a chat

- **Write messages:** Enter sends, Shift+Enter adds a line; @ mentions a member (they see "@you"); sent messages can't be edited or recalled.
- **Input box:** one box that starts one line tall and grows as you type. References, files and people you @ waiting to be sent sit as small chips at the top of the box; click x to drop one, and more than one file folds into "N files". The bottom row holds the tools:  send a file, the experiment chip,  reference attachment,  share one result, and @ in group chats.
- **Send a file:**  in the bottom row, or drag files into the chat or paste a screenshot.  sends a copy from your computer;  references an attachment already in the experiment and copies nothing. Up to 50 MB per file and 10 files per message; images are shown inline and open enlarged, other files are downloaded with "Download". Files are kept in the private storage of sciblock's official collaboration relay; only members who can see that message right now can download them, and there are no direct links. Files uploaded but never sent are cleared within 24 hours.
- **Mention experiment / Reference attachment:** see 11.5.
- **Tag messages by experiment:** one chat often covers several experiments. Before sending, choose in the experiment chip which experiment this message is about, and the message carries that experiment's tag; choose nothing for small talk. The chip only takes what you choose: entering through "Discuss" picks that experiment for you, while the experiment selected in the left column only appears as the first menu item, "Selected in the left panel", and is never applied on its own. The menu also lists the five experiments most recently discussed in this chat and "Choose from all experiments...".
- **Reading tags:** when the topic changes, a small grey line with the experiment name sits right above the first message (left or right, following that message); click it to see only that experiment. Switching back to small talk just leaves a little space. Several messages one person sends within a few minutes sit close together, with the name shown once and the time only at the end of the last one; hover the others to see theirs. When you scroll up, the top shows "Now viewing: ...".

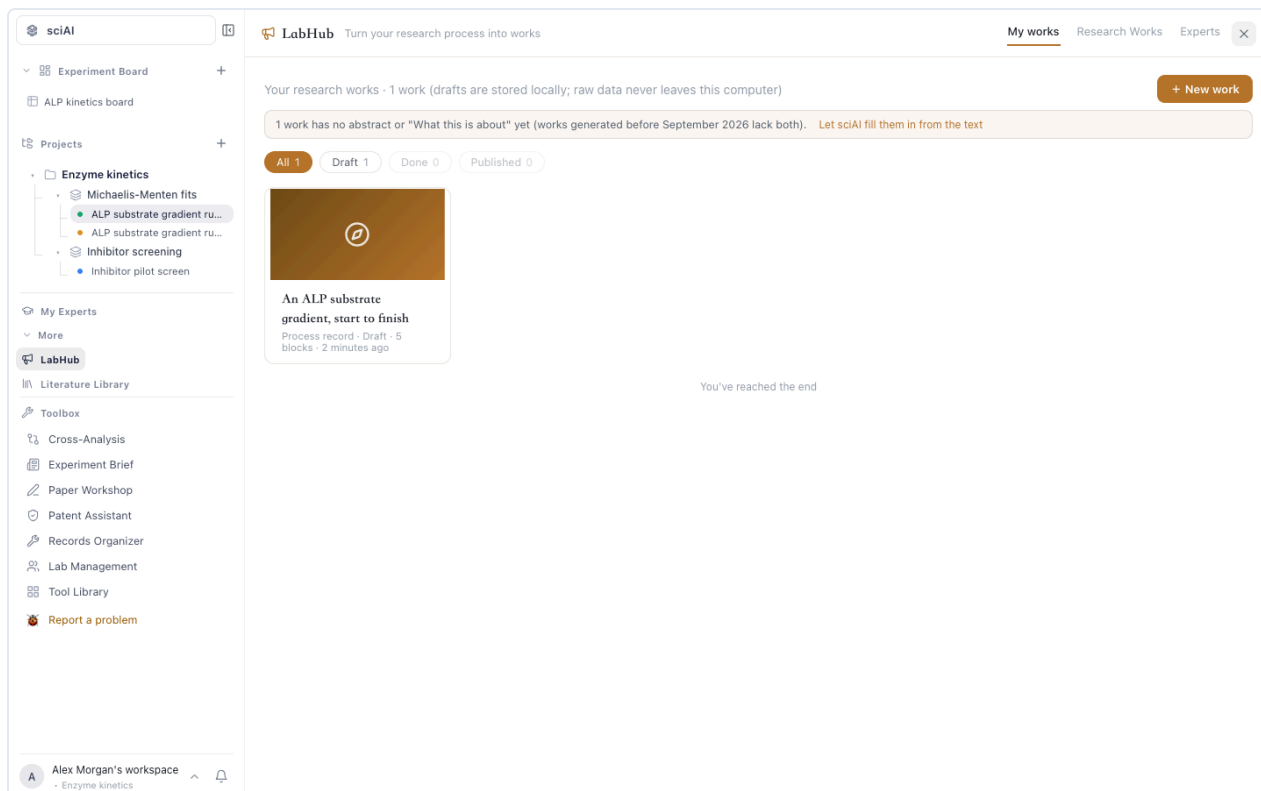
- **Filter by experiment:** the chat header has a single "All experiments ▼" button. It opens a searchable list grouped by project › module (by person first in group chats), three per group with the rest folded into "N more experiments". Pick one to see only its messages; what you write next is tagged with it by default. "Show all messages" takes you back.
- **Tagged messages can be saved too:** hover a message to see "Save...". The rules are the same as under a reference card (the experiment owner saves to notes or next steps; the advisor saves their own expertise).
- Experiment names are resolved on each person's own computer with their own permissions. Anyone without access sees only "Unshared experiment"; several unshared stretches in a row merge into one, labeled once. In the filter, that group folds into a single row, "Experiments not shared with you (N)", and searching by name won't find them.
- **Share one result:** only the student who owns the data can pin one of their results (value, unit, provenance) as a snapshot into the chat. Before sending, it lists everyone who will receive it and who among them is an external collaborator, and notes "Does not change with the original experiment". An advisor who wants a student's result sends a "Result sharing request" card in a group, which the student answers with "Confirm sharing" or "Not now"; in a direct chat, just ask.

What it doesn't do: no online status, no typing indicators, no read receipts; nobody is shown whether you have read something. Messages arrive in real time; if the connection drops, the chat refetches every 15 seconds and refreshes when the window comes back to the front.

Chapter 12 • LabHub Research Community

LabHub is a community platform for experimental methods and know-how. You can turn mature experimental workflows, method guides and process records into works and publish them, and you can also read, save and cite your peers' works, and install experts that others have made public.

