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Genedata Screener vs IDBS ActivityBase vs Dotmatics

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Executive Summary

Genedata Screener, **IDBS ActivityBase**, and **Dotmatics** offer overlapping routes from assay measurements to interpretable results, but the useful comparison is the workflow that a buyer will actually license and configure. Genedata documents assay annotation, historical performance monitoring, and cross-assay result management. (www.genedata.com) ActivityBase's current page describes screening analysis alongside compound registration and plate management. (www.idbs.com) Dotmatics documents reusable assay protocols, curve-fit calculators, plate layouts, and custom definitions. (www.dotmatics.com) These are vendor-supported capability statements, not independent measurements of relative scientific accuracy.

The strongest documented fit for Genedata is a screening-analysis program that needs instrument ingestion, automated quality control (QC), and specialized analysis workflows. Its import interfaces explicitly include Python and Java, while its imaging workflow distinguishes original images from calculated results. (www.genedata.com) ActivityBase merits evaluation where a screening organization needs continuity between existing analysis and operational records; historical customer material describes retaining the complete analysis in a test set. (www.idbs.com) Dotmatics merits evaluation where assay processing must feed a broader discovery environment, including downstream structure-activity relationship (SAR) analysis. (www.dotmatics.com) Those fit statements are editorial interpretations of documented workflows, not product rankings.

A useful selection test is an identical, exportable assay challenge. This report proposes a **120-plate, 46,080-well** scenario and a reproducible synthetic plate generator. These are analyst-designed workload units, created on October 15, 2026, with no geographic population or measured vendor runtime. The **Hypothetical Example** control calculation gives **Z-prime = 0.8833**, using the Assay Guidance Manual's formula; it establishes an expected mathematical result, not observed platform performance. (www.ncbi.nlm.nih.gov) Scientific acceptance should also distinguish technical replicates from independent runs and preserve raw, normalized, aggregated, and fitted results separately. (www.ncbi.nlm.nih.gov)

The reviewed material does not establish comparable public prices, deployment-specific scale ceilings, or a controlled benchmark across these products. Procurement should therefore require current module entitlements, a replayable analysis history, exception handling, and a full export demonstration. The FAIR principles explicitly call for persistent identifiers and detailed provenance, while W3C's provenance model separates data objects, processing activities, and responsible agents. (www.nature.com) (www.w3.org) A defensible choice is the configured platform that can reproduce a reviewed hit list and explain every inclusion, exclusion, and revision within the buyer's operating constraints.

Introduction and Background

A screening database becomes useful when a scientist can explain how an instrument signal became a candidate for follow-up. The Assay Guidance Manual provides a helpful separation: instrument-level raw measurements, normalized well values, within-run aggregates, model-derived results, and summaries across runs. These are distinct analytical records, even when a software interface displays them together. (www.ncbi.nlm.nih.gov) This report follows those records from assay definition to a reviewed hit list.

For procurement, define the lifecycle explicitly:

- **Register the assay:** record its biological purpose, method, endpoint, protocol version, and expected units.
- **Describe the plate:** assign sample identities, control roles, concentrations, and replicate relationships.
- **Ingest measurements:** preserve the original file and the mapping from instrument coordinates to wells.
- **Normalize and inspect:** calculate control-relative responses and expose missing or suspect observations.
- **Fit and review:** retain model settings, exclusions, warnings, and the scientist's interpretation.
- **Select candidates:** apply declared criteria and capture the reason for follow-up.
- **Publish evidence:** transfer results with identifiers and enough context to reconstruct the decision.

This lifecycle is an evaluation framework. BioAssay Ontology (BAO) supplies reference terms for describing assays and results; it does not dictate a particular vendor's registration screen. (bioassayontology.org) Likewise, the FAIR principles require rich metadata and persistent identifiers without prescribing one software architecture. (www.nature.com)

The system boundary matters. For this comparison, the electronic laboratory notebook (ELN) records experimental narrative, the registry owns entity identity, instruments produce measurements, and the assay platform owns the reviewed analytical result. A data lake can receive these records, but the buyer must decide which system may amend each one. W3C PROV offers a useful conceptual language for describing the objects, activities, and agents involved. (www.w3.org)

The report takes IntuitionLabs' adjacent advisory perspective: specify the evidence and responsibilities needed for a platform decision. It excludes general [ELN selection](#), [molecular registration design](#), and virtual screening algorithms. Research was refreshed on October 15, 2026. Vendor statements, scientific guidance, and the report's hypothetical evaluation design are identified separately throughout.

