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CortexQ Predictive Immune Escape Interception Across Pathway and Molecular Scales

George Soto

georgesoto@mindnetq.com

MindNetQ https://orcid.org/0009-0004-2394-4562

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Additional Declarations:
The authors declare potential competing interests as follows: George Soto is the founder and president of Infinity Software Architects, Inc. and founder of MindNetQ, Inc. He has commercial interests in the CortexQ platform and related intellectual property. These interests present potential financial competing interests related to the methods and applications described in this manuscript.

Ethics approval and consent to participate: Not applicable. This computational study used exclusively publicly available, de-identified data, including TCGA, Frangieh Perturb-CITE-seq, and GSE166181. No participants were recruited, no identifiable personal information was accessed, and no new human samples were collected. No new human-participant, animal, or wet-laboratory experiments were conducted for this study.

CortexQ Predictive Immune Escape Interception Across Pathway and Molecular Scales

George Soto

MindNetQ Inc. | Infinity Software Architects Inc.
Proposed computational invention and research progress | 22 October 2026 | Version 5.0

Abstract

CortexQ develops a computational method for anticipating immune recovery, subsequent tumor escape and molecular strategies for intercepting resistance. QEPD supplies intervention-conditioned pathway forecasts. SPE challenges escape hypotheses using known resistance explanations and perturbation evidence. Functional Pocket Dynamics extends the investigation to molecular behavior across protein motion. The proposed invention connects these pathway and structural challenges to a common intervention decision, with explicit treatment of uncertainty, contradictory evidence and unavailable measurements. CortexQ-CRC-01 supplies the lead colorectal research setting. CortexQ-EC-01 supplies a proposed endometrial transfer setting.

The candidate technical contribution is a disproof-conditioned computation across pathway and molecular scales. Here, disproof conditioning challenges candidate behavior against credible known explanations. A forecast identifies resistance to challenge, functional evidence tests persistence under independent route blockade, and structural evidence tests whether a molecular opportunity survives known-motion explanations. Compatible results inform a ranked research hypothesis. Missing required evidence identifies the experiment needed next. Recorded outcomes are intended to update biological models and subsequent research strategies through controlled training and evaluation. Quantum-assisted molecular hypothesis acceleration is a supporting research direction.

Development records include retrospective colorectal gene recovery, a revised perturbation layer, preliminary longitudinal state prediction, molecular prototypes and quantum hardware execution. An archived post-repair relevance benchmark reports AP 0.8347 versus 0.7832 for its reference, with unresolved comparison restrictions. A longitudinal prototype reports accuracy 0.5455 on eleven held-out state-change transitions from four patients. Structural demonstrations are constructed, and the reported quantum-device result was noise dominated. These results document component progress. Integrated predictive superiority, molecular efficacy and practical quantum advantage require separate evaluation.

Central invention question

Does coupling resistance forecasts with pathway and molecular challenges produce a technically distinct and more useful method for selecting immune-escape interception experiments? This paper defines the proposed construction, explains the comparison needed to assess patentability, and reports completed work without equating component tests with an end-to-end biological result. Standard endpoint mathematics and implementation diagnostics appear in the appendices and companion package.

1 Research objective and technical distinction

A candidate intervention must address both the current immune-suppression mechanism and the escape response expected afterward. CortexQ organizes research around this sequence: predict the biological transition, challenge competing explanations, identify a molecular intervention and test the resulting interception hypothesis. The intended advantage is more informative laboratory selection across cancer contexts. CRC-01 and EC-01 make the first questions concrete without limiting the method to one cancer.

1 1 The proposed invention

The invention hypothesis concerns the coupling between computations. The forecast specifies which resistance routes matter for a proposed intervention. The pathway challenge asks whether an effect persists when declared routes are independently blocked. The molecular challenge asks whether an apparent pocket opportunity persists after credible known motions are considered. A common decision record links compatible results to one intervention, endpoint and horizon. Unresolved evidence restricts the claim and specifies the next measurement. Learning updates the underlying models while retaining declared evidence requirements [1,2,14].