12.1 Read works



LabHub: the My works / Research Works / Experts tabs

1. In the left column, go to "More" → "LabHub". On the "Research Works" tab you can filter by "All / Relevant to me / Saved by me", or "Browse by research area".
2. When you open a work, the page has three columns: on the left, the table of contents (the section you are reading is highlighted) and an index of figures and tables; in the middle, the body text; on the right, the author, version, license, length, and Save / Cite / Report.
3. The body may begin with "What this is about": 2 to 3 one-sentence conclusions.
4. You can tick off procedure steps as you go; ticked steps are struck through and the work shows "Done 3/5". Progress is stored only on your computer; "Start over" clears it.
5. Click a figure in the body to enlarge it (scroll to zoom, drag to pan, Esc to close).
6. "Cite this work" at the end: add it to your own Literature Library in one click, or copy the GB/T 7714 reference, BibTeX or permanent link (pinned to the version you read).
7. The end of the work also shows "More works by this author" and "Same research area".
8. If the author has published an expert, "The author published the expert "X" (N entries)" appears above the body, and you can click "Install" right there.

12.2 Create and publish works

1. In LabHub, click "New work", choose a type and enter a title.
2. "AI one-click generate": The AI fills in the procedure steps, required materials, precautions and so on from your experimental data. It uses only the real content and images in your materials; anything

missing is skipped, never made up.

3. Upload or insert images and videos (up to 300 MB each).
4. You can use "AI revise" on each section to polish the wording. "What this is about" can be edited, deleted or written by yourself.
5. Byline: your account's name, school, major and email are filled in automatically. You can change them and add co-authors before publishing; click "Set as my default byline" so new works use it from then on.
6. When the preview looks good, click "Publish". Once published, the work is visible in the public feed, categorized by research area.

Republishing: After making changes, click "Publish" again; images and videos you haven't changed are not uploaded again. **Unpublishing:** Click "Unpublish" on the right side of the work; once unpublished, others can no longer see it. **Takedown:** If a work is reported and taken down after review, you receive an in-app message stating the reason. A work that has been taken down cannot be republished; if you disagree, reply to that message.

12.3 Saves and experts

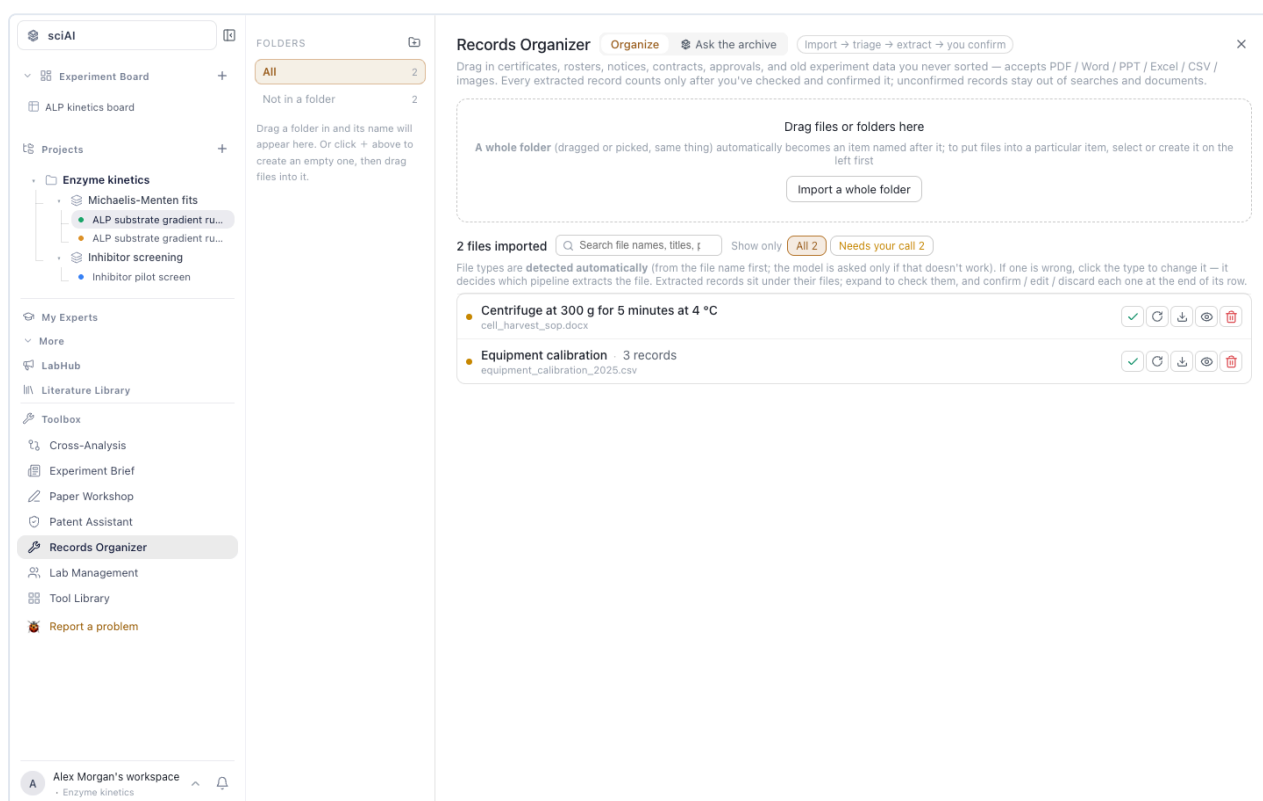
- Click "Save" on the right side of a work, and it appears under "Saved by me" at the top of the "Research Works" page.
 - The "Experts" tab lists experts that people have published; see Section 7.4 for how to install them.
 - Use the "My works" tab to manage the works you have published.
-

Part 7 · Records Organizer

Chapter 13 · Records Organizer: turn certificates, lists, and notices into searchable records

When to use it: You work in research administration, academic affairs, or as a lab secretary, and you have a pile of certificates, award lists, official notices, contracts, and approvals. You want to turn them into structured records you can search, cite, and trace back to the original, and then produce documents and tables as needed. It is also a good way to bring in older experiment data that was never organized.

The top of the page shows the workflow: "Import → triage → extract → you confirm". Every extracted record counts only after you have reviewed and confirmed it; unconfirmed records are not searchable and do not go into documents. The page has two tabs: "Organize" (import, review, confirm) and "Ask the archive" (search, produce documents, draw charts).