Genedata Screener

Capabilities

Genedata describes a screening-specific chain from assay registration to historical result comparison. Assays can be annotated using public ontologies and structured sources; its performance-monitoring dashboard brings together historical session, plate, and sample metrics. (www.genedata.com) The software page documents Python or Java import application programming interfaces (APIs), which are relevant when instrument exports need repeatable parsing rather than manual spreadsheet cleanup. (www.genedata.com)

For high-throughput screening (HTS), Genedata identifies absorbance, luminescence, fluorescence, and related readouts, and explicitly documents calculation and tracking of Z-prime. (www.genedata.com) Its high-content screening (HCS) workflow shows original images alongside calculated results. Raw-image processing through Imagence and integration with other image-analysis tools are distinguished on the application page, so an image-analysis component should be specified in the offer. (www.genedata.com)

Automation is documented at several boundaries: triggering upload after a run, processing results, and releasing results that satisfy business rules. (www.genedata.com) Recalculation after parameter changes is also described, but that statement alone does not establish the exact persistence and versioning behavior of every previous analysis. (www.genedata.com)

Adoption

The relevant adoption question is integration fit with the laboratory's actual equipment and scheduler. Genedata distinguishes maintained integrations from customer-specific integrations; its connectivity page explicitly labels a Biosero integration as custom work. (www.genedata.com) A familiar instrument or automation brand on a compatibility page should therefore lead to a release-specific demonstration.

Genedata's brochure describes on-premises and cloud deployment options. (www.genedata.com) Its software page describes modular architecture, including assay-specific functionality, which makes a scoped module list more useful than a generic platform quotation. (www.genedata.com) Neither statement establishes an implementation timeline for the buyer's environment.

Strengths and Limitations

The documented strength is the connection between screening analysis, specialized assay handling, and automated data flow. Exact normalization algorithms, curve-model catalogs, replicate aggregation, and export completeness remain questions for detailed documentation or a demonstration. A supplier's capability claim should be tested against the intended configuration.

Prioritize these acceptance cases:

- **Control review:** reproduce the agreed normalization and Z-prime calculations, including excluded controls.
- **Image lineage:** navigate from a result to its originating image and analysis configuration.
- **Reanalysis:** change a parameter, preserve the earlier decision, and export both analysis versions.

The current product page claims immutable records and complete audit logs. Treat those as vendor-described capabilities and request evidence of the configured record lifecycle, including retention and review behavior. (www.genedata.com) That evidence is more decision-relevant than an unqualified claim that a platform is validated.

IDBS ActivityBase

Capabilities

ActivityBase's current public page was readable during this research refresh. It describes biochemical, cellular, and biophysical assay support, statistics and nonlinear regression, and genealogy linking samples, containers, and results. It also names imaging-store integrations. These current statements establish a substantive screening scope; they do not specify every available model, normalization algorithm, or connector version. (www.idbs.com)

Historical documentation adds useful implementation detail when clearly dated. The **February 2021** ActivityBase XE release notes describe propagation of point exclusions to associated wells and an optional imaging-provider plugin. Those are historical, version-specific behaviors, not a statement about the latest release or today's license. (knowledgebasecontent.s3.amazonaws.com) The same documentation says paired XE and standalone runner installations must use matching versions. (knowledgebasecontent.s3.amazonaws.com)

Adoption

IDBS's historical Pfizer account describes importing through a web client while preserving the complete analysis in an ActivityBase test set. (www.idbs.com) Its historical Inventiva account describes images displayed alongside analysis data and integration with laboratory equipment. (www.idbs.com) Both are vendor-hosted descriptions of particular implementations. They support questions about workflow continuity, not assumptions about current customer counts or comparative speed.