This construction makes predictions about the intervention, the resistance expected afterward and the molecular opportunity needed to act. Retrieval, agents, shrinkage and generic uncertainty thresholds support implementation. The proposed patentability argument concerns the specific operations and their dependence on one another. A complete prior-art comparison must assess the actual computation.

1 2 Closest scientific methods

Precedent	Established capability	CortexQ distinction to test
Network analysis [3]	Relational gene and module ranking	Prediction of intervention response and subsequent resistance beyond association ranking.
CPA and GEARS [9,10]	Cellular perturbation-response prediction	Whether route challenges and molecular linkage improve the downstream interception decision.
Causal optimization [4-6]	Intervention selection and active experimental design	Whether the complete two-scale computation adds value beyond an adapted causal policy.
Interaction screens [7,8]	Genetic interactions and immune-evasion mechanisms	Whether forecast-dependent route testing improves prospective hypothesis selection.
Selective prediction [11]	Abstention under a declared risk criterion	Whether mechanism-specific challenges add value beyond ordinary uncertainty thresholds.

Zhang and colleagues evaluated causal active intervention design with Perturb-CITE-seq [6], making their work a close comparison. The present literature review identifies relevant precedents. It does not establish absence of the complete CortexQ construction in earlier disclosures.

2 Computation across pathway and molecular scales

The public method describes the dependencies between forecasts, challenges, molecular hypotheses and experimental feedback. Selected operators, weights and program-specific molecular details remain confidential. The diagram depicts the proposed integration. Available software implements components, with unresolved links recorded in Section 4.

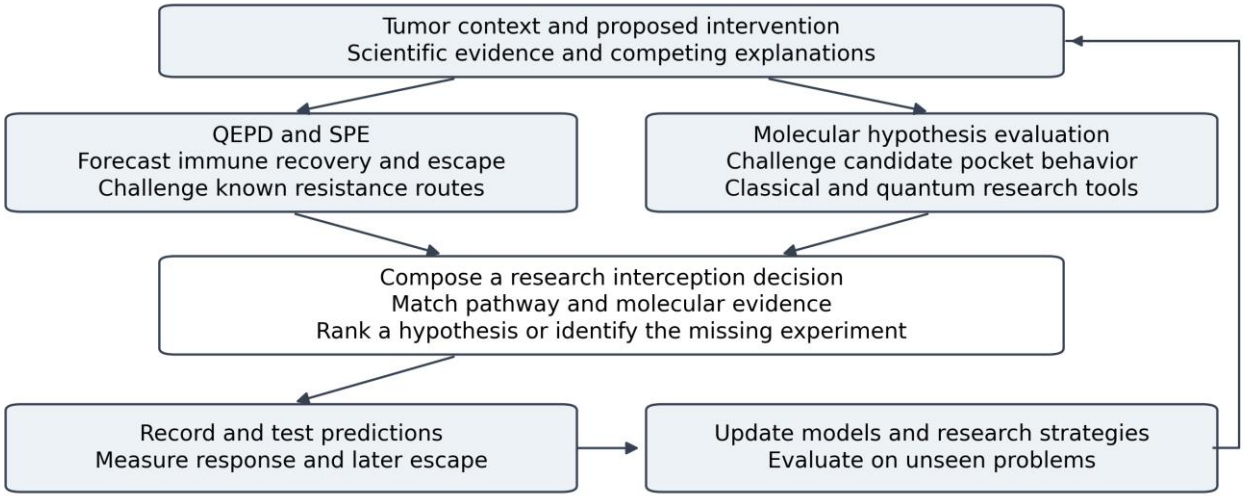


Figure 1. Proposed predictive interception computation. Pathway and molecular challenges inform one research decision. Experiments supply outcomes for subsequent model and strategy updates. The diagram expresses intended dependencies and supplies no performance measurement.

2 1 Pathway challenge

QEPD represents intervention-conditioned changes and candidate escape routes. SPE separates observational relevance from pressure-specific perturbation effects and persistence under independent route blockade. Bulk co-expression supplies association-level evidence. Measured perturbation and longitudinal data are required for functional and temporal claims. Spatial claims additionally require measured regions. The earlier covariance-residual independence interpretation was withdrawn after negative testing [1,2].

