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Quantum Computing in Molecular Design and Drug Discovery: A Systematic Literature Review

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Abstract. This study examines how quantum computing (QC) is being applied to molecular design and drug discovery. This study aims to investigates how QC surpasses classical limitations, focusing on empirical performance in precision, accuracy, and optimisation tasks. Study design use PRISMA 2009 guidelines, 15 empirical studies (2020-2025) were included. Data were extracted on the drug-discovery stage, the algorithm used, evaluation metrics, benefits, and limitations. The findings show QC outperforms classical methods particularly through hybrid quantum–classical models. Thirteen studies reported superior gains, including AUC–ROC values of 0.80–0.95, +30% improvement in drug-likeness (QED), +6% increase in prediction accuracy, and up to 99% accuracy in drug–target interaction tasks. However, noisy intermediate-scale quantum (NISQ) hardware limitations and poor scalability limit real-world deployment, due to noise, and limited qubit counts. Consequently, current performance results are largely simulation-based rather than hardware-validated. In contrast to prior algorithm-centric reviews, this study provides a consolidated empirical synthesis and proposes a hybrid quantum–classical pipeline that maps high-performing algorithms across the drug discovery workflow under NISQ-era constraints. These findings inform pharmaceutical research and development by identifying realistic adoption pathways and the boundaries of current technological readiness.

Keywords: quantum computing, molecular design, drug discovery, quantum algorithms, hybrid quantum-classical, NISQ

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1. INTRODUCTION

Drug discovery is an important process for developing therapeutic agents that address both long-standing and emerging health issues [1]. Despite significant advances such as artificial intelligence (A.I.), the drug discovery pipeline is characterised by developmental timelines, high costs and the exponential scaling of molecular interactions [2], [3], [4]. Classical methods such as molecular mechanics (MM) and molecular docking (MD) have accelerated the drug process, but they heavily rely on approximations that fail to capture the quantum nature of molecules[5], [6]. This has resulted in diseases being underserved due to poor safety profile predictions and the wastage of therapeutic candidates due to ineffectiveness [2], [7], [8], [9].

Quantum computing (QC) utilises quantum bits (qubits), superposition, and entanglement to address classically intractable molecular problems [2], [10], [11]. These principles enable more accurate representations of molecular states, supporting property prediction, constrained optimisation, molecular screening, and the generation of novel compounds [12], [13]. Compared to classical approaches, QC can improve computational efficiency, reduce experimental effort, and offer scalability advantages for high-dimensional molecular data [7], [9]–[12]. In practical drug discovery pipelines, such improvements are particularly valuable at early stages, where molecular screening, property prediction, drug–target interaction modelling, and toxicity assessment determine which compounds advance to costly laboratory validation and clinical trials [10]. Early-stage computational accuracy is critical, as prediction errors propagate through the pipeline: false positives waste synthesis resources. In contrast, false negatives discard viable therapeutics [2], [7]. Limitations of classical methods in capturing quantum-mechanical effects further contribute to late-stage failures [5], [6], [11], making improved early-stage precision essential for reducing development costs and timelines.

The objective of this review is to systematically analyse and synthesise empirical evidence on the application of QC in drug discovery, focusing on where and how QC and hybrid quantum–classical approaches provide measurable advantages over classical methods. Specifically, this study maps the stages of the drug discovery pipeline into a conceptual framework and examines how current technological constraints shape practical deployment. Recent progress in QC-enabled drug discovery has demonstrated

promising performance over classical approaches [12], [13]. However, practical adoption remains constrained by the NISQ-era environment [14] , which is characterised by limited qubit counts, hardware noise and errors. These restrict the performance of fully quantum pipelines, making hybrid quantum–classical workflows the most practical near-term solution. Table 1 summarises the key differences between classical, quantum and hybrid paradigms to contextualise the reasons for integrating quantum computing into drug-discovery processes.