A migration team should inventory the logic already embedded in its installation: templates, calculations, exclusion rules, scheduled processing, and reports. The historical ActivityBase release notes require coordinated updates of the client, database, and web server, illustrating why an upgrade assessment should cover the complete deployed system. (knowledgebasecontent.s3.amazonaws.com) Current topology and supported versions must be obtained from IDBS.

Strengths and Limitations

ActivityBase merits consideration when continuity of screening records and analysis behavior drives the decision. The evidence supports a configurable screening system, but current public packaging, comprehensive API contracts, export coverage, and deployment-specific approval behavior were not established in the retrieved materials. Missing public detail remains an open question.

Require these demonstrations:

- **Legacy reconciliation:** reproduce a representative historical test set and explain every changed result.

- **Exclusion semantics:** distinguish excluding a fitted point, a well, and an entire replicate group.
- **Dependency mapping:** identify each analysis component, plugin, runtime, and supported version.

The historical XE announcement identifies XE as part of the ActivityBase Suite. (www.idbs.com) That relationship should be refreshed in the current bill of materials. Similarly, a software-platform support document dated **July 2021** is evidence of historical requirements, not a current infrastructure recommendation. (s3.amazonaws.com) Buying against an explicit, supported configuration is essential when evaluating ActivityBase alternatives.

Dotmatics

Capabilities

The **Dotmatics assay data management** page describes a flexible capture and processing environment, including manually reviewed experiments or processing driven by an automation layer. (www.dotmatics.com) A vendor screening demonstration identifies the Studies application and shows plate-reader file ingestion, plate-format selection, and review of dilution and sample placement. (www.dotmatics.com) This is more specific evidence of a workflow than the general platform label.

The demonstration also shows well exclusion with updated statistics and curve review with configured classification rules. These are demonstrated behaviors in that environment; the exact equations, weighting, bounds, and business rules still need to be disclosed for the buyer's assay. (www.dotmatics.com) Completion can include an optional countersigner, followed by access to results and the originating experiment. (www.dotmatics.com)

Dotmatics separately markets Luma as a composable platform. (www.dotmatics.com) Its named Luma Lab Connect product documents interfaces including Java Database Connectivity (JDBC), event-based exchange, GraphQL, and representational state transfer (REST) APIs. Those interfaces should be attributed to that product and scoped explicitly in a screening proposal. (www.dotmatics.com)

Adoption

The documented adoption pattern is configurable workflow delivery. A vendor-hosted implementation account describes protocol creation, plate layouts, sample identifiers, well editing, and curve calculation as parts of delivered assay systems. (www.dotmatics.com) This supports testing configuration effort and maintainability, rather than assuming every implementation arrives with identical templates.

The small-molecule discovery page connects assay analysis to downstream SAR work. (www.dotmatics.com) That is relevant where assay review must connect to project decisions across applications. Current Studies or Studies Ultra contractual packaging was not established in the retrieved sources; a buyer should ask which named applications and services deliver each promised step.

Strengths and Limitations

The documented strength is a connected discovery workflow with configurable assay processing. Package boundaries deserve close attention. Dotmatics explicitly describes adding tools such as GraphPad Prism and other scientific applications as needed; portfolio membership alone does not establish entitlement in an assay-platform contract. (www.dotmatics.com)

Use these acceptance cases:

- **Rule ownership:** show who can change classification criteria and how previous classifications remain interpretable.
- **Processing boundaries:** identify which application parses, normalizes, fits, reviews, and publishes.
- **Portable decisions:** export the fit configuration, excluded points, reviewer action, and experiment link together.

For collaboration, the assay page advertises web access and cloud-hosted deployments.

(www.dotmatics.com) Luma's workflow offering separately describes configurable tasks, data models, and governance settings. (www.dotmatics.com) These statements are useful starting points, but neither proves a particular regulated-use configuration, current deployment limit, or complete proprietary-object export.