2 2 Structural challenge and shared decision

Functional Pocket Dynamics examines candidate opportunities across protein motion. Its intended challenge separates a proposed pocket event from behavior explained by admitted known motions [14]. The pathway and structural challenges address different quantities. Their outputs require a justified link to the same intervention before composition. A missing route contrast or unsupported molecular mapping produces an unresolved research decision. This coupling is the invention hypothesis under examination, rather than a completed efficacy result.

2 3 Contradiction and feedback

For a fixed claim, unresolved material contradictions restrict the authorized claim level. Outcome learning updates empirical route models, conformational bases and research priorities through reviewed records. No monotonic performance improvement follows from accumulating data alone. Held-out evaluation determines whether each update improves prediction and experimental selection.

3 Disease programs and molecular hypothesis acceleration

3 1 CortexQ CRC 01

CRC-01 asks whether a molecular intervention restores suppressed immune sensing, which escape response follows and which subsequent intervention deserves testing. The prospective record specifies tumor context, intervention direction, immune pressure, response endpoint, horizon and rejection criterion. A sensing marker addresses a mechanism. Immune killing or an appropriate fitness assay addresses the escape outcome. The candidate molecular target and structures remain confidential.

An informative challenge measures the candidate intervention under immune pressure with and without a distinct resistance-route blockade. The necessary factorial groups distinguish candidate action, route action and their interaction. A single knockout does not identify a double-perturbation effect. A knockout increasing escape also requires separate evidence before supporting therapeutic inhibition. The program seeks forecasts of immune recovery and later escape within this experimental structure.

3 2 CortexQ EC 01

EC-01 supplies a proposed transfer question involving impaired tumor recognition after checkpoint exposure. The research decision concerns a recognition-restoring intervention, a subsequent checkpoint intervention and the resistance persisting after the sequence. Each intervention alone and the proposed sequence need suitable controls. No independent endometrial prediction benchmark or efficacy result is reported. Transfer requires new calibration and validation of the relevant mechanisms.

3 3 Molecular and quantum research

Functional Pocket Dynamics adds a dynamic molecular hypothesis to the pathway question: whether a candidate opportunity persists across protein conformations and supports the intended intervention. Existing demonstrations include constructed trajectories and prototype simulation work [14]. Replicated real trajectories, active and inactive controls, and binding or functional measurements are needed to connect structural calculations to a biological effect.

Quantum-assisted molecular hypothesis acceleration targets selected chemical calculations within this research process. The internal record includes classical reference calculations, simulator work and a real IBM device run [1]. Hardware execution is completed engineering work. The reported device output was noise dominated. A practical advantage requires matched scientific accuracy and end-to-end comparisons covering preparation, optimization, repeated runs, device access and cost [15]. Quantum execution alone does not establish faster molecular discovery.

3 4 Learning how to investigate

The cognitive architecture connects a custom scientific model, inference engine, research agents and discovery metadata. Retrieval supplies evidence at inference time. Controlled training updates model behavior. Versioned datasets, scientific evaluations and deployment checks support traceability. Reviewed outcomes are intended to improve later reasoning strategies and hypothesis selection. The team reports autonomous colorectal investigation and Rust services on Amazon ECS. Quantitative learning and production gains require workload-specific evaluation.

4 Completed work and computational progress

Development has progressed through biological ranking, negative tests, revised functional endpoints, longitudinal modeling, molecular prototypes and hardware execution [1,2,14]. The table separates reported results from the scientific conclusion each supports. Biological datasets were not rerun for this revision.