Records Organizer: folders on the left; the import area, filter bar, and list of imported files on the right

13.1 Importing materials

1. In the "Tool Library", add "Records Organizer" to your toolbox and open it.

- The middle column lists folders: "All", "Not in a folder", and the folders you create. Click the new-folder icon in the top-right corner to create a folder, for example "2024 Teaching Award Materials" or "Contracts and Approvals". Folders can be renamed and deleted.
- There are two ways to import: - **A whole folder**: drag the folder onto the "Drag files or folders here" area, or click "Import a whole folder" to pick one from your computer. An entry is created under the folder's own name, and nested subfolders are merged into that same entry. - **Individual files**: first select a folder on the left, then drag files in or click "Import files". The files go into the selected folder.
- You can import PDF / Word / PPT / Excel / CSV / image files, up to 30 MB each. Convert HEIC and TIFF images to JPG or PNG first; both **.ppt** and **.pptx** can be imported directly.
- Files with identical content are never added twice; dragging the same file in again does not create a second copy.

13.2 Triage, extraction, and confirmation

After import, the system first **triages** each file: it decides whether to extract page by page (certificates, notices) or row by row (lists and tables). The reason is shown next to the file; if it's wrong, click it to change it. It then **extracts** fields: title, level, date, issuer, owner, and so on. Categories (such as "Teaching Excellence Award") are names that grow out of your own library, not a fixed menu.

The screenshot displays the sciAI Records Organizer interface. On the left is a sidebar with navigation options like 'Experiment Board', 'Projects', 'My Experts', and 'Records Organizer'. The main area is divided into three panels. The first panel, 'FOLDERS', shows 'All' and 'Not in a folder' with counts. The second panel, 'Records Organizer', has tabs for 'Organize', 'Ask the archive', and 'Import → triage → extract'. It contains instructions for dragging files and a search bar. Below, it lists '2 files imported' with a filter 'All 2' and a status 'Needs your call 2'. The first file is 'Centrifuge at 300 g for 5 minutes at 4 °C' (cell_harvest_sop.docx), showing extraction by page. The second file is 'Equipment calibration' (equipment_calibration_2025.csv), showing extraction by row. The third panel on the right shows the expanded CSV data table.

#	Equipment	Serial No	Owner	Calibration date
1	Centrifuge	CF-1102	Alex Morgan	2025-03-02
2	Pipette set	PS-3301	Alex Morgan	2025-04-11
3	Spectrophotometer	SP-0207	Sam Lee	2025-05-20

An expanded file: one row per record, with ✓ Confirm / ⬇ Download original / 👁 View original / 🗑 Discard at the end of each row

The file list is also the review area. The "Show only" filter sorts files into four groups:

- "Needs your call": some extracted records are uncertain — a missing date, a level that can't be determined, or no person assigned yet.
- "All clear · ready to confirm": all extracted records look fine and are waiting for you to glance over and confirm.
- "Fully confirmed": every record in this file has been confirmed.
- "No records yet": extraction hasn't been run, or it ran and produced nothing.

Record by record: click a file row to expand it. Each record row ends with ✓ "Confirm this record", ↓ download original, 👁 "View original", and 🗑 discard. Click the record itself to edit its fields, and to change "Which field is which" (title / date / issuer / level). Whole file at once: click "Confirm the N clean records in this file". Records marked "Needs your call" must be handled one by one first; a record with no person assigned can't be found in searches even after you confirm it, so pick a person below first. You can expand "Text read during extraction" to check against the original text.

Merging categories: if the same kind of material has ended up under two names (for example "Teaching Reform Project" and "Education Reform Project"), when you rename the category you can choose "Just this record", "All N records in this file", or "All M records of ..." in the library".

Manual entry: for material that can't be extracted, click "Fill in manually" to add a record; it still needs to be confirmed to count. **Re-extract:** recognizes the material again in a different way and creates a new record; any edits you made are lost. **Trash:** discarded records keep their originals, so you can "Restore" them (exactly as they were, including edited fields), "Re-extract" them, or "Delete permanently" together with the original.

Only confirmed records go into searches and documents. Editing a confirmed record keeps it confirmed.

13.3 Ask the archive: search, produce documents, draw charts

sciAI

Experiment Board

ALP kinetics board

Projects

Enzyme kinetics

Michaelis-Menten fits

ALP substrate gradient ru...

Inhibitor screening

Inhibitor pilot screen

My Experts

More

LabHub

Literature Library

Toolbox

Cross-Analysis

Experiment Brief

Paper Workshop

Patent Assistant

Records Organizer

Lab Management

Tool Library

Report a problem

Alex Morgan's workspace

Enzyme kinetics

Records Organizer

Organize

Ask the archive

Import → triage → extract → you confirm

Materials for Alex Morgan

Drag in certificates, rosters, notices, contracts, approvals, and old experiment data you never sorted — accepts PDF / Word / PPT / Excel / CSV / images. Every extracted record counts only after you've checked and confirmed it; unconfirmed records stay out of searches and documents.

No conditions given, so this lists everything confirmed. Sorted by material date, newest first. (2 more record(s) awaiting confirmation aren't counted — only confirmed ones are searched.) 2 records in total

There are 3 calibration records.

#	Name	Linked to	Level	Time	Serial No	Valid until	Calibrated by
1	Spectrophotometer	Sam Lee	—	2025-05-20	SP-0207	2026-05-19	MetroCal
2	Pipette set	Alex Morgan	—	2025-04-11	PS-3301	2026-04-10	MetroCal

Make materials from these 2 records →

View original

View original

equipment_calibration_2025.csv

#	Equipment	Serial No	Owner	Calibration date
1	Centrifuge	CF-1102	Alex Morgan	2025-03-02
2	Pipette set	PS-3301	Alex Morgan	2025-04-11
3	Spectrophotometer	SP-0207	Sam Lee	2025-05-20

Ask it to find materials or download original files...

Ask the archive: only confirmed records are visible; ask by person, category, year, or level

Switch to the "Ask the archive" tab and ask in plain language:

- **Search:** "Which provincial / ministerial-level or higher awards has Jane Smith received?", "Which teaching reform projects were added in 2024?", "Who is in the School of Life Sciences?". The table below the answer and its "N records in total" are what count: the system counts the records itself, the AI doesn't estimate. Every record links back to its original, with the matching part highlighted in yellow. If nothing matches, it says so; there is no fuzzy matching.
- **Produce a document:** say "Put together Jane Smith's materials", or click "Make a new document with the current conditions" below an answer. An "Archive materials list" preview appears in the right panel, with a header stating the search conditions, record count, sort order, and generation time, and "Download Word" at the bottom. While a document is open, a follow-up such as "Remove the municipal ones" edits that document by default.
- **Draw charts:** say "Draw a trend chart by year" to get a trend line, a school × year heatmap, or a dot plot. All the data is counted by the system.
- Click "New conversation" in the top-right corner to start a new thread; earlier conversations are kept in the history.

13.4 Filling an official template

Received a blank form from an administrative office to fill in? On the "Organize" page, click "Fill an official template": upload the blank Excel template → the system recognizes the headers → it proposes which archive field goes in each column (uncertain ones are flagged for you to decide) → it fills in the original file, keeping letterheads, borders, and merged cells → it tells you right away which columns weren't fully filled. You can save the template and reuse it with one click next year.