Feature Comparison

Table 1 compares assay data management platforms using documented scope. **Confirm** marks insufficient public evidence about a precise configuration, not absent functionality. General notebook features are outside scope.

Lifecycle step	Genedata Screener	IDBS ActivityBase	Dotmatics
Assay definition and sample context	Ontology-assisted assay registration; confirm protocol-version and control-role schema. (www.genedata.com)	Built-in compound and plate management; confirm authoritative identity boundaries. (www.idbs.com)	Standard protocols and layouts plus reusable custom definitions. (www.dotmatics.com)
Normalization and curve review	Automated QC and recalculation documented; demonstrate exact equations and replicate rules. (www.genedata.com)	Statistics and nonlinear regression documented; demonstrate model catalog and fit constraints.	Demonstration shows curve review and configured classification; disclose actual rules. (www.dotmatics.com)
Image-derived results	Original images and calculated results displayed together; specify the image-processing component. (www.genedata.com)	Current page names imaging-store integrations; confirm supported releases. (www.idbs.com)	HCS accommodation advertised; demonstrate image links, features, and processing boundary. (www.dotmatics.com)
Provenance and release	Audit-log capabilities and rule-based downstream reporting described. (www.genedata.com)	Genealogy documented; historical implementation preserves analysis in test sets. (www.idbs.com)	Traceable interactions described; demonstration includes optional countersigning. (www.dotmatics.com)
APIs and exchange	Import APIs documented; demonstrate complete analysis-object export. (www.genedata.com)	Obtain current ActivityBase-specific API and export documentation.	Lab Connect documents interfaces; confirm inclusion and Studies integration. (www.dotmatics.com)

The crosswalk identifies shortlist priorities: analysis automation, continuity, and connected discovery. These are editorial interpretations of documented workflows. Apply identical acceptance data when evaluating **Genedata Screener vs ActivityBase**, **Genedata Screener vs Dotmatics**, or **IDBS ActivityBase vs Dotmatics**.

Registration, controls, and replicate meaning

Define endpoint, units, biological context, protocol identity, and replicate meaning. BAO's reference terms support consistent annotation across datasets. (bioassayontology.org) The Assay Guidance Manual distinguishes technical replicates within a run from independently prepared or inter-run observations. Averaging these groups indiscriminately would erase information needed to interpret a result. (www.ncbi.nlm.nih.gov)

For a demonstration, specify rather than infer:

- **Control roles:** identify the high and low signal populations and the handling of excluded controls.
- **Replicate identity:** preserve sample, concentration, preparation, plate, and run membership.
- **Unit semantics:** retain original and standardized units, including any conversion rule.
- **Review states:** separate provisional calculations, accepted results, and follow-up decisions.
- **Ownership:** assign responsibility for assay definitions, entity identifiers, and published results.

ChEMBL's documentation illustrates the units requirement by retaining published units while also standardizing activity data. (chembl.gitbook.io) This is a useful downstream example, not evidence that any compared platform implements ChEMBL's transformation rules.

APIs, images, and export

Evaluate communication and representation separately. SiLA's documentation describes functionality-oriented laboratory connectivity, and its FAQ distinguishes a communication standard from an analytical data format. This report does not establish SiLA support for any contender. (sila-standard.com) A working connection therefore still needs an agreed payload, identifiers, retry behavior, and error response.

Image exchange has its own structure. OME-TIFF combines image planes with descriptive metadata; the OME next-generation format specifies a hierarchy for plates, wells, and fields of view. (docs.openmicroscopy.org) (ngff.openmicroscopy.org) A numeric feature table should retain links to the relevant images and image-analysis configuration.