Component	Completed or source reported work	Evidence boundary
Colorectal foundation	Recovery of five known mechanisms and known-gene recovery AUC 0.896, permutation p = 0.0005.	Relational foundation on established biology. A separate computation from the proposed integrated invention.
Updated relevance	Archived post-repair AP 0.8347 versus 0.7832. Both precision and recall at six are 0.8333.	Nonzero reference restored. Equal held-out exclusions (the prior 0.9167 reflected OOV anchor leakage, now removed), AP ties and estimator normalization restrict comparison.
Pathway challenge	Covariance independence interpretation withdrawn. Perturbation layer separates effect, null, inconclusive and unestimable states.	All assessed Qpert values remain null because required route evidence is unavailable. Matched estimation also needs repair.
Longitudinal forecast	State-change accuracy 0.5455 versus uniform reference 0.3333 on eleven test transitions from four patients.	Preliminary CD8 state-cluster task. Calibration and mapping to tumor escape routes remain incomplete.
Molecular challenge	Functional Pocket Dynamics method and prototype code, including constructed trajectory demonstrations.	No independent binding, target-engagement or molecular efficacy validation reported.
Quantum computation	Classical references, simulator work and a real IBM device execution.	Reported device output noise dominated. No practical quantum advantage demonstrated.

4 1 Progress in scientific interpretation

The perturbation revision separates immune-program transcription from guide enrichment under pressure. The reported CD58 enrichment effect is 0.1439 in natural-log odds units, with bounds 0.0072 to 0.2908. Its lower bound does not exceed the declared 0.10 magnitude threshold. The result addresses guide enrichment and leaves effect magnitude unresolved under this rule. It is neither an immune-killing measurement nor a new therapeutic finding.

4 2 Progress in implementation

The dimension-driven reference collapse was reproduced and repaired. Ten repository regression methods pass under direct invocation. Twelve companion regression tests and eleven mathematical diagnostic groups also pass on their declared controls. These checks preserve useful engineering progress while exposing remaining endpoint, reference-state and joint-uncertainty mismatches. The detailed audit supports the invention discussion and appears in the companion package.

5 Invention hypothesis and patentability assessment

The proposed invention couples resistance forecasts, known-route challenges, structural challenges and an intervention experiment. Its technical object is the dependency between these computations and their contribution to selection. Patentability requires assessment of a sufficiently defined construction against the applicable requirements. Architecture labels and performance targets alone do not establish those requirements.

5 1 Public mathematical objective

$$u_* \in argmin_{u \in U(E)} sup_{H \in M(E)} R_{escape}(X, u, c, H)$$

X denotes biological state, u an intervention and c context. U(E) is a finite eligible intervention set. M(E) is an evidence-admissible family of mechanism models H. Rescape is a bounded escape-risk score at a fixed horizon. For nonempty sets and an available score, the expression selects a minimizer of worst-case risk. Otherwise selection is unestimated. Robust optimization is established. The invention hypothesis concerns how the two-scale challenges construct and support this decision. The notation supplies no proprietary transition operator, causal identification or new optimization theorem [1,4,5,14].

Question	Specific assessment needed
Novelty	Map the complete proposed claim to qualifying earlier disclosures. Compare the arrangement and dependence of its operations, not the platform name.
Nonobviousness	Assess whether the complete combination would have been obvious from the relevant art. Identify a supported technical effect from the coupling.
Technical application	Explain the concrete computation and biological research operation. Mathematical scoring or generic computer execution alone does not resolve eligibility.
Enabling disclosure	Supply enough of the actual computation to support the intended claim scope. Distinguish executed examples from proposed experiments.

These are separate assessment requirements [21]. A completed clinical or commercial demonstration is not a prerequisite to every patent filing. An enabling disclosure is still required. Proposed examples must remain distinguishable from work performed. The present public interface supports scientific discussion, while confidential invention review requires the actual operators and an element-level prior-art comparison.

5 2 Scope of the proposed distinction

Pathway prediction, interaction analysis, selective prediction, molecular simulation and quantum chemistry have substantial prior work. The candidate distinction is the specific cross-scale composition and its effect on intervention selection. Authority contraction and withholding a composite when a required term is unestimated are supporting properties of this construction. Neither property is treated here as independently proven novel. Molecular targets, compounds and quantum implementations represent separate claim questions when sufficiently specified.

