PCR (Endpoint Amplification) Experiment Template

Structured Documentation for DNA Amplification — From Primer Design and Reaction Setup Through Thermal Cycling and Gel-Verified Product

Applies to

- Academic and molecular-biology research laboratories
- Biotechnology and life-sciences R&D groups
- Cloning, genotyping, and sequencing-prep teams
- Contract research organizations (CROs)

Relevant compliance & integrity frameworks

- **FDA 21 CFR Part 11** — Electronic records and signatures
- **GLP** — Good Laboratory Practice for preclinical documentation
- **Data integrity (ALCOA+)** — Attributable, contemporaneous, defensible records
- **NIH / NSF** — Reproducibility and data-management requirements

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1. Executive Summary

PCR is the workhorse of molecular biology, and its output is decision data: a band of the expected size on a gel is what tells you the amplification worked, the primers are specific, and the product is ready for cloning, sequencing, or genotyping. But a PCR result is only as trustworthy as the reaction and the record behind it. A band called “the right size” with no recorded primer pair, annealing temperature, or expected product size is not a weak result — it is one that cannot be reproduced or defended. And when primer sequences, cycling parameters, polymerase lots, and gel images live scattered across a thermocycler, a primer spreadsheet, and a gel-doc drive, reactions cannot be compared reliably across runs — which is exactly what troubleshooting a failed amplification requires.

The ELabELN PCR (Endpoint Amplification) Experiment Template solves this by providing a pre-built, fully structured reaction record that loads from the template library in a single click. It ships with a 10-step protocol covering primer prep through gel verification, validated polymerase references, pre-wired cycling fields, and typed inputs for template DNA source, input mass, primer pair, primer Tm, annealing temperature, polymerase, extension time, cycle count, expected product size, and gel result. The primers, polymerase, and dNTP mix link to the ELabELN inventory, and the tamper-evident audit trail captures every primer-pair choice, every cycling change, and every gel image.

This white paper describes what the template contains, the amplification use case it is designed to support, the upstream and downstream workflows it connects to, the benefits it delivers to the scientist, and how a laboratory can deploy it and begin running PCR within days.

> **Key benefit**
> Labs that adopt the PCR template stop rewriting the reaction scaffold every run and lose no primer sequence, cycling parameter, or gel result between the thermocycler, the imager, and the notebook. The reaction setup is captured beside the verification, every run carries its primers and polymerase lots, and outcomes become queryable across amplifications — the structured, comparable foundation reproducible amplification and defensible result provenance depend on.

2. What Is Endpoint PCR, and Why Does Documentation Matter?

2.1 The Technique

The polymerase chain reaction amplifies a specific DNA sequence exponentially. A reaction is assembled from template DNA, a forward and reverse primer pair that flank the target, a thermostable polymerase, dNTPs, and buffer, and then driven through repeated temperature cycles in a thermocycler. Each cycle has three steps: a high-temperature denaturation that separates the DNA strands, an annealing step at a temperature set by the primers' melting temperature where the primers bind, and an extension step at which the polymerase synthesizes new strands. Roughly thirty cycles later, the target has been copied a billion-fold. In endpoint PCR, the product is read at the end of cycling — typically by running it on an agarose gel and confirming a single band of the expected size against a ladder.

A band is only meaningful if the reaction and the reading support it: primers specific to the target, an annealing temperature matched to their Tm, a polymerase and cycle count suited to the amplicon, and a gel that resolves the product against a ladder. Weakness anywhere — an annealing temperature that is too low, a mispriming event, or a product sized by eye without a ladder — produces a result that looks conclusive and is not.

Because the product decides what gets cloned, sequenced, or genotyped, and because a failed or ambiguous reaction has to be diagnosed against its parameters, **the primer pair, the annealing temperature, the cycling program, and the gel result are what make a PCR trustworthy and comparable to the next run — which is exactly why they must live in one structured, queryable record rather than a thermocycler screen and a gel-doc folder.**

2.2 The Documentation Problem

Recording PCR across thermocycler screens, primer spreadsheets, and gel-doc drives creates a set of interconnected risks:

- The primer pair and its Tm are recorded loosely, so the exact primers behind a result — and the annealing temperature they dictate — are easily lost.
- The cycling program is set on the thermocycler and rebuilt from memory next time, so an inconsistent run quietly makes results non-comparable.
- The expected product size is not recorded, so an observed band is judged "about right" by eye rather than against a documented expectation.
- The gel image sits in a gel-doc export, disconnected from the reaction, primers, and cycling that produced it.
- Polymerase and primer lots are not captured, so a sudden amplification failure cannot be traced to a reagent batch.
- Per-run results are noted inconsistently, so a primer pair's track record across reactions cannot be queried when a run fails.
- Prior reactions for the same target cannot be retrieved to compare conditions, so optimization restarts from memory each time.