Table 1. Classical vs Quantum vs Hybrid frameworks

Dimension	Classical Computing	Quantum Computing	Hybrid Quantum-Classical
Computational principle	Deterministic logic	Quantum superposition and entanglement	Parallel integration of classical pre-processing and quantum kernels
Example Algorithms	SVM, CNN	VQE, QAOA, Quantum GAN	Hybrid VQE-DNN, Quantum CNN
Strengths	Mature, scalable, interpretable	Exponential state-space exploration	Balance between accuracy and hardware feasibility
Limitations	High time complexity	Hardware noise, NISQ instability	Integration and interoperability complexity

Previous reviews have examined quantum computing in molecular design and drug discovery. Notable works include [4], [15], [16], which explored molecular simulation, QML-based molecule generation, and property prediction, respectively, each reporting improvements in modelling performance. However, these studies were highly task-specific, lacked comparative evaluation against classical baselines and did not analyse scalability or end-to-end pipeline applicability. Moreover, reviews such as [2], [17] outlined the theoretical foundations and accuracy gains of QC, but similarly noted that NISQ-era noise, limited hardware stability and the need for error correction continue to restrict practical real-world applications.

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Although several reviews have explored the potential of quantum computing in drug discovery, most remain largely theoretical, algorithm-centric, focused on isolated tasks, with limited systematic comparison between hybrid quantum–classical and classical methods. Collectively, existing literature is fragmented and lacks an empirical synthesis across the full drug discovery workflow. Moreover, no comprehensive framework currently demonstrates how to integrate quantum algorithms across the major stages of the drug-discovery pipeline. While QC-enabled workflows promise improved molecular modelling and shorter development timelines, there remains no systematic empirical review identifying where QC is practically applied and how its performance compares with classical approaches under NISQ constraints. This review directly addresses this gap through a consolidated empirical synthesis and a stage-mapped hybrid quantum–classical pipeline.

The urgent need for such a consolidated empirical synthesis arises from the rapid growth of experimental quantum studies in molecular modelling and drug discovery. As hybrid quantum–classical approaches increasingly report performance gains, the absence of a unified empirical framework makes it difficult to distinguish practical capability from theoretical promise. Without structured integration guidance, researchers and industry practitioners lack clear direction on realistic deployment points, expected benefits, and current limitations of quantum methods. A consolidated synthesis is therefore essential to support informed methodological selection, system design, and long-term investment decisions in quantum-driven pharmaceutical research.

This review addresses these gaps by systematically mapping and critically analysing empirical studies between 2020 and 2025. It provides a quantitative and qualitative synthesis of comparative insights between quantum and classical models and proposes a hybrid quantum–classical conceptual framework that demonstrates its utilisation across the drug discovery pipeline. This research will answer the following questions:

1) RQ1. At which stages of the drug discovery pipeline is quantum computing being applied?
2) RQ2. How are quantum computing algorithms utilised within the drug discovery processes?
3) RQ3. How does quantum computing enhance the identification of novel drug candidates in molecular discovery?

4) RQ4. How do current technological and technical limitations influence the application of quantum computing in drug discovery?

The rest of the paper is structured with the following order of topics: 2. Methodology used in this systematic review, 3. Results and Discussion, 4. Conclusion.

2. METHODS

The PRISMA (2009) framework guided the literature analysis of this study through the stages of Identification, Screening, Eligibility, and Inclusion, which were used to determine, select, prioritize, analyze and summarize all relevant published findings [18], [19].

2.1. Search Strategy

This review was conducted in the following databases: IEEE Xplore, PubMed, ACM Digital Library and Springer Nature Link. The core Boolean search string is shown as follow.

(("quantum computing*") AND ("drug discovery" OR "molecular design*") AND ("pharmaceutical" OR "biomedicine*" OR "healthcare"))

2.2. Inclusion and Exclusion Criteria

Table 2 shows the inclusion and exclusion criteria used in this study.

Table 2. Inclusion and Exclusion criteria

Criterion	Inclusion	Exclusion
Study Type	Peer-reviewed empirical studies reporting experimental or simulation-based evidence.	Theoretical, conceptual, perspective, opinion papers, or reviews without empirical evaluation.
Quantum Computing Relevance and Application Scope	Studies that apply quantum computing or hybrid quantum–classical methods to any computational task within the drug discovery pipeline.	Generic quantum computing studies with no drug-discovery relevance.
Application	Papers situated in	Papers from domains

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Criterion	Inclusion	Exclusion
Domain	pharmaceutical science, biomedicine, healthcare-related molecular modelling, or computational drug discovery.	unrelated to biomedical or pharmaceutical applications
Timeframe	2020–2025	Pre-2020
Language	English	Non-English

To maintain methodological rigour, grey literature such as preprints, theses, and non-peer-reviewed reports was intentionally excluded. Only peer-reviewed empirical studies were included, as the review aimed to evaluate practical algorithm performance, comparisons with classical baselines, and NISQ-related constraints, which cannot be reliably assessed using purely theoretical or conceptual works.