6 Demonstrating the technical advantage

A meaningful comparison tests whether the complete construction selects more independently confirmed interception hypotheses under matched data access, experimental budget and useful coverage. The comparator set includes strong relational or linear predictors, compatible response models, an adapted causal or active-design policy, and ordinary uncertainty-based selection [3-13]. Remove the pathway challenge, structural challenge and cross-scale linkage separately to measure each contribution. The molecular arm needs its own active and inactive controls.

The planning target remains a 10 percentage-point selection-precision gain at 50% coverage. This target is unmeasured and not power-justified or preregistered. The archived AP difference of 0.0515 concerns gene ranking under unresolved comparison restrictions. It is a different endpoint. A paired 95% interval with lower bound above zero supports superiority. A lower bound above 0.10 is needed to support a gain exceeding 10 percentage points. Missing outcomes and abstentions remain visible in the denominators.

6 1 Prospective experimental record

For CRC-01, freeze predictions of initial immune response and subsequent resistance before testing. Record intervention direction, assay, horizon, route definitions and rejection criteria. Score both successful and failed forecasts. Split development and evaluation by the relevant patient, donor or independent experimental unit. EC-01 requires its own calibration. A regional prediction requires regional measurements. Laboratory savings require measured cost and independently confirmed outcomes.

6 2 Present limitations and next scientific step

The remaining work includes a fair relevance comparison, matched perturbation persistence, calibrated longitudinal forecasts, validated pathway-to-molecular mapping and an integrated intervention experiment. Bulk co-expression does not establish spatial geography or causal direction. Melanoma perturbation evidence does not establish CRC-01 or EC-01 efficacy. The current longitudinal composition uses pooled destinations and unvalidated route mappings. Resolving these links advances the proposed predictive invention beyond component demonstrations.

Patentability and freedom to operate require separate assessments. The companion U.S. screen identifies three patent records for implementation-to-claim follow-up. It is not a clearance conclusion [20]. Selected molecular information and internal operators remain confidential. This manuscript presents a computational and preclinical research method. No diagnostic, treatment or clinical efficacy claim is made.

Declarations

Data and code. Sources include TCGA, Frangieh Perturb-CITE-seq and GSE166181. Private repositories contain development records. The companion package supplies proposed repairs, executed diagnostics, source hashes, reference checks and invention-review notes, excluding patient data and proprietary model code. Biological results remain source-reported.

Interests and support. George Soto has a commercial interest through MindNetQ Inc. and Infinity Software Architects Inc. Funding information is not reported. This revision reports no new human-participant, animal or wet-laboratory experiment. AI tools assisted review, diagnostics and drafting. The author retains responsibility for verification.

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Appendix A Perturbation estimands and endpoint scales

For a fixed candidate g, admitted route m and biological context, let A indicate candidate perturbation, P immune pressure and B a distinct route blockade. Define μ(a,p,b) as the conditional mean of a declared response Y in factorial cell (a,p,b). The following is a standard interaction contrast on the mean-response scale. Its algebra alone does not identify a causal effect.

$$\theta_{g,b} = [\mu(1,1,b) - \mu(0,1,b)] - [\mu(1,0,b) - \mu(0,0,b)]$$

The source function _did computes this contrast for a transcriptional endpoint [2]. A causal interpretation requires justified intervention assignment, appropriate controls, effective target engagement, positivity and assumptions about interference and sampling. The same mean contrast applies to a suitable killing assay only after defining its direction and units. An IFN program response is a mechanism readout, separate from measured tumor survival.

A 1 Guide enrichment uses a different estimator

The source fitness function does not compute a difference of mean Y values. It computes a natural-log odds ratio for guide presence among sampled cells under pressure versus control. Let n(apb) count cells in each candidate-by-pressure group within a fixed blockade state. The implemented 0.5 correction yields:

$$\ell_{g,b} = ln[(n_{11b} + 0.5)(n_{00b} + 0.5) / ((n_{01b} + 0.5)(n_{10b} + 0.5))]$$

Positive ℓ means relative enrichment of candidate-guide cells in the sampled pressure arm. This is a fitness proxy. Capture, growth, sampling and guide effects require assessment before attributing enrichment to immune escape. ℓ has log-odds units, whereas θ has units of Y. The two estimators must not share a numerical effect margin without endpoint-specific justification. A log-odds margin of 0.10 corresponds to an odds ratio of exp(0.10), approximately 1.105. It is not a 0.10 z-score change.