These are the gaps that make PCR results hard to trust, compare, and troubleshoot, and they are the gaps this template was designed to close.

3. Template Overview: What Ships with the Template

The ELabELN PCR (Endpoint Amplification) Experiment Template is a pre-populated experiment record available to all ELabELN subscribers directly from the template library. It ships configured for endpoint amplification of a 498 bp GAPDH fragment from human genomic DNA, with a 10-step protocol covering primer working-stock prep through agarose gel verification. The default protocol assumes Q5 High-Fidelity polymerase in a 25 µL reaction, an annealing temperature of 58 °C derived from the primer Tm, 30 cycles with a 72 °C extension, and 1% agarose gel imaging at 100 V for 35 minutes with SYBR Safe stain. Every section is editable — the configuration is a tested baseline, not a locked format.

3.1 Template Sections at a Glance

The template populates the existing ELabELN experiment sections your lab already works in. Your team edits a working baseline instead of rewriting the reaction scaffold from scratch every run.

Section	What it pre-populates
Main Text	The reaction summary, primer notes with Tm, and expected product size, authored in the TinyMCE rich-text editor and linked to the template prep.
Extra Fields	Eleven structured, typed fields grouped as Template, Reaction, and Cycling — template DNA source, input mass, primer pair, primer Tm, annealing temperature, polymerase, extension time, cycle count, reaction volume, expected product size, and gel result. Typed values make reaction parameters queryable across runs.
Steps	A 10-step workflow checklist covering primer prep through gel verification. Each tick is timestamped to the audit trail, and the thermocycler run is auto-logged.
Compounds	The forward and reverse primers, Q5 polymerase, dNTP mix, and gel reagents pre-linked from the compound database, with lot numbers carried in automatically and primer designs shown inline.
Links & Resources	Pre-wired to the lab's PCR Standard SOP v2.1, the GAPDH primer database entry, and the gel-imaging protocol.
Storage & Files	−20 °C primer-stock storage and polymerase aliquot tracking, plus labelled attachment slots for gel images (TIF or PDF).

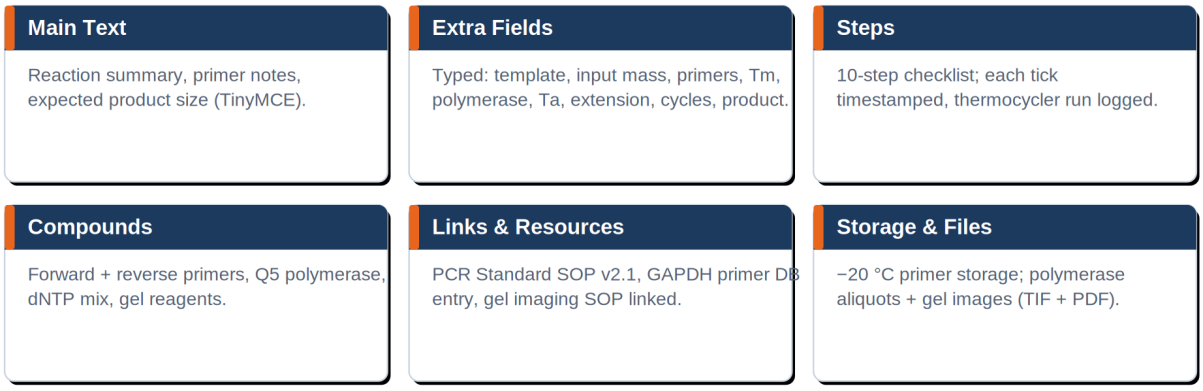


Figure 1. The six ELabELN experiment sections pre-populated by the PCR (Endpoint Amplification) template.