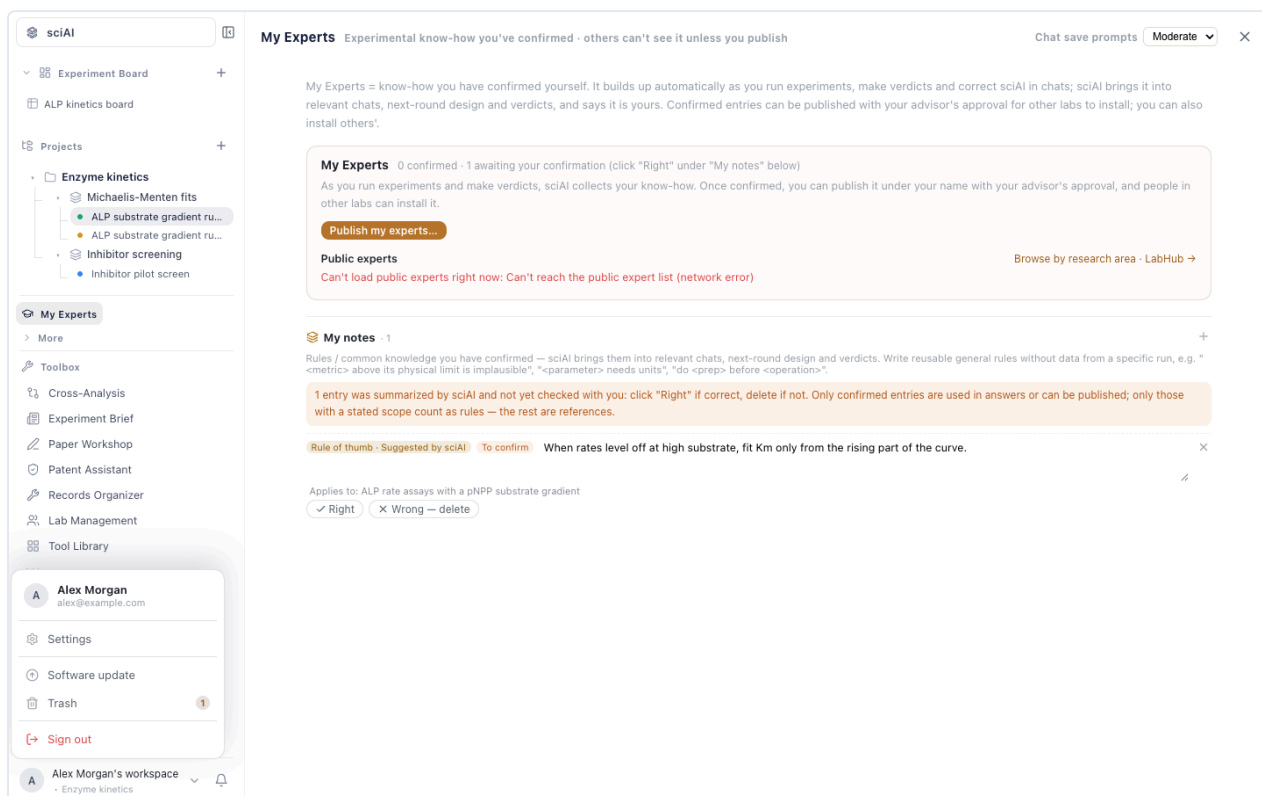
13.5 Linking to a project

By default, Records Organizer records don't appear in the project tree on the left, and the AI can't see them in experiment chats. When you need them, click "Link to project" on a folder: each document in that folder is attached to the chosen project as one experiment, named after the file, and can then be cited in experiment chats. They don't appear in the tree on the left; the project node just gets one extra "Archived data · N experiments" row.

Part 8 · Settings and maintenance

Chapter 14 · Settings and profile

Click your name at the bottom of the left panel to open your account menu: Settings / Software update / Trash / Sign out.



Account menu: Settings / Software update / Trash / Sign out

The Settings window has a section list on the left and the content on the right. Changes take effect only after you click "Save". Sections covered in this manual:

- **Profile:** name, research area, university, major; "Brief cover byline" (student name / advisor name / advisor email), used on the cover page when you generate a brief.
- **Cloud sync:** see Chapter 15.
- **Software update:** see Chapter 16.

Chapter 15 · Cloud backup and restoring on a new computer

15.1 Two rules

- **The cloud is only a backup.** Your computer is the single source of truth. Nothing is ever downloaded to or wiped from any computer automatically; when you switch computers, the backup is restored to the

new one only after you confirm it yourself.

- **Backups are always kept.** Turning off sync only stops uploading; content that is already backed up is not deleted.

15.2 Turning on backup

If your lab runs its own server, first connect to it with "Connect to a server" on this page (see Chapter 17), and backups go to that server; otherwise they go to the official cloud.

1. Open "Settings → Cloud sync", or click the "Local data" bar at the top of the center column (hard-drive icon + the name of your current data folder).
2. Check "Sync to the cloud", read the sync notice that pops up, and click "I understand, turn on sync".
3. Optionally check "Also upload original files" (experiment attachments, board images, literature PDFs, Records Organizer originals, etc.). If you leave it unchecked, only structured data is synced, and advisors won't be able to see images.
4. Once it's on, local changes are uploaded automatically after about 20 seconds. If the network drops, it retries automatically; anything not uploaded before you shut down is uploaded the next time you open the app. To upload right away, click "Sync now". The "Status" area shows "Last sync ... · N experiments and M original files synced"; anything still waiting shows as "N pending".
5. If sync is already on and you see "Sync scope updated", click "Review and agree"; only then do the newly added areas (conversations, literature library, paper drafts, Records Organizer, etc.) start being backed up.

15.3 Switching computers: restoring on a new computer

1. If the old computer still works, complete the backup first: if you see "Sync scope updated", click "Review and agree", then click "Sync now" and wait until nothing is pending. Check the "Skipped" list for any files you care about. You don't need to turn off sync on the old computer.
2. Install sciblock on the new computer, choose a new data location on first launch, and sign in with your existing account.
3. If the new data folder is empty and there is a backup in the cloud, a prompt appears automatically: "Your account has a cloud backup: N projects, M experiments, K conversations, F original files. Restore it to the data folder you just chose on this computer?" Click "Restore my data".
4. If you didn't see the prompt or clicked "Cancel" at the time: go to "Settings → Cloud sync" and, under "Restore on a new computer", click "Restore from the cloud to this computer".
5. Restoring runs in the background; progress is shown at the top of the window or on the button.
6. When it finishes, you're asked "Keep backing up to the cloud on this computer?". Click "Keep backing up" to continue with your original scope, or "Not now".