A 2 Persistence needs a matched reference

$$\omega_{g,m} = \ell_{g,Bm=1} - \ell_{g,Bm=0}$$

Persistence asks whether the effect under an independent route blockade stays within a prespecified equivalence margin of its unblocked value. The mean-response version substitutes θ throughout. These are different effect scales. A nonsignificant difference does not establish equivalence. Under a suitable test model, two one-sided tests at level 0.05 correspond to a 90% two-sided confidence interval inside the declared equivalence limits [18]. These intervals are pointwise and provide no automatic simultaneous guarantee across routes.

All required A × P × B groups and suitable independent replicates must be available. Candidate perturbation cannot substitute for the independent route blockade. The inspected _theta implementation uses all cells when block_mask is absent. Its reference is therefore pooled over blockade states, rather than restricted to B = 0. In a balanced constructed design, unblocked and blocked effects of 2 and 5 yield a pooled effect of 3.5. The intended change is 3; comparison with the pooled reference gives 1.5. This implementation mismatch needs repair before claiming the matched persistence estimand.

Appendix B Joint support and implementation checks

For a nonempty required route set H, all effects in one indicator use the same resampling draw j, endpoint scale and prespecified margins. L is the positive number of valid joint draws. With no valid draws or a missing required route, support is unestimated.

$$h_j = 1\{\ell_{g,0}^{(j)} > \delta \wedge |\omega_{g,m}^{(j)}| < \Delta \, \forall \, m \in H\}$$

$$Q_{boot} = (1/L)\sum_{j=1}^{L} h_j$$

Qboot is a bootstrap event frequency under the declared resampling procedure. It is not automatically a Bayesian posterior or calibrated confidence level. The source drops invalid draws independently and aligns the compressed arrays by position. A constructed example changes event frequency from zero to one under this misalignment. Retain common draw identifiers and every required route. The example does not recalculate a biological Q.

B 1 Composition quantities

$$K = estimable \wedge compatible \wedge calibrated \wedge traceable$$

$$J_{g,r} = p_r \times \ell_{g,0,r} \times Q_{g,r}$$

K is a proposed eligibility policy. J is reported only when K holds. The forecast, effect and support must refer to compatible contexts, endpoints, directions, routes and horizons. J has log-odds units and dependent terms. It is a heuristic priority index, not a response probability. It does not establish expected therapeutic benefit. A downstream molecular mapping needs independent evidence.

B 2 Supporting benchmark diagnostics

The earlier shrinkage rule forced full shrinkage at 80 samples and 222 genes. The repair gives intensity 0.0867 and maximum absolute off-diagonal value 0.6376 on structured synthetic data. All ten repository methods pass under direct invocation. The patch combines n−1 covariance with an n-based variance expression. A consistently normalized reference matches scikit-learn on six cases [16,17]. Conventional Ledoit-Wolf agreement is not established for the repository patch.

The inspected AP implementation is order-dependent for ties. With 203 constant scores and six positives, source AP ranges from 0.017385 to 1.000000 after label reordering. Threshold-group AP is 6/203, approximately 0.029557 [19]. The relevance call also omits the full target-exclusion set used by its comparator. These issues require matched evaluation and raw predictions for a fair biological comparison.

Twelve constructed composition controls include one compatible positive case. The proposed guard rejects eight unsupported combinations accepted by the bare interface and retains the positive. Twelve companion regression tests and eleven mathematical check groups pass. These are bounded software checks. Complete source hashes and results are retained in the companion package.