3.2 The 10-Step Protocol

The workflow checklist is the operational spine of the template. Each step maps to a discrete bench or analysis action and writes a timestamped, user-attributed entry to the audit trail when checked off. The thermocycler run is auto-logged, and the cycling and gel imaging are done on the instruments, with the resulting result recorded as typed fields.

Step	Action	What it captures
1	Prep primer stocks	Primer pair; working-stock concentration
2	Thaw template DNA	Template source; input mass
3	Assemble master mix (Q5)	Polymerase; dNTPs; reaction volume
4	Aliquot + add template	Per-reaction setup
5	Load thermocycler	Cycling program; annealing temperature
6	Thermal cycling (30×)	Cycle count; extension (thermocycler)
7	Run agarose gel	Gel setup
8	UV image (gel doc)	Gel image (imager auto-logged)
9	Score band vs ladder	Observed band vs expected size
10	Record result	Gel result; e-signature

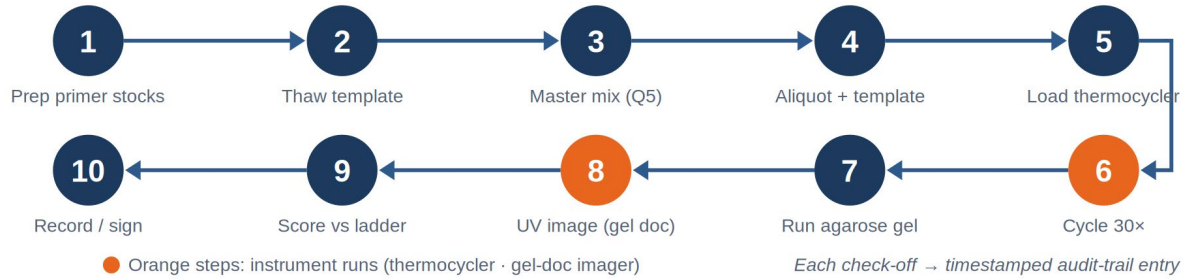


Figure 2. The 10-step endpoint PCR workflow — orange steps are instrument runs (the thermocycler and the gel-doc imager); every check-off writes a timestamped entry to the ELabELN audit trail.

4. The Use Case: When and How the Template Is Used

The template is intended as a tested baseline for academic and life-sciences research labs running endpoint PCR. It is configured around a recognizable reference — a GAPDH amplification from human genomic DNA — but the scenarios it serves span the reaction bench and the projects it feeds.

4.1 Amplification for Cloning and Sequencing Prep (Primary Use Case)

The core scenario: amplifying a target for a downstream cloning or sequencing step. The template captures the primers, the cycling program, the expected size, and the gel result in one structured record, so a reaction is fully reconstructable — which primers, which annealing temperature, which polymerase, which product — rather than a tube detached from the conditions that produced it.

4.2 Genotyping and Colony Screening

PCR is the fastest way to ask whether a sequence is present — in a genotyping assay or a colony screen after transformation. Because each reaction's primers, conditions, and result are structured and queryable, positives and negatives are triaged from the records rather than reconstructed from a strip of tubes and a gel.

4.3 RT-PCR From cDNA Template

Amplifying from cDNA extends PCR to expression work. Because the template DNA source is a typed field, moving from genomic DNA to a cDNA template is a matter of editing the reaction section, with the source recorded so a result is never ambiguous about what was amplified.

4.4 Primer and Condition Optimization

A new primer pair often needs its annealing temperature and cycling optimized. Because primer Tm, annealing temperature, and cycle count are typed and queryable, optimization becomes a comparable series — each run's conditions and result side by side — rather than a set of remembered attempts.

4.5 Amplification QC Across Runs

Because primers, conditions, and gel results are typed and queryable, the template doubles as a running amplification-QC record. A team can pull every reaction with a primer pair, compare which conditions gave a clean single band, and flag a lot or condition that correlates with failure — before it derails a downstream step.

4.6 Teaching, Onboarding, and Multi-PI Collaboration

PCR is a technique every new lab member learns. Because every ELabELN edition includes unlimited users, students, rotating researchers, and collaborators can all work from the same tested baseline, and granular permissions let the PI control who can edit PCR runs versus only review them — useful for onboarding and multi-PI collaboration alike.

5. Dependencies and Connected Workflows

The PCR template does not exist in isolation. It sits inside a network of connected workflows — upstream, parallel, external, and downstream — that give the reaction record its full scientific and decision-making value.