15.4 Turning off backup

Uncheck "Sync to the cloud". The confirmation says "This only stops further uploads. Data already backed up stays in the cloud". Click "OK". Your local data is not affected.

15.5 Common situations

- "There is no backup to restore in the cloud yet.": make sure you signed in to the same account on the new computer, and that sync was turned on on the old computer.
- No restore prompt on the new computer: the prompt only appears when the new data folder has no projects or conversations yet. If it already has data, use "Restore from the cloud to this computer" on the Settings page.
- "This computer already has N of your projects or conversations. Continuing will overwrite local items with the same id using the cloud backup": click "Restore from the cloud anyway" only if you're sure you want the cloud copy to replace what's on this computer.
- Network drops during a restore: whatever has already been saved locally is kept; click "Restore from the cloud to this computer" again to fill in the rest.
- Projects you deleted on the old computer reappear after restoring: the cloud never deletes anything, so they come back with the restore. Delete the ones you don't need on the new computer.
- Items in "Skipped": original files over the 50 MB limit are not uploaded; "local file no longer exists" means the original file has been moved away.
- "Cloud storage is full (limit 5 GB); uploading original files is paused": projects, experiments, and conversations are still backed up as usual, and uploading resumes automatically once there is space.
- "This computer has no usable cloud credentials": click "Sync now" first; if that doesn't help, sign out and sign in again.
- "N items were overwritten by a newer version from another computer": both computers edited the same project at the same time. Click "View old values" to check them one by one, and "Restore old value" where needed. When you use two computers, try not to edit the same project on both at the same time.

Chapter 16 · Software updates and reporting problems

Software updates

- sciblock checks for updates automatically when it starts, and then every few hours; when a new version is available, a notice appears in the bottom-right corner.
- You can also check manually: "Software update" in the account menu, or "Settings → Software update", shows the current version. Click "Check for updates" → download → "Restart to install". You can also choose "Skip this version".
- Updating never loses your existing data or conversations.

Reporting problems

If the interface misbehaves, an AI answer is clearly wrong, or a file can't be parsed, you can submit a report with "Report a problem" in the toolbox: it automatically captures the current window (you can mask parts of it), you choose the problem category and severity, add a one-line description, and submit. We'll follow up from there.

Antivirus false positives when installing on Windows

If the installer shows "sciblock was not installed successfully... it has almost certainly been quarantined as a virus by antivirus software", follow the steps in the dialog in order: first go to "Protection history" in Windows Security, find the sciblock entry, and choose "Allow on device"; then add the installation folder to "Exclusions"; finally, run the installer again. If you use 360, Tencent PC Manager, or Huorong, restore the files from its quarantine, add the installation folder to its trusted zone, and reinstall. If clicking the icon after installation says the item "has been changed or moved", or the app crashes during use and disappears, the cause is the same and so is the fix.

Part 9 · Lab Server Deployment

Chapter 17 · Your Lab's Own Server (Private Deployment)

Who this is for: research groups that have bought their own server and want to bring the whole group's data together on a machine the lab controls. The first half is for the administrator (installation, handing out codes, operations); the second half is for members (how to connect). The whole process takes about 20 minutes.

17.1 Three things to know first

- **This server runs the same server software as the official cloud**, just with a different configuration. Once it is installed, the whole group's cloud backup, restoring on a new computer, and lab management all go through this machine.
- **Every member has a complete copy of their data on their own computer; the server is only the meeting point.** If the server's disk fails, any member's computer can rebuild the group's data. Backing up the server is still your own responsibility, though (see 17.6).
- **This server does not send email.** Members register with an **invitation code** that the administrator issues from the admin console, not with an email verification code.
- Each member's sciblock must be a version that supports "Connect to a server". Clients that are too old cannot connect, and pairing will tell them plainly to update. So the first step is to have the whole group update.

17.2 What you need

Item	Requirement
Machine	An always-on machine. 8 CPU cores, 16 to 32 GB of RAM and a 1 to 2 TB SSD are enough; no GPU is needed
OS	Any Linux that can run Docker (Ubuntu / Debian / CentOS all work)
Software	Docker and Docker Compose v2. If you don't have them, install them first: docs.docker.com/engine/install
Network	The group's computers only need to be able to reach this machine; a local network is fine. Whether you need a public domain name is covered in 17.5

17.3 Installation

We will send the administrator **an archive** that contains no source code. Unpacked, it holds these files:

```
sciblock-lab-server-<date>/
  install-lab-server.sh      <- run this
  docker-compose.lab.yml    <- used by the script, don't move it
  部署文档.md               <- deployment guide (in Chinese)
  README.txt
  sciblock-cloud-api.tar    <- offline image (for machines on an internal network)
```

If the machine cannot reach the internet (true of most lab servers), keep `sciblock-cloud-api.tar` in the same folder. The script uses it automatically, with no internet connection and no sign-in to any image registry.

```
tar -xzf sciblock-lab-server-<date>.tar.gz
cd sciblock-lab-server-<date>
./install-lab-server.sh
```

The script asks two questions:

- **What this server is called:** this is the name members see when they pair, so choose one they will recognize at a glance (for example, "Zhang Lab"). The script won't continue without it.
- **Administrator email:** the first account registered with this email *and* the install token becomes the administrator.

The script handles everything else: the database password is generated at random and written to `.env.lab`, so you don't need to remember it. At the end it prints a **pairing code** and a **first-admin install token** (also stored in `.env.lab`). The pairing code looks like this:

```
http://192.168.1.50:8788#51b4b07b19db6f9a
```

Running it again is safe: the keys and data live in Docker volumes, so a second run won't change the site identity or touch the data. If the installation fails halfway, fix the problem and run it again.

17.4 What the administrator does, in order

After installation, members still can't connect, because two things are missing. What you send each member is:

	What it is	Where it comes from
① Pairing code	<code>http://192.168.1.50:8788#51b4b07b19db6f9a</code>	The line printed at the end of the install script; the whole group shares the same one
② Account	An email + password on this server	Members register themselves, but you need to issue invitation codes

The most common mix-up: the email and password in item ② are **an account on this server**, not a sciblock official-cloud account. The two are unrelated, and members need to register a new account on this server.

The order:

1. **Run the script** and note the pairing code and the first-admin install token it prints.
2. **Register an account with the administrator email you entered, and enter the install token in the sign-up form.** With an empty database, the right email and the right token, that account becomes the administrator; a random email or a missing token can't claim it. The token is spent after one successful sign-up.
3. **Issue invitation codes** to the group from the admin console. Ordinary members enter only the invitation code and leave the install token field empty.
4. **Have the whole group update sciblock to the new version first.**
5. Post the **pairing code + invitation codes** in your group chat. Each member connects → registers or signs in → (if they already have data) claims their own data.