For analysis exports, request raw values, normalized values, units, plate coordinates, exclusions, model settings, fitted parameters, result qualifiers, review state, and historical identifiers. (www.nature.com) W3C PROV's distinction between entities and processing activities provides a useful way to test whether these relationships survive a handoff. (www.w3.org)

Performance and Benchmarks

The reviewed sources do not provide a controlled comparison of throughput, curve-fit agreement, review effort, or total cost across the three configured systems. Vendor automation statements describe capabilities. For example, Genedata's scheduler-pause example depends on a customized call to scheduling software, while Dotmatics' documented instrument interfaces belong to a named integration product. Neither establishes a common workload benchmark. (www.genedata.com) (www.dotmatics.com)

For **high throughput screening data analysis software**, define a **benchmark contract** before demonstrations. All workload quantities in this section are analyst-designed on October 15, 2026; geography is not applicable. They describe scheduled observations, not vendor capacity. *Table 2* gives the proposed volume and expected arithmetic.

Workload item	Declared design	Expected count or interpretation
Primary screen	120 plates, 384 scheduled wells per plate	46,080 scheduled well records
Controls	16 high and 16 low controls per plate	3,840 control wells
Sample positions	352 positions per plate	42,240 scheduled sample wells
Missing-data challenge	12 blank sample signals per plate	1,440 missing signals; 44,640 numeric signals
Confirmation challenge	40 selected samples, 10 concentrations, duplicate wells	800 scheduled sample wells, separately plate-mapped with controls
Timing measures	Ingestion, computation, review, publication, recovery	Measure each in elapsed time; report computing resources and concurrency

The confirmation workload is a separate fixture; its controls are additional to the stated sample-well count. Repeating the primary fixture tests volume handling, but repeated identical plates do not approximate the biological diversity or image volume of a real campaign. Image-heavy work needs a declared file-size distribution and fields-per-well specification.

Run the comparison under a common protocol:

- **Freeze inputs:** use identical files, identifiers, assay definitions, and scientific rules.
- **Declare resources:** record deployment topology, compute allocation, storage, network, and concurrent activity.
- **Separate clocks:** distinguish file arrival, finished computation, scientist acceptance, and downstream availability.
- **Inject exceptions:** submit duplicate files, unknown samples, missing signals, and an interrupted transfer.
- **Replay revisions:** change an exclusion and show the earlier and revised decision paths.
- **Inspect exports:** rebuild selected results outside the platform using the exported evidence.

Scientific agreement is as important as elapsed time; measurement fitness remains a separate acceptance question. (www.nist.gov) The Assay Guidance Manual accepts three- or four-parameter logistic fits and cautions against fixing the Hill coefficient without statistical support. (www.ncbi.nlm.nih.gov) Compare results only after aligning the model, constraints, weighting, concentration units, and exclusions.

A reported half-maximal inhibitory concentration (IC50) also needs a definition. The manual distinguishes relative potency, halfway between fitted asymptotes, from an absolute response threshold, and discusses appropriate handling beyond the tested range. (www.ncbi.nlm.nih.gov) For the proposed challenge, include a well-behaved curve, a partial response, a flat series, and a flagged point. Their expected disposition is a scientific acceptance rule, not a presumption that every series deserves a numeric IC50.

Synthetic Dataset and Evaluation

Reproducible synthetic plate input

The following standard-library Python script prints comma-separated values (CSV) to standard output. It is an **evaluation script, not production assay processing**. The fixture contains the workload declared above. Control offsets are scaled so their sample standard deviations match the inputs in Data Analysis and Evidence before decimal rounding.

```
import csv
import math
import sys

writer = csv.writer(sys.stdout)
writer.writerow(["assay", "plate", "well", "role", "sample",
                "signal_rfu", "protocol_version"])
scale = math.sqrt(15 / 16)
for plate in range(120):
    for index in range(384):
        well = f"{chr(65 + index // 24)}{index % 24 + 1:02d}"
        if index < 16:
            role, sample = "high_control", ""
            signal = 1000 + (-1 if index % 2 else 1) * 30 * scale
        elif index < 32:
            role, sample = "low_control", ""
            signal = 100 + (-1 if index % 2 else 1) * 5 * scale
        else:
            role = "sample"
            sample = f"S{plate:03d}_{index:03d}"
            signal = None if index < 44 else 100 + ((index * 37) % 901)
        writer.writerow(["SYN_INHIBITION", f"P{plate:03d}", well,
                        role, sample,
                        "" if signal is None else f"{signal:.6f}",
                        "fixture_v1"])
```

The script deliberately leaves concentration-response and image files to separate fixtures. It tests well mapping, control assignment, deterministic import, and missing-data handling. Supply the vendor the same field dictionary and declare that **protocol_version** identifies this synthetic assay definition, not a vendor software version.