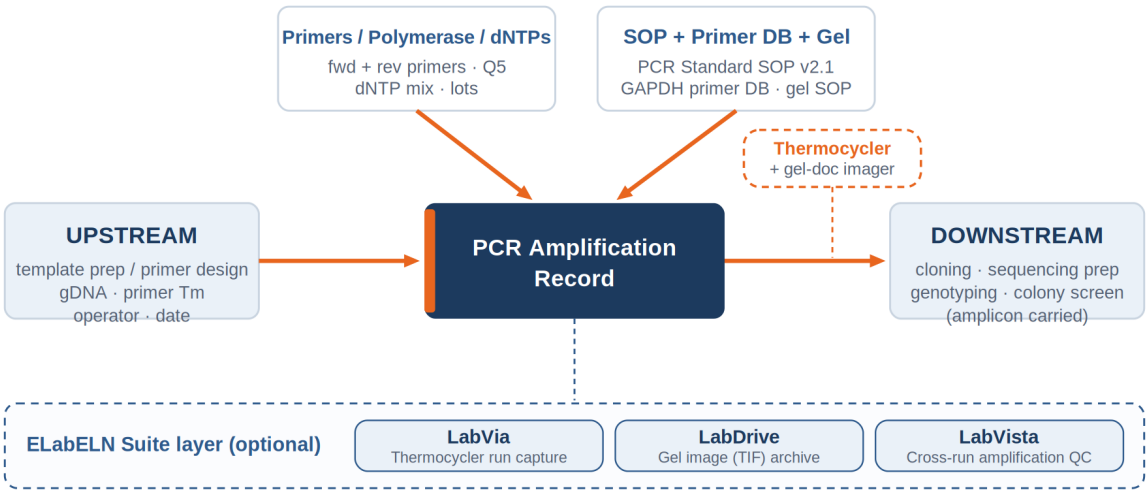


Figure 3. The template connects an upstream template-prep and primer-design workflow, parallel primer/polymerase/dNTP inventory and SOP/primer-DB/gel systems, the external thermocycler and gel-doc imager, and downstream cloning, sequencing-prep, genotyping, and colony-screen workflows.

5.1 Upstream: Template Prep and Primer Design

Every reaction begins with a prepared template and a designed primer pair. The template links to the upstream template prep and the primer design, so opening a reaction surfaces the template source, the primers and their Tm, the operator, and the date — connecting each product to the design and material behind it.

5.2 Parallel: Primer, Polymerase, and dNTP Inventory

The Compounds section links the forward and reverse primers, Q5 polymerase, and dNTP mix directly to the ELabELN inventory. Because reagent identity bears on whether a reaction amplifies, this traceability is decisive. Through the link the record automatically carries:

- **Lot numbers and primer-design references** for the primers, polymerase, and dNTPs, so an amplification failure can be traced to a reagent batch.
- **The primer sequences and Tm, shown inline**, so the exact primers and their annealing temperature are on the record and reproducible.
- **Expiry and stock levels**, with low-stock warnings before a run, so a reaction is not started against a depleted or expired reagent.

Barcode and QR scanning can populate these links from the physical tube, keeping lot capture effortless across runs.

5.3 Parallel: SOPs, the Primer Database, and the Gel Protocol

The Links section connects the reaction to the lab's PCR Standard SOP, the primer database entry, and the gel-imaging protocol. The primer-database link is what makes conditions

coherent: each reaction opens alongside the primer entry that fixes its target and annealing temperature, so the setup is built in rather than recalled.

5.4 External: The Thermocycler and Gel-Doc Imager

Cycling and verification run on instruments outside ELabELN: the thermocycler drives the temperature program, and the stained gel is imaged on a gel-documentation system. ELabELN is the system of record around them: per-lane gel results (sample, expected size, observed band, intensity) live in the spreadsheet editor, the gel image (TIF or PDF) attaches in the Storage & Files section, and the gel result is written back into the typed fields. The reaction setup, the run, and the verification stay together in one record.

5.5 Downstream: Cloning, Sequencing, Genotyping, and Screening

The verified amplicon feeds cloning, sequencing prep, genotyping, and colony screening — and, because primers, conditions, and results are typed and queryable, cross-run comparison. A decision to clone, sequence, or call a genotype rests on a documented, comparable reaction rather than a band recalled from a gel image.