Don't split the pairing code. The 16 characters after `#` are this server's identity fingerprint. The client compares it with the one the server reports, and if they don't match it refuses on the spot, with no "Continue anyway" option. This is the only guarantee that you have connected to your lab's real server and not to an impostor on the local network. Copy and paste the whole line; don't send just the address and leave members to check the fingerprint themselves.

17.5 Do you need HTTPS on the internal network?

Approach	When to choose it
Plain HTTP on the internal network	Least effort; generally acceptable on a lab network
Self-signed certificate	More robust; the client already trusts this server's identity fingerprint anyway
Campus domain + the university's certificate	Best if you have one; once set up, use <code>PUBLIC_BASE_URL</code> to override the address the script prints

```
PUBLIC_BASE_URL=https://sciblock.lab.edu.cn ./install-lab-server.sh
```

17.6 Day-to-day operations

Check status and logs

```
docker compose -f docker-compose.lab.yml --env-file .env.lab ps
docker compose -f docker-compose.lab.yml --env-file .env.lab logs -f cloud-api
```

Backups (do these regularly): all the data lives in two Docker volumes. The simplest approach is to export the database regularly:

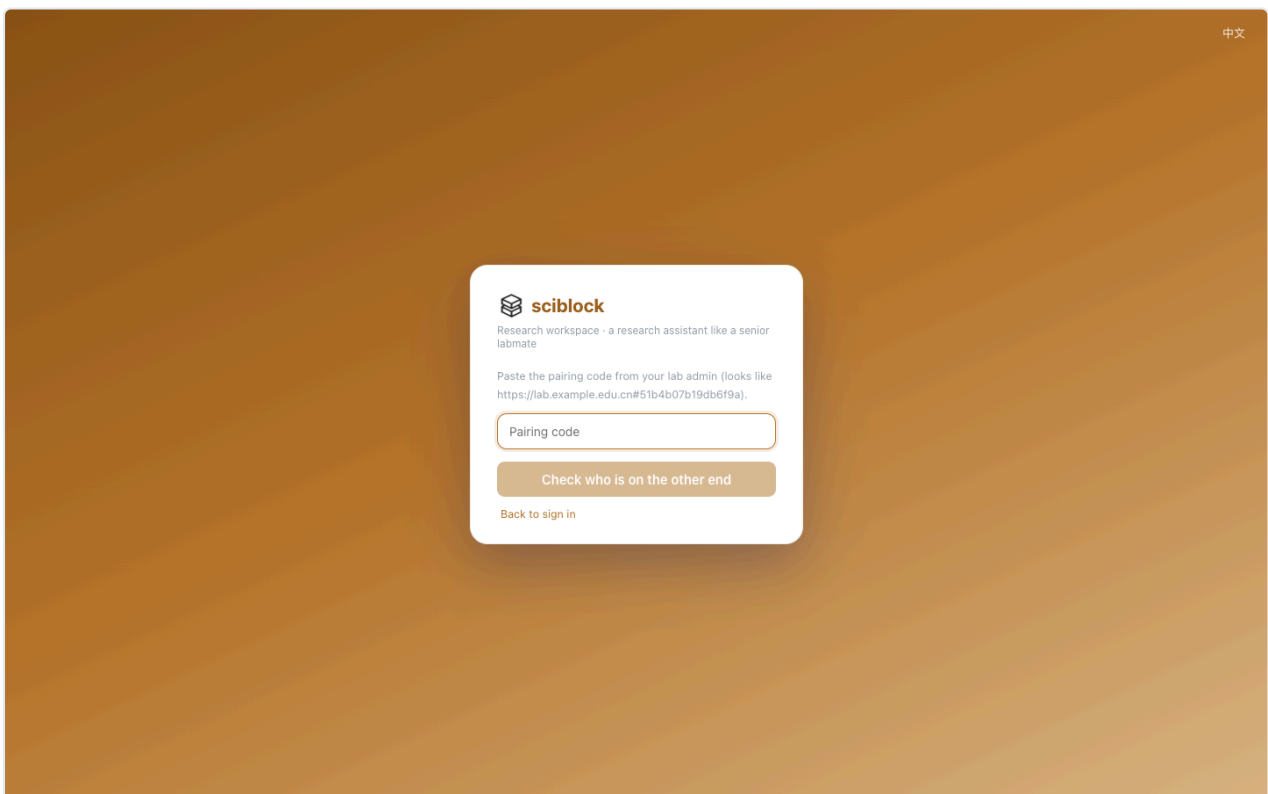
```
docker exec sciblock-lab-pg pg_dump -U sciblock sciblock_lab | gzip > backup-$(date +%Y%m%d).sql.gz
```

Upgrades: when you receive a new image package, first take a backup as above, then put the package in the folder and run the install script once. Upgrades don't touch the data; if the database structure needs to change, that happens automatically when the service starts. **Upgrade the server first, then have members update their clients.** After upgrading, check the container status Docker prints: you need to see Recreated, not Running. Running means the image was never replaced and the upgrade did nothing.

The one thing you must never do: don't delete the `sciblock_lab_storage` volume, and don't change `SCIBLOCK_JWT_DIR`. The site identity (the 16-character fingerprint in the pairing code) is derived from the keys, and the keys are stored in that volume. If the keys change, every member who has already paired will be locked out at once, and no error message will point you here. If you really must change them (for example, if you suspect the keys have leaked): change the keys → issue a new pairing code → tell the whole group to pair again.

17.7 How members connect

There are two kinds of members and two paths. Both paths show the site name the administrator chose.



The "Connect to a server" option at the bottom of the sign-in page: paste the pairing code, then "Check who is on the other end"

New members or new computers (sciblock has never been used on this computer, or you have no official-cloud account)

1. Open sciblock and, at the bottom of the sign-in page, click "Does your lab run its own server? Connect to it".
2. Paste the pairing code, click "Check who is on the other end", check the site name and fingerprint shown, and confirm the connection.
3. From then on the sign-in page says "Signing in to: your site name", and both registration (with the invitation code; leave "First-admin install token" empty) and sign-in happen on this server.
4. Do the same when you switch computers: "Restore from the cloud" on first launch after signing in pulls from this server.

Members who already use sciblock (with an official-cloud account and data on their computer)

1. First sign in with your existing account.
2. Go to "Settings → Cloud sync → Connect to a server", paste the pairing code and click "Check who is on the other end". This step only identifies the server and writes nothing; it shows the site name so you can confirm you've reached the right place.
3. Only after the server checks out does the next step appear: enter your email and password **on this server**, then pick one set of local data to "claim".
4. Once connected, you are switched to your account on this server and the local data is placed under it. If you don't claim anything, this account is empty for now, and your original data stays exactly as it was.