After migration or a pilot import, map the exported CSV to the same columns and run this reconciliation script with the original and exported filenames as arguments. It compares identifiers, metadata, and missingness, with signals rounded to the fixture's six-decimal RFU precision. Extra analysis objects require the separate rubric below.

```
import csv
import sys

def load(path):
    with open(path, newline="") as handle:
        rows = list(csv.DictReader(handle))
        result = {}
        for row in rows:
            key = (row["assay"], row["plate"], row["well"])
            assert key not in result, "Duplicate well identifier"
            value = row["signal_rfu"]
            row["signal_rfu"] = None if value == "" else round(float(value), 6)
            result[key] = row
        return result

assert load(sys.argv[1]) == load(sys.argv[2]), "Reconciliation failed"
print("Canonical fixture records reconciled")
```

For the separate confirmation fixture, add concentration, concentration unit, replicate identifier, source sample, and run identifier. Preserve a response qualifier when a fitted potency lies outside the measured range, rather than manufacturing a precise estimate. (www.ncbi.nlm.nih.gov) For imaging, keep the source image identifiers and fields of view alongside derived features, consistent with the OME hierarchy. (ngff.openmicroscopy.org)

Data Analysis and Evidence

A transparent control and hit calculation

The Assay Guidance Manual defines Z-prime using high- and low-control means and variability. (www.ncbi.nlm.nih.gov) Written without a vendor-specific implementation:

```
Z-prime = 1 - 3 * (s_high + s_low) / abs(mean_high - mean_low)
```

For this **Hypothetical Example**, assume high-signal controls have mean **1,000 relative fluorescence units (RFU)** and standard deviation **30 RFU**, while low-signal controls have mean **100 RFU** and standard deviation **5 RFU**. These are analyst-created inputs dated October 15, 2026, with no geographic population. Substitution

gives $1 - 3 \times 35 / 900 = \mathbf{0.8833}$, dimensionless. The manual describes values above **0.5** as excellent, but the fixture's value is not an assessment of a real assay or any platform. (www.ncbi.nlm.nih.gov)

For an inhibitory assay, define the fixture's control-relative response:

```
inhibition_percent = 100 * (mean_high - sample_signal) / (mean_high - mean_low)
candidate_hit = inhibition_percent >= chosen_threshold AND accepted_QC
missing_well_rate_percent = 100 * missing_signals / scheduled_wells
```

Converting wells to control-relative activity or inhibition before concentration-response fitting follows the manual's guidance. (www.ncbi.nlm.nih.gov) The **50%** candidate threshold here is an editorial test rule, not a universal scientific recommendation. A sample signal of **550 RFU** yields **50% inhibition** under the example controls. With **12 missing signals among 384 scheduled wells**, the missing-well rate is **3.125%**. Blank signals remain missing; they are never converted to zero or allowed to become candidate hits. All values in this paragraph are synthetic arithmetic in the stated units.

A high control-separation statistic does not answer whether metadata were mapped correctly or a candidate should advance. Preserve plate-level dynamic range and review it across the run; the manual specifically recommends defining that range on each plate. (www.ncbi.nlm.nih.gov) NIST also distinguishes measurement traceability, which requires a calibration chain and uncertainty information, from a software record of processing history. (www.nist.gov) These are complementary evidence questions.

Evaluation rubric and downstream evidence

Table 3 defines evidence to collect during the pilot. Its outcomes are **demonstrated**, **requires configuration**, **requires services**, and **not tested**. These are local observations, not scores inferred from public documentation.