5.6 The ELabELN Suite: Instruments and Dashboards

Everything above is available in ELabELN Standard. Labs on the ELabELN Suite gain three layers that connect to the same record: LabVia captures runs directly from the thermocycler, gel-doc system, and other instruments; LabDrive adds metadata search, versioning, and role-based access across gel-image archives; and LabVista builds cross-run amplification and QC dashboards on the structured reaction metadata. The same audit trail and data-integrity controls span all layers.

6. How the Scientist Benefits

The template is built to deliver value at the bench and to the project alike. The benefits compound with every reaction a lab runs.

6.1 Start From a Tested Baseline, Not a Rewritten Scaffold

The scaffold — protocol, typed fields, primer and polymerase links, SOP, and primer-database link — is already built. The scientist edits a working configuration to match the target they actually amplify, rather than rewriting the reaction scaffold from scratch every run. The first reaction is faster, and every subsequent one is consistent and comparable.

6.2 Document by Doing

Checking off each of the 10 steps as it happens produces a contemporaneous, timestamped record as a by-product of the run, and the thermocycler run is auto-logged. There is no separate write-up to reconstruct later.

6.3 Never Lose the Primers or Cycling Program Again

Because the primer pair and cycling parameters are structured fields and the reagents are linked to inventory, the primers, annealing temperature, program, and lots are captured permanently on every run. When a reaction fails, its exact conditions are on the record — closing the most common PCR troubleshooting gap by default.

6.4 Cross-Run Amplification History You Can Query

Typed primers, conditions, and gel results make the project queryable. A team can pull every reaction with a primer pair, compare which conditions gave a clean band run by run, and gate on the ladder-referenced result at a glance — turning a drawer of tubes and a gel-doc folder into a live amplification view.

6.5 Reproducible Reactions and Defensible Result Provenance

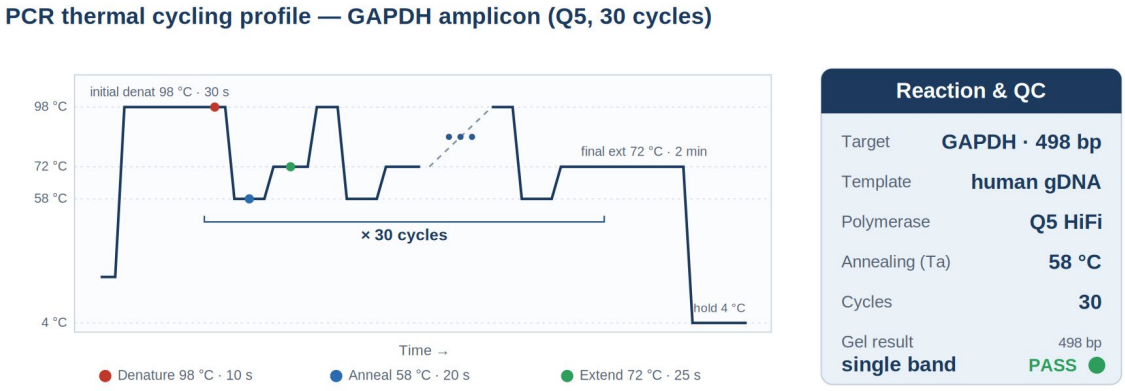
Capturing the full reaction setup beside the gel result makes each amplification reproducible rather than a remembered recipe, and the tamper-evident audit trail, reagent-lot traceability, and electronic signatures give each result a defensible provenance — structured to support reproducibility documentation and FDA 21 CFR Part 11 review when the lab's quality system requires it.

> **At the bench, in practice**
>
> A scientist opens the template, sets the primers and expected product size to match today's target, scans the polymerase and primer tubes to capture their lots, and checks off each step as the master mix is assembled, the thermocycler is loaded, and the reaction is cycled. The gel-doc image is attached, the band is sized against the ladder, and the gel result is recorded against the expected size — confirming a clean single product. Weeks later, comparing runs, the project lead queries every reaction with that primer pair and sees which conditions worked, run by documented run.