After connecting: cloud backup, restoring on a new computer and lab management all go through this server. Members who had official-cloud backup turned on will see "Backup destination changed"; backups to this server start only after they click "Review and agree" once. The earlier copy on the official cloud is not deleted. You can **disconnect or switch back to the official cloud** at any time (at the bottom of the sign-in page or in Settings), and your local data stays exactly as it was.

17.8 Troubleshooting

The member says	Most likely
"Can't reach this address"	Their computer has no network path to the server, or the address sent was the server's 127.0.0.1
"There is no sciblock site at this address"	The address is right but the port is wrong, or the server version is too old
"The fingerprint doesn't match the one in the pairing code"	Don't bypass it. Either the pairing code is outdated (the keys were changed) or someone is in the middle. Send a fresh pairing code
"This site requires version X or later"	Their sciblock is too old; update the client first

The member says	Most likely
Registration asks for an invitation code	That's expected: this server can't send email verification codes, so the administrator issues codes from the admin console
Registered with the administrator email but not an administrator	The install token wasn't entered, or someone already used it (the token only works once). An existing administrator can promote the account from the admin console
The whole group suddenly can't sign in	See "The one thing you must never do" in 17.6: check whether the volume was deleted or the key directory was changed

If you still have problems, send us the output of this command:

```
docker compose -f docker-compose.lab.yml --env-file .env.lab logs --tail 50 cloud-api
```

17.9 What this server doesn't have

These are deliberately not set up, so don't go looking for them:

- **Object storage:** attachments are stored directly on the machine's disk (the `sciblock_lab_storage` volume).
- **Email service:** it can't send verification codes, so registration uses invitation codes.
- **LabHub public feed:** this stays on the official cloud, not on this machine.

Part 10 • Reference

Chapter 18 • UI Element Index

17.1 Left column

Element	What it does
"♦ sciAI"	Global research assistant: ask general questions, and it can also search all your experiment records
"Experiment Board"	List of board pages + " + New board page"
"Projects" tree	Project › Module › Experiment; inline " + " to create, "🖱" to rename, "X" to delete; "🔍" on a project row starts a research thread in one click
"More"	Collapsible group containing LabHub, the Literature Library and more
"My Experts"	Know-how you have confirmed; publish / install experts
"Toolbox"	Tools you have added + "Tool Library"
User header	"{name}'s workspace" + menu (Settings / Software update / Trash / Sign out) + notification bell

17.2 Center column (chat panel)

Element	What it does
Connection status	Colored dot at the top left; hover to see "Connected", "Connecting..." or "Backend not connected"
Scope Bar	The AI's current analysis scope + the experiment status control (In progress / Needs refinement / Succeeded / Failed / Discarded)
"Local data" strip	Name of the current data folder; click it to manage cloud sync
Icon row on the right	Draft / Attachments / Record sheet + " : More panels" (Evidence / Analysis / Assets / Experts)
"📦 Handoff package"	Completeness bar: "Complete · ready for the next cohort" or "N items missing"
Input box	Enter to send, ▲ to send / ■ to stop, "@" to reference an attachment or mention something to compare, 📎 to add files

17.3 Right-column panels

Panel	Contents
Draft	AI experiment record draft with a source tag on each item; "Confirm" endorses the whole draft; decisions and notes
Attachments	Upload, parse status, preview of the first 12 rows, re-parse, delete, add to the Literature Library
Record sheet	Factors prefilled, responses filled in cell by cell, saved as a CSV attachment
Evidence	Facts / metrics / images / data / literature / documents, each with a traceable source
Analysis	Structured analysis: facts / metrics / inferences / limitations / next steps / missing evidence / overall confidence
Assets	Materials / sample locations / SOP / handoff
Experts	Your own know-how in use, others' know-how, expert reviews

17.4 Toolbox tools

Tool	In one sentence
Cross-Analysis	Pick experiments across experiments / modules / projects for comparative analysis; outputs Word
Experiment Brief	Generate a progress brief (weekly / monthly style) from selected experiments; outputs Word / PDF
Research Proposal	Enter your research idea and a proposal is built in several passes, even without data; outputs Word
Research Report	Progress update / mid-term review / final summary, automatically including real experiment data; outputs Word
Paper Workshop	Outline → key claims → claim list → body text → Word; Chinese and English, academic papers / theses
Patent Assistant	Generate a patent disclosure from experimental results; outputs Word
Lab Management	Create research topics and invite students; the advisor view shows progress and results (read-only); LabAI Q&A
Records Organizer	Turn certificates, rosters, notices, contracts and approvals into searchable, citable, traceable records
Report a problem	Takes a screenshot automatically and submits the problem

Chapter 19 • File Formats and Limits

Limit	Current value
Maximum rows parsed from CSV / Excel	500 rows; anything beyond that is not parsed
Rows shown in attachment preview	First 12 rows
Experiment attachment size	300 MB
Literature Library upload size	40 MB
LabHub single image / video	300 MB
CSV encoding	Must be UTF-8
Excel worksheets	Every worksheet is parsed; each sheet has the row limit above
Document text length	Extraction has a cap; the end of very long documents may be cut off
Python computation timeout	25 seconds
Number of @ mentions to compare	Up to 12
Module / project scope	With many experiments, the AI gives a high-level overview rather than a detailed data-by-data analysis
Single original file in cloud sync	50 MB; larger files are listed under "Skipped"
Cloud storage space	5 GB; when it is full, original-file uploads pause, while projects, experiments and conversations keep being backed up
Files sent in chats	50 MB per file, up to 10 per message; 2 GB in total per person on the relay
Brief format templates	.docx / .xlsx / .doc / .pdf / .txt; Word and Excel templates are filled back in as they are, other formats only provide section names and the brief uses sciblock's layout

Chapter 20 • Glossary

- **Scope:** the AI's analysis scope, set by the experiment / module / project you select in the left column.