Evaluation area	Acceptance evidence	Recorded outcome
Scientific calculation	Expected controls, normalization, Z-prime, and curve settings reproduced	Result difference, tolerance, and explanation
Exception handling	Blank wells, duplicate files, and unknown IDs handled explicitly	Observed disposition and recovery evidence
Provenance	Raw file, processing execution, operator, revision, and accepted result linked	Exported lineage and reproducible replay
Decision capture	Candidate rule, reviewer rationale, and superseded decisions preserved	Reviewed hit list and change history
Portability	Values, units, qualifiers, exclusions, fit settings, and identifiers exported	Reconstruction result and unresolved objects

The rubric requires evidence for a classification and leaves untested requirements open. Provenance should include both an analysis execution and the participating agent; W3C's primer explicitly treats agents as participants with roles in activities. (www.w3.org) FAIR's provenance principle reinforces the requirement for reusable records rather than isolated numeric endpoints. (www.nature.com)

Downstream standardization needs similar care. Official ChEMBL documentation gives **1 nanomolar IC50** as **pChEMBL 9**, a dimensionless negative logarithm of an eligible molar activity value. This is a documented unit-conversion example accessed October 15, 2026; the page is undated and geography is not applicable. (chembl.gitbook.io) EMBL-EBI separately describes pChEMBL as a standardized potency measure. (www.ebi.ac.uk) Those sources explain representation, not equivalence of different assays or evidence that a selected candidate will reproduce.

Implications and Future Directions

Migration and ownership

Replacing spreadsheets or a legacy database requires migration of meaning as well as values. Retain original and standardized units, relational qualifiers, assay definitions, and revision links. ChEMBL's distinction between published and standardized units provides a concrete reference for this separation.

(chembl.gitbook.io) BAO provides a vocabulary reference for annotating assay meaning without pretending that matching column names establish scientific comparability. (bioassayontology.org)

An executable migration plan should include these steps:

- **Inventory:** enumerate assays, templates, calculation rules, scripts, and reports.
- **Assign owners:** identify the authoritative source for assay, entity, sample, and result identifiers.
- **Map semantics:** document units, control roles, replicate types, and response qualifiers.
- **Reconcile:** compare scheduled wells, imported signals, exclusions, fitted results, and accepted candidates.
- **Replay:** rerun representative analyses with recorded settings and explain differences.
- **Export:** reconstruct selected decisions from the proposed exchange package.
- **Cut over:** define the last legacy write, catch-up transfer, and controlled release of the new workflow.
- **Retain evidence:** preserve historical identifiers, source files, decision records, and unresolved exceptions.

Corporate ownership informs procurement; interfaces and roadmaps require product-specific evidence. Danaher's current directory lists both Genedata and IDBS, and its Genedata business page records the company's joining in **2024**. (www.danaher.com) Siemens' announcement dated **July 1, 2025** states that its Dotmatics acquisition completed and places Dotmatics in Digital Industries Software. (news.siemens.com) These are corporate event dates, with no geographic performance population. Request support, roadmap, and contractual commitments.

Scope discipline, validation, and cost

A proposal should identify the licensed analysis engine, instrument parsers, image-processing components, interfaces, hosting, environments, implementation, migration, support, and exit assistance. The reviewed public material does not establish comparable prices for this bundle. Request itemized commercial terms and evaluate internal configuration and review work alongside supplier fees.

Validation language should be equally specific. Genedata advertises audit and record capabilities, while the Dotmatics demonstration shows an optional countersigner. (www.genedata.com) (www.dotmatics.com) Those are different kinds of evidence. A regulated-use decision needs a configured-system assessment of intended use, access, records, review, retention, and change control. Software feature descriptions alone do not document the buyer's completed validation.

Avoid importing an unrelated exchange requirement merely because it is familiar. CDISC describes its Laboratory Data Model as designed for clinical-trial laboratory interchange; that scope does not establish a universal schema for discovery screening. (www.cdisc.org) Similarly, SiLA's communication role does not by itself define the analytical payload to archive. (sila-standard.com)

The likely direction of useful automation is greater reuse of structured, attributable results. That is an editorial implication of FAIR's provenance requirements and the separation of data from processing in PROV, not a prediction of any vendor's roadmap. (www.nature.com) (www.w3.org) NIST's caution that traceability alone does not guarantee fitness for purpose is a valuable reminder to evaluate measurement suitability alongside software lineage. (www.nist.gov)

Conclusion

The choice among Genedata Screener, IDBS ActivityBase, and Dotmatics should follow the assay dataset to a reviewed decision. Genedata's documentation emphasizes integrated screening analysis and automation. ActivityBase's current and historical materials make analysis continuity, operational context, and version-specific behavior important evaluation topics. Dotmatics' documented workflow links configurable assay processing with broader discovery activities. These are supported shortlist rationales, not measured overall rankings.