7. The Cycling Program and Reaction Quality

7.1 The Default Reference: A GAPDH Amplification

The template ships configured for an endpoint amplification of a 498 bp GAPDH fragment from human genomic DNA with Q5 High-Fidelity polymerase: a 25 µL reaction, an initial denaturation, thirty cycles of denaturation, annealing at 58 °C set by the primer Tm, and a 72 °C extension, a final extension, and a hold, with the product verified on a 1% agarose gel against a ladder. This concrete reference demonstrates the full primer-to-verification workflow out of the box; swap the primer pair, template, polymerase, or cycling to match what your lab amplifies. Note that this template covers endpoint PCR read on a gel — for real-time quantitative PCR with cycle-threshold readings and fold-change analysis, the ELabELN library offers a separate qPCR template.



Illustrative — the cycling profile reflects the typed reaction parameters; Ta, cycle count and gel result are recorded as typed fields in ELabELN.

Figure 4. The thermal cycling profile for the GAPDH reference — initial denaturation, thirty cycles of denature, anneal, and extend, a final extension, and a hold — alongside the reaction-and-QC panel (with the gel-verified product). Illustrative; the profile reflects the reaction's typed cycling parameters, and the annealing temperature, cycle count, and gel result are recorded as typed fields in ELabELN.

7.2 How the Template Handles the Reaction, Cycling, and Verification

The reaction setup and cycling program — template source, primers and Tm, annealing temperature, polymerase, extension time, and cycle count — live in the typed fields, and the per-lane gel results (sample, expected size, observed band, intensity) live in the spreadsheet editor. The gel image (TIF or PDF) attaches in the Storage & Files section, and the gel result is written back into the typed fields. Because these values are structured and queryable, cross-run comparison is straightforward: query every reaction with a primer pair, gate on the ladder-referenced result, and review which conditions gave a clean band side by side — the amplification view a project runs on.

Element	Default configuration	Editable to
Target / amplicon	GAPDH, 498 bp	Any target and product size
Template DNA	Human genomic DNA	cDNA, plasmid, colony lysate
Polymerase	Q5 High-Fidelity	Phusion, Taq, KAPA HiFi
Annealing (Ta)	58 °C (from primer Tm)	Any Ta; touchdown
Cycling	30 cycles, 72 °C extension	Any cycle count / extension
Mode	Standard endpoint PCR	Colony, touchdown, nested; RT-PCR

Figure 5. The template's default configuration — fully editable for any target, template, polymerase, annealing temperature, cycling program, or mode.

8. Configuring the Template for Your Reaction

Adapting the template to a different target or mode is a matter of editing the relevant sections — not rebuilding the structure.

8.1 Swap the Primers and Template

Change the primer pair — custom or catalog — and the template DNA source (genomic, cDNA, plasmid) by editing the Template and Reaction sections, and record each primer's Tm so the annealing temperature stays tied to the primers that dictate it.

8.2 Change the Polymerase and Annealing Temperature

Switch the polymerase — Q5, Phusion, Taq, or KAPA HiFi — and set the annealing temperature from your primer Tm by editing the Reaction and Cycling sections. The verification fields apply regardless of the enzyme or temperature.

8.3 Adjust the Cycling and Mode

Change the cycle count and extension time, and move from standard PCR to colony PCR, touchdown PCR, or nested PCR by editing the Cycling section. Amplifying from a cDNA template turns the same reaction into an RT-PCR readout.

8.4 Save a Custom Version

Once configured, save your edits as a private template scoped to your lab, or publish back to the ELabELN template library. Every subsequent reaction opens from your configured baseline, and separate versions can be maintained for different targets, polymerases, or modes.

9. Getting Started

ELabELN Standard is a cloud-hosted SaaS deployment typically live within one to two business days of account creation. There is no hardware to buy, no IT project, and no per-seat licensing.

1. **Start an ELabELN account.** Visit elabeln.com/get-started. ELabELN Standard runs on LabLynx's managed cloud infrastructure.
2. **Provision your instance.** LabLynx provisions the instance within one to two business days; you receive a URL, admin credentials, and onboarding documentation.
3. **Load the PCR template.** From the template library, select the PCR (Endpoint Amplification) template and click "Use This Template." An editable instance opens immediately.
4. **Add your primers, polymerase, and reagents to the inventory.** Enter your primers, polymerase, and dNTP mix with lot numbers and −20 °C storage locations. This is a one-time setup step.
5. **Link your SOP, primer database, and gel protocol.** Upload your PCR SOP and connect the primer database entry and gel-imaging protocol to the template's Links section.
6. **Customize the template for your reaction.** Edit the primer pair, template source, polymerase, annealing temperature, and cycling, then save as a private team version.
7. **Run your first reaction.** Open your saved template, complete the 10-step checklist, attach the gel image, score the band against the expected size, and sign off.