2.3. Screening

The initial search on November 4 yielded a total of 1291 papers, distributed as follows: 35 from IEEE Explorer, 122 from PubMed, 1040 from SpringerLink, and 94 from the ACM Digital Library. 2 duplicate sets were identified and merged, yielding 2 unique papers. One thousand two hundred twenty-nine papers were excluded during title and abstract screening because they focused on classical or quantum methods with no contribution to the drug discovery pipeline. This resulted in 60 papers qualifying for the full-text screening process. Two reviewers independently screened titles and abstracts, followed by full-text assessment, following the predefined inclusion and exclusion criteria. Disagreements during the screening process were resolved through structured discussion until consensus was reached. A Cohen's K = 0.87 which indicates substantial agreement was calculated using the standard formula as shown in Equation 1.

$$\kappa = \frac{P_o - P_e}{1 - P_e} \quad (1)$$

where P_o is the proportion of observed agreement, and P_e represents the expected chance agreement.

2.4. Eligibility

Sixty papers were eligible for the full-text screening process, and 45 were removed because they did not involve biological concepts such as molecules or biological targets, or because they were purely theoretical algorithm development. As a result, a total of 15 papers qualified for the systematic analysis.

2.5. Inclusion

The inclusion stage of the review shows how studies were identified, screened, and selected. After applying the predefined inclusion and exclusion criteria, 15 studies were found to be suitable for inclusion in the final review. These selected studies provide the foundation for the analysis and discussion that follow. A detailed PRISMA flow diagram is shown in Figure 1.