For organizations seeking Genedata Screener alternatives or IDBS ActivityBase alternatives, the same comparison method applies: agree on scientific rules, submit identical inputs, inspect exceptions, and reconstruct the final hit list from exported evidence. Preserve technical and inter-run replicate identity because they describe different observations. (www.ncbi.nlm.nih.gov) Preserve the raw, normalized, aggregated, and fitted levels because an endpoint alone cannot explain the analytical path. (www.ncbi.nlm.nih.gov)

A successful pilot ends with reproducible calculations, an attributable review, a clear bill of materials, and an understandable exit package that remains useful after the original analyst has moved to another project. W3C's provenance concepts offer a practical reference for that evidence chain. (www.w3.org) Where current public information is missing, the correct outcome is an explicit procurement question and an untested requirement. The defensible platform is the one whose configured workflow meets the laboratory's declared acceptance criteria and preserves enough context for another scientist to assess the decision.

Source links

Links cited in this article, in order of first appearance. Full addresses are provided for readers using extracted text.

1. <https://www.genedata.com/screener/assay-data-management>
2. <https://www.idbs.com/activitybase/>

3. <https://www.dotmatics.com/capabilities/assay-data-management>
4. <https://www.genedata.com/platform/screener/software>
5. <https://www.idbs.com/2017/05/pfizer/>
6. <https://www.dotmatics.com/solutions/streamline-small-molecule-discovery>
7. <https://www.ncbi.nlm.nih.gov/sites/books/NBK550206/>
8. <https://www.nature.com/articles/sdata201618>
9. <https://www.w3.org/TR/prov-overview/>
10. <https://www.ncbi.nlm.nih.gov/sites/books/NBK91993/>
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12. <https://intuitionlabs.ai/articles/gxp-eln-comparison-benchling-idbs-labarchives>
13. <https://intuitionlabs.ai/articles/mosaic-regmol-dotmatics-certara-registration-comparison>
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IntuitionLabs is an AI consulting, custom software development and data engineering firm serving pharmaceutical, biotechnology, medical-device and other life-science organizations. We work with clinical, regulatory, medical-affairs, commercial, quality and IT teams to connect technology decisions with the work people need to accomplish.

AI consulting and adoption

Our AI enablement services cover readiness assessments, use-case selection, governance and policies, team workshops, adoption measurement and ongoing advisory support. We help organizations structure the information layer behind AI: source material, context, permissions and maintained knowledge that make generated answers useful and reviewable. Private LLM inference and hosted AI options support teams evaluating how to operate AI with appropriate control over their data and infrastructure.

Software, data and life-science workflows

IntuitionLabs develops custom software for pharma and biotech, integrates enterprise systems, and builds data engineering and business intelligence solutions. Areas of focus include AI agents, regulatory research, medical writing, medical affairs, CMC information, competitive intelligence and clinical-document workflows. Our eTMF intelligence work includes cross-system reconciliation and inspection-readiness support.

Enterprise platforms and regulated delivery

We provide Veeva services, application support, managed services, integrations and custom applications, alongside enterprise content work involving platforms such as Egnyte. For regulated workflows, our services include GxP enablement, computer-system validation and software development addressing 21 CFR Part 11 requirements. The applicable controls, validation responsibilities and acceptance criteria are defined for each engagement.

Work with IntuitionLabs

Explore [AI enablement](#), [pharma and biotech software development](#), [data engineering and BI](#), and [Veeva services](#). [Contact IntuitionLabs](#) to discuss your workflow, information sources and implementation needs.

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