> **Typical timeline**
> Day 1: Account requested at elabeln.com/get-started. Day 2–3: Instance provisioned; primer, polymerase, and reagent inventory populated; SOP, primer database, and gel protocol linked. Day 3–4: Template configured and saved as a private version for your target. Day 4–5: First reaction documented in ELabELN with the cycling program, gel image, and result captured and an e-signature.

9.1 ELabELN Standard vs. ELabELN Suite

Capability	Standard	Suite
PCR template access	Included	Included
Unlimited users	Included	Included
Audit trail and e-signatures	Included	Included
Primer / polymerase / dNTP inventory with lot tracking	Included	Included
SOP, primer-database & gel-protocol linking	Included	Included
Per-lane gel results + gel image (TIF) attachments	Included	Included
LabVia direct thermocycler / imager capture	—	Suite layer
LabDrive gel-image archive search & versioning	—	Suite layer
LabVista cross-run amplification & QC dashboards	—	Suite layer

10. Frequently Asked Questions

Can I configure the template for my primers and target?

Yes. Every section is editable. Swap in any primer pair (custom or catalog), change the template DNA source (genomic, cDNA, plasmid), adjust the annealing temperature based on your primer Tm, change the polymerase (Q5, Phusion, Taq, KAPA HiFi), or move from standard PCR to colony PCR, touchdown PCR, or nested PCR by editing the cycling section. Save your edits as a private template scoped to your lab, or publish back to the ELabELN template library.

How does the template differ from the qPCR template?

This template covers endpoint PCR for amplification and gel verification — cloning prep, colony screening, and sequencing prep. The qPCR template covers real-time quantitative PCR with cycle-threshold readings and fold-change analysis. Both share the underlying reaction-setup pattern but diverge on readout: a gel image here versus amplification curves for qPCR.

Does the template handle gel verification?

Yes. The spreadsheet editor captures per-lane results (expected size, observed band, intensity), and the Storage & Files section has a labelled slot for the gel image (TIF or PNG). Paired with the standard ladder reference in your gel-imaging SOP, this gives a complete reaction-to-verification record.

Is it included in every ELabELN plan?

Yes. Every published template in the ELabELN library is available to all subscribers in both the Standard and Suite editions, with unlimited users in either edition and no per-template fee.

Can my whole lab use this template?

Yes. Every ELabELN edition includes unlimited users, so the PI, postdocs, grad students, rotating researchers, and visiting collaborators can all use the template without per-seat charges. Granular permissions let the PI control who can edit PCR runs versus only review them.

How quickly can my lab start running PCR in ELabELN?

ELabELN Standard cloud deployment is typically live in one to two business days. Once the instance is provisioned, the template loads from the library in a single click, with the primers, polymerase, and cycling parameters editable to match the reactions your lab actually runs.

11. Conclusion

The ELabELN PCR (Endpoint Amplification) Experiment Template is not simply a digital copy of a thermocycler program and a gel image. It is a structured, audit-ready, searchable record that connects to your primer, polymerase, and reagent inventory, your SOPs and primer database, the template and design the reaction followed, your thermocycler and gel-doc imager, and the downstream cloning, sequencing, and genotyping workflows — and, in the Suite edition, cross-run amplification dashboards. It turns a routine reaction into a record whose primers, conditions, program, and result are captured, comparable, and defensible.

For a laboratory that runs PCR constantly, the benefit compounds with every project. Primer pairs, cycling programs, and gel results accumulate into one queryable amplification history, and every reagent lot is traceable. Every reaction is reproducible from its record, and every result carries a defensible provenance — so a band judged “about right” by eye can no longer quietly drive a decision, and a failed run can be diagnosed against its documented conditions rather than from memory.

The template is available to all ELabELN subscribers today — a new instance is live in one to two business days, with the first structured reaction typically documented within a week of account creation.

> **Get started**
> Visit elabeln.com/get-started or contact LabLynx at 866.522.5969 / info@lablynx.com. Load the PCR (Endpoint Amplification) template, configure it for your primers and target, and run your next reaction from a tested, audit-ready baseline.