- **Scope Bar:** the scope indicator at the top of the center column; the single visible source of truth for what the AI is looking at.
- **Evidence:** structured data parsed from uploaded files, each item with a traceable source. The AI can only cite evidence in its answers.
- **Source marker:** the superscript [1][2] in a reply; click it to jump to the original evidence or attachment.
- **Grounding bar:** the label at the top of an answer that states the evidence boundary of that answer.
- **Draft:** an experiment record the AI generates from evidence and the conversation, with a source tag on each item; you need to confirm and endorse it.
- **Measured / Inferred / To confirm:** measured values come from real numbers in files; inferred values are worked out by the AI; values still to confirm are left out of analysis until you confirm them.
- **Research thread:** the top-level DOE container built around one scientific question, holding the main hypothesis and a number of experiment rounds.
- **DOE:** the design-of-experiments loop: hypothesis → design → run → verdict → iterate, until it converges.
- **Verdict:** the AI's judgment of the hypothesis based on the current round's data, "supported / refuted / inconclusive", along with statistical test results.
- **Board:** a table organized as one row per experiment, with category containers, AI estimates and confirmation, a kanban view, and Excel export.
- **My Experts:** experimental know-how you have confirmed; you can publish it and install other people's.
- **Notes (sediment):** general know-how distilled from conversations (rules of thumb / methodology / terminology), accumulated into "My Experts".
- **Handoff package:** the completeness bar at the top of the right column, which checks whether the draft, attachments and assets are complete.
- **SOP:** standard operating procedure; it can be saved in the draft's "Methods" section and also viewed in a board column.
- **Lab:** an organization created by an advisor; after students accept an invitation, they share projects with the advisor.
- **Mirror:** the read-only copy of a student's shared projects that the advisor pulls to their own computer.
- **Discussion:** a chat message with an experiment or attachment attached. The student saves the conclusion into their own experiment notes or next steps; the advisor can save it as their own expertise. Earlier "co-research" exchanges are kept read-only as "Discussion record".
- **Contact:** two people who have accepted each other's invitation; used only for talking and opens no data. Your advisor, students and labmates are listed on the Contacts page automatically.
- **Chat:** direct chats, research topic groups and group chats; joining a chat grants no experiment permissions.
- **Brief format:** a Word / Excel report template you uploaded; briefs follow it and are filled straight back into the template.

- **LabAI:** AI Q&A within a lab group; you can switch the scope (research topic / all members / one member), and answers name the person.
- **LabHub:** the community platform for research works and experts.
- **Records Organizer:** the tool that turns materials such as certificates and rosters into structured records, each of which you must confirm.
- **Cloud sync:** an optional switch that backs up local data to the cloud; this computer is the sole source of truth, and you restore manually when switching computers.

Chapter 21 · Frequently Asked Questions

What is sciblock? What do I need to get started? A desktop research workbench for scientists. Register and sign in, and you can start using it.

Will the AI make up values that aren't in my data? No. The AI can only cite parsed evidence, and every fact carries a source marker; when data is insufficient, it says so plainly.

What are the [1][2] in replies? Source markers; click one to jump to the original evidence or attachment.

I uploaded data but the AI doesn't cite it. What should I do? Check in this order: whether that experiment is selected in the left column; whether the attachment status in the right column is "Parsed"; and try asking a more specific question.

The AI replies with empty content? Make sure the file has finished parsing and the scope isn't empty, then rephrase and try again.

How do I use research threads? Click " " on a project row to start one in one click; see Chapter 9.

Can I use the cells the AI estimated on a board? They need "Confirm as measured"; until then, AI analysis does not treat them as measured.

What are the yellow / orange tags in a draft? Inferences / AI suggestions. They are less reliable than measured values and are what you should review most closely.

Why does literature search mention "fallback mode"? The local retrieval model hasn't been downloaded. Download it in Settings; search still works without it.

What is "My Experts" for? It lets sciAI bring in your own know-how. It builds up automatically as you run experiments, make verdicts and correct sciAI, and only confirmed entries are used.

Can my advisor see all my data? No. Your advisor only sees the projects you choose to share, and only read-only. The scope is listed when you accept the invitation, and you can turn sharing on or off per project afterwards.

How do I restore my data on a new computer? On the old computer, click "Sync now" first and let it finish uploading. On the new computer, choose a new data location on first launch, sign in with your original account and click "Restore my data" when prompted, or go to "Settings → Cloud sync" and click "Restore from the cloud to this computer". See Chapter 15.

Paper generation seems stuck. What should I do? Multi-pass background generation is slow; wait for the completion notice. The task can reconnect in the background; restart the app if necessary.

Which formats are supported? CSV, Excel, PDF, Word, PPT, images, and video (archive only); see Chapter 19.

Can I change my registered email? The current version doesn't let you change your registered email yourself; please contact the administrator.

Not receiving the verification code? Check your spam folder. Sending is rate-limited within 60 seconds, so wait a moment before clicking again.

Chapter 22 · Troubleshooting

Symptom	Check in this order
AI doesn't respond	Is the connection status at the top "Connected"? → stop and send again → restart the app
AI replies with empty content	Same as above + is the scope empty, and is the question complete?
File parsing failed	See the failure reason under Attachments in the right column → "Re-parse" → check the encoding (CSV must be UTF-8) and format
File upload failed	Check the size limits (attachments 300 MB / literature 40 MB) → network → retry
Garbled Chinese text	The CSV isn't UTF-8; save it as UTF-8 and upload again
Data didn't become evidence	Confirm the attachment is "Parsed" → re-parse → select the correct scope
Can't connect to the cloud	Check the network → "Retry"; the same applies to sync, the inbox and the lab
Data didn't come back after switching computers	Did you sign in with your original account? → "Settings → Cloud sync" → "Restore from the cloud to this computer" → did the old computer agree to back up personal materials, and was "Also upload original files" turned on?
Literature indexing failed	Status "Failed / Metadata only" → delete and upload again; for scanned copies, make sure OCR is possible
"Judge this round" is grayed out	Has this round's experiment been uploaded and finished parsing?
Board AI estimate doesn't appear	"The AI didn't estimate this cell: not enough evidence" → add evidence or fill it in manually
Project tree is blank	Backend not connected → restart the app; if startup isn't ready after more than 90 seconds, a diagnostics page opens
Draft wasn't saved automatically	Check whether the status says "Unsaved..." → keep the app running; after editing, click outside the field or press Enter

Symptom	Check in this order
Exported PDF is blank	Make sure the document has been confirmed and the cited experiments haven't been deleted, then export again
Square brackets in chemical names show up as superscripts in a report	First update to the latest version and export again; abbreviations like "CB[7]" may still be treated as citations, so change them back to plain text in Word or write out the full name
App is sluggish	Clear the chat history, narrow the scope, restart the app
Can't accept an invitation	"This invitation came from an older version and is no longer valid" → ask your advisor to invite you again; if the cloud can't be reached, the app blocks it first
App disappears after installing on Windows	Quarantined by antivirus software; see Chapter 16
A confirmation box or the settings window is hidden behind the right drawer	A display issue in older versions; update to the latest version. In an older version, close the right drawer first
Some characters in a downloaded PDF turn into boxes	Update to the latest version and export again; to keep special symbols exactly as they are, use Word