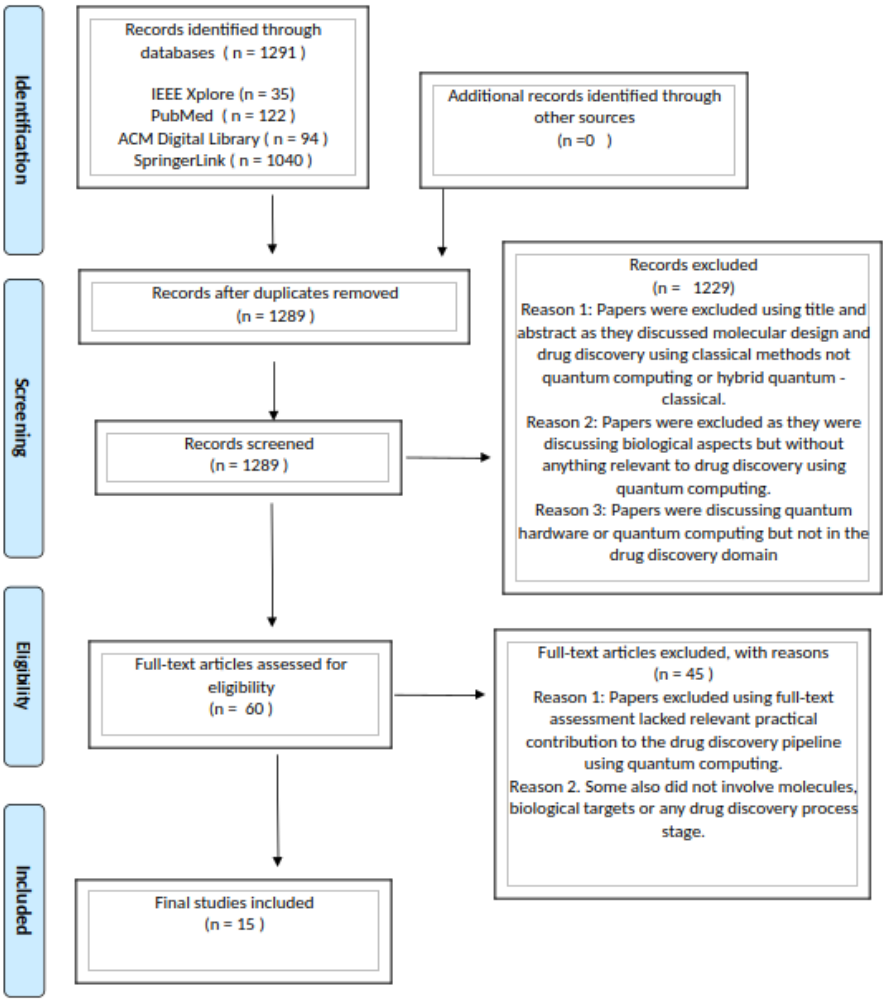

Figure 1. PRISMA diagram to show the screening process

2.6. Quality Appraisal

The quality of the selected studies was evaluated using the Critical Appraisal Skills Programme (CASP) Checklist (2018). The CASP tool is a set of appraisal checklists developed to evaluate the methodological quality, reliability and applicability of research studies [28]. The checklists were altered to suit the practical nature of the research and adapted structured judgments by dividing the appraisal into five major domains, as shown in Table 3.

Table 3. CASP Checklist domains and scoring

Checklist Domain	Description	Scoring range
Method clarity	Is the method or algorithm adequately described?	0 - 2 points
Research objectives clarity	Explicit definition of study goals.	0 – 2 points
Drug discovery stage coverage	Relevance to one or more drug discovery pipeline stages.	0 – 2 points
Outcomes and limitations transparency	Were outcomes and limitations clearly presented?	0 – 2 points
Reproducibility	Transparency of data collection, parameters set and algorithms used.	0 – 2 points

The scoring system was:

2 points – fully addressed with high quality

1 point – partially addressed or moderate quality.

0 points – not addressed or insufficient quality.

Table 4 presents the quality assessment of the studies included in this study.

Table 4. CASP Quality Assessment of included studies

Author	Method Clarity	Research Objectives Clarity	Drug-Discovery Stage Coverage	Outcomes & Limitations Transparency	Reproducibility	Score
[20]	2	2	1	2	2	9
[21]	1	1	2	2	1	7
[22]	2	2	2	2	1	9
[23]	2	2	2	2	2	10

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Author	Method Clarity	Research Objectives Clarity	Drug-Discovery Stage Coverage	Outcomes & Limitations Transparency	Reproducibility	Score
[24]	2	2	1	2	2	9
[25]	2	2	1	2	2	9
[26]	2	2	2	2	2	10
[27]	2	2	2	2	2	10
[28]	2	2	1	2	2	9
[29]	2	2	1	2	1	8
[30]	2	2	1	2	2	9
[31]	2	2	2	2	2	10
[32]	2	2	1	2	2	9
[33]	2	2	1	2	2	9
[34]	2	2	1	1	1	7

Thirteen papers scored above or equal to 8/10 (high quality), and two scored 7/10 (moderate quality). All included studies demonstrated sufficient contextual relevance to justify inclusion. Low-scoring studies were not excluded due to the limited volume of empirical quantum computing research. Instead, they were retained to ensure thematic completeness and were interpreted cautiously within the synthesis, rather than being weighted equally in algorithm performance comparisons.

2.7. Data Extraction

The screening and data extraction process was conducted using Mendeley Reference Manager (Version 2.139.0) for reference management, deduplication, and inclusion-exclusion tracking; RIS and BibTeX formats for standardised citation tracking and exporting and PRISMA (2009) for data logging. No AI-assisted screening tools were used. All screening, data extraction and appraisal activities were performed manually by the two reviewers to ensure methodological transparency.

Extracted variables included author, publication year, country, quantum algorithm, quantum algorithm type, drug discovery stage, benefits, benchmark dataset, and reported limitations. Table 5 shows articles included in the study and their extracted characteristics.