Figures

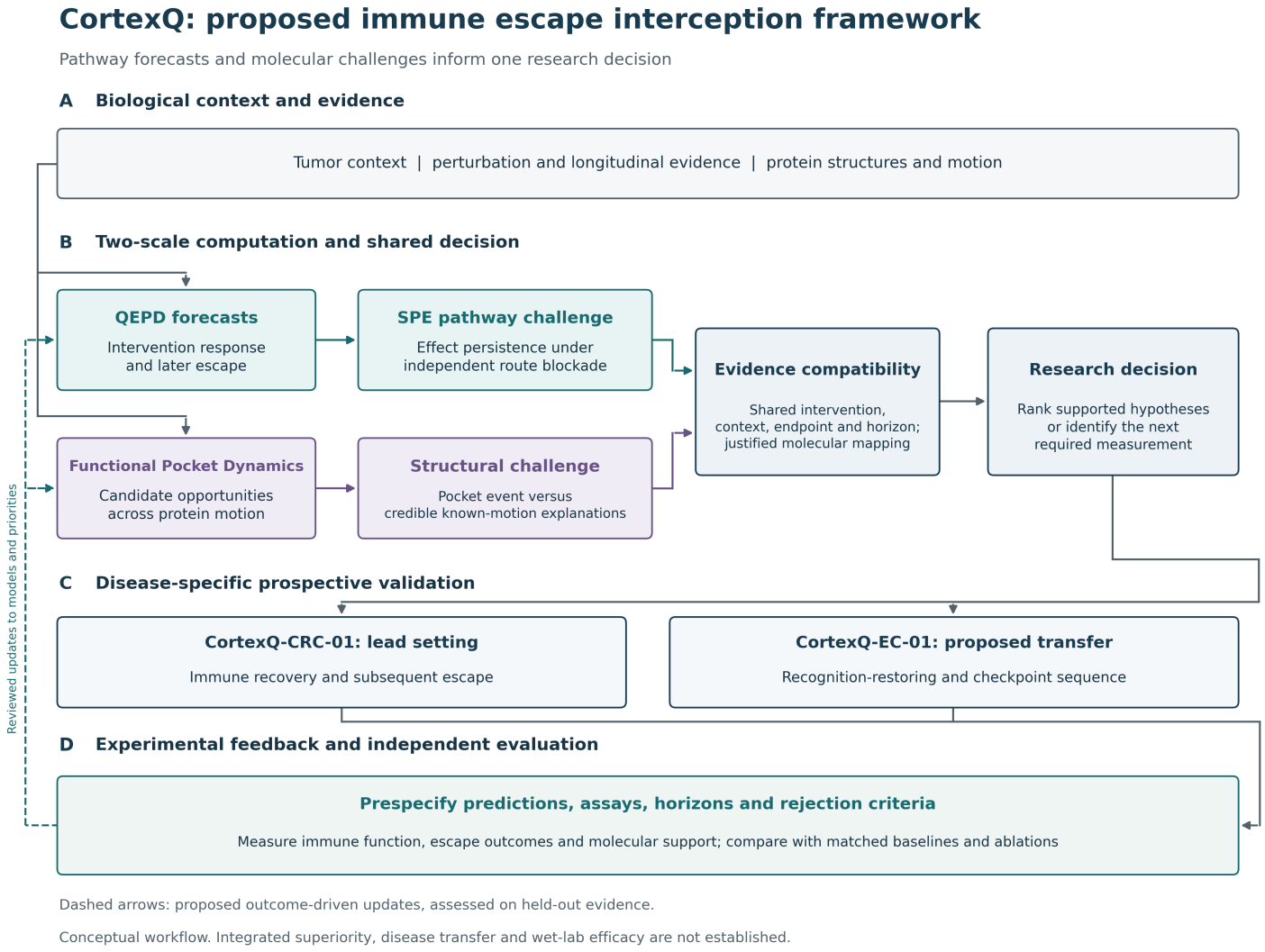


Figure 1

CortexQ predictive immune escape interception framework. Tumor context and a proposed intervention inform QEPD pathway forecasts, SPE resistance challenges, and molecular hypothesis evaluation. Compatible evidence supports a ranked research hypothesis, while missing evidence identifies the next experiment. Experimental outcomes inform subsequent model and research strategy updates. The diagram depicts the proposed integration of tested components.