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Table 5. Characteristics of included studies

Country	Drug Discovery Stage	Algorithm Used	Type	Benefits	Evaluation Metrics	Challenges
[20] India	Drug-target interaction	QSVR	Hybrid quantum-classical	94-99% accuracy gain in DTI prediction	The DAVIS dataset achieved 94.21% accuracy, and the KIBA dataset achieved 99.99%	- NISQ noise. - Scalability of feature mapping
[21] India	Phytopharma modelling. -electronic structure prediction, -network pharmacology, -bioactivity modelling	Hybrid simulation	Hybrid quantum-classical	Improved complex-interaction modelling	-	- Immature NISQ hardware
[22] USA	- Protein folding	Grover's algorithm	Pure quantum	accelerated and optimised search in protein folding and drug discovery modelling	Classical exhaustive search	-NISQ noise - High qubit count required for realistic proteins.
[23] China	-Simulation of ground state energy. -Pro drug activation.	VQE	Hybrid quantum-classical	- Higher precision and feasibility of quantum-classical integration	- Classical MM	- NISQ Hardware. - Limited scalability to a full drug discovery pipeline.
[24] China	- Molecular conformation (creating 3D structures of small molecules). - Optimisation	-Quantum Approximate Optimisation Algorithm (QAOA), - Quantum-inspired Simulated Bifurcation Algorithm (SB)	Hybrid quantum-classical	- Time-to-target factor reduced (faster optimisation)	- QM9 dataset	- Quantum hardware maturity. - Encoding/ representing molecular structures complexity - Experiment is simulated, not run on quantum hardware.
[25] India	-molecular interactions - Identification of drug candidates.	Quantum Support Vector Machines (QSVM) - Quantum Neural Networks (QNN)	Hybrid quantum-classical	improved accuracy	- Classical SVM and NN algorithms	- NISQ Hardware. - Noise and error rates -Scalability issues

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Country	Drug Discovery Stage	Algorithm Used	Type	Benefits	Evaluation Metrics	Challenges
[26] China	- De novo molecular generation.	QGAN	Hybrid quantum-classical	- Generated novel molecular structures with improved drug-likeness scores.	- Classical GAN - QED score	- NISQ Hardware - Limited molecular complexity
[27] USA	- Binding affinity prediction.	Hybrid QML	Hybrid quantum-classical	- increased speed and accuracy - +6% increased prediction	- PBDbind dataset	- NISQ hardware -quantum hardware error and noise
[28] Switzerland	- Small Molecule generation	- QGAN	Hybrid quantum-classical	+30% in druglikeness score -QED score +30% vs classical GAN	- QM9 datasets - - PC9 dataset - QED	- Noisy quantum devices - simulation not validated on quantum hardware -smaller training datasets with a small range of chemical compounds and molecular structures
[29] India	- ADME-Tox prediction	- QSVC	Hybrid quantum-classical	- better classification results with an AUC ROC of 0.80-0.95 across various ADME-Tox datasets	- HIA datasets-CYP2D6 datasets - DILI dataset	- Immature quantum hardware -immature quantum software. And algorithms.
[30] India	- Molecular energy estimation - Protein-ligand binding	VQE	Hybrid quantum-classical	- greater molecular energy estimation accuracy	DFT/HF	-NISQ noise -Molecules simulated were from a small test set
[31] USA	-Molecular generation. - Property prediction.	QAOA	Hybrid quantum-classical	- Improved predictive performance. - Efficient generation of novel molecules that accurately fill target constraints.	- Zinc dataset	- NISQ hardware - limited qubit counts. - Scaling to larger drug-like molecules is difficult.
[32] India	- binding energy simulation	- VQE - QAOA	Hybrid quantum-	- Accurate folding and structural analysis	- Hartree-Fork	- NISQ hardware

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Country	Drug Discovery Stage	Algorithm Used	Type	Benefits	Evaluation Metrics	Challenges
	- Structure analysis		classical			
[33] USA	- screening - molecular generation	- QGAN - QCNN	Hybrid quantum-classical	- Quantum GAN/CNN outperformed classical GAN/CNN in terms of accuracy. - No advantage over VAE	- Classical GAN/CNN - VAE	- Designing qubit qubit-efficient circuit architecture for data encoding -NISQ noise
[34] UK	- Electronic structure calculation.	VQE	Hybrid quantum-classical	- higher accuracy with fewer computational resources	-	-NISQ hardware -Scaling constraints

3. RESULTS AND DISCUSSION

3.1. Publication Trends

Studies on quantum computing in molecular design and drug discovery have shown steady interest, with the peak period from 2023 to 2024 accounting for 9 of the 15 studies. The year 2024 had the most publications, with five papers accounting for 33% of the total, followed by 2023, with four publications accounting for 27%. Although the upward trajectory indicates growing interest in quantum-enabled molecular design, a slight decline in publications was observed in 2025. Figure 2 shows the number of publications per year.

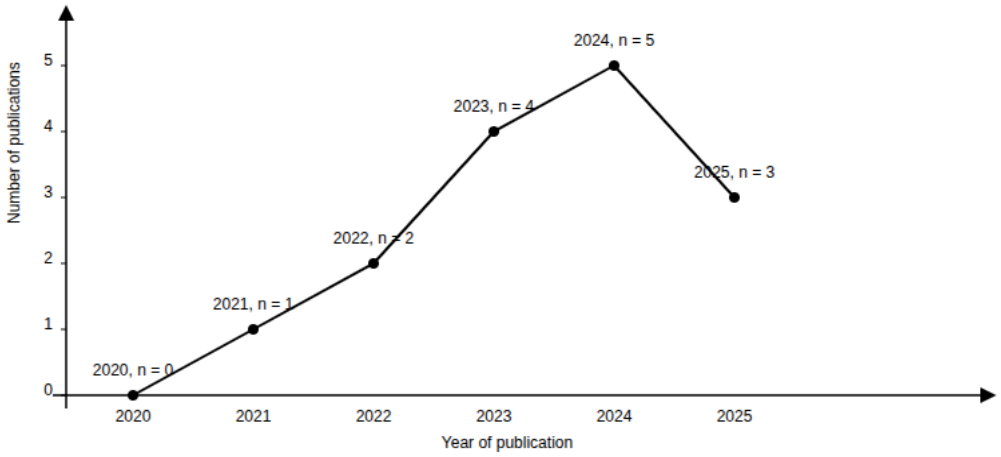

Figure 2. Publication Trends

3.2. Geographic Distribution

At the country level, India contributed the most publications (6), followed by the United States of America (4), China (3), and the United Kingdom and Switzerland, each with 1 paper. When grouped by continent, Asia emerges as the leading contributor with nine studies (60%), driven primarily by India and China. North America follows with 4 studies (26.67%) from the USA, while Europe accounts for two studies (13.33%), contributed by the UK and Switzerland. Asia's dominance in publication output can be attributed to coordinated national quantum strategies, large-scale public research funding, and strong integration between academic institutions and government-supported quantum programmes. In particular, India and the USA lead QC-driven drug discovery due to strong national quantum initiatives, significant government investment, and ready access to cloud-based Noisy Intermediate-Scale Quantum (NISQ) hardware from providers such as IBM and Google. In contrast, other regions, including Africa and Oceania, remain underrepresented due to limited research funding, restricted access to quantum hardware, and the absence of dedicated national quantum programmes. Figure 3 shows the geographic distribution of the 15 studies included in this review.

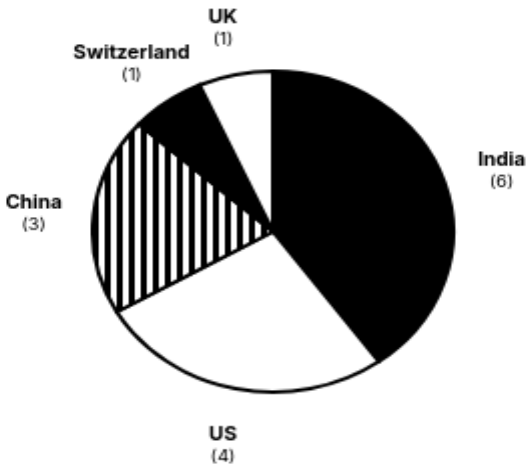

Figure 3. Country-wise distribution trends

3.3. Drug discovery stages discussed

The distribution shows that current work is more concentrated in the early stages of property prediction, discussed 7 times, followed by molecular generation, discussed 5 times and then drug-target interaction, which was discussed 3 times. These tasks are computationally intensive and the most crucial, making them the functions that can

benefit greatly from quantum accuracy and speedup. These findings provide the empirical foundation necessary to answer Q1, as they reveal where quantum computing is currently being applied within the drug-discovery pipeline. Figure 4 shows the frequency of discussion of algorithms.

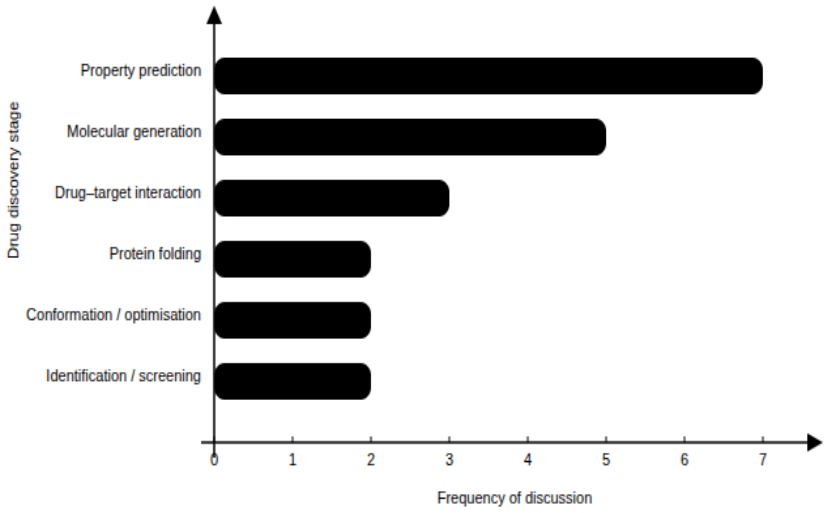

Figure 4. Drug discovery stages and frequency of discussion

3.4. RQ1: Which stages of the drug discovery pipeline is quantum computing being applied?

The findings from the synthesis of these 15 empirical studies show that quantum computing applies to several stages of the drug-discovery pipeline, with the strongest concentration being early-stage computational tasks. Evidence from Figure 4 shows that property prediction is one of the stages where QC was applied. Examples include [26], [27], [28], who estimated properties such as binding affinity and ADME-Tox behaviour. QC is also applied in drug–target interaction prediction and molecular screening, as shown by [22], [27], and [33]. Another major area of application is molecular generation, where quantum generative models are used to explore chemical space and propose new, drug-like structures, as shown by [33]. In addition, quantum computing contributes to structural and conformational optimisation shown by [21], [22], [32]. Altogether, these works indicate that quantum computing is applied across the spectrum of drug discovery stages, including property prediction, screening/interaction prediction, structural optimisation, and molecular generation.

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Across the 15 empirical studies, a total of 12 different quantum algorithms were identified. Figure 5 shows the frequency distribution across all studies, with VQE being the most widely adopted algorithm, followed by QAOA and QGAN. This reflects the dominance of variational algorithms and quantum machine-learning methods. Figure 5 shows the algorithms utilised and their frequency of application.

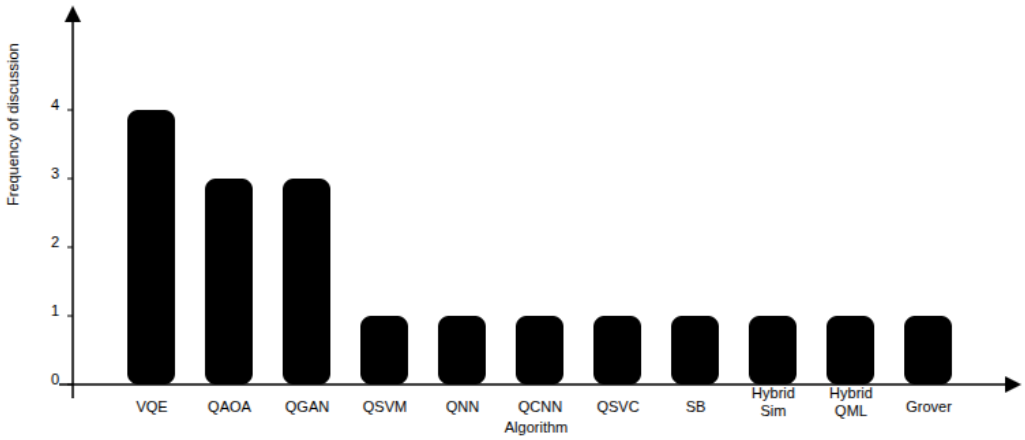

Figure 5. Algorithm frequency distribution

Table 6 shows the drug discovery stages discussed and the algorithms utilised in each stage.

Table 6. Algorithm vs Drug Discovery Stage

Drug Discovery Stage	VQE	QAOA	QSVM	QNN	QGAN	QCNN	QSVC	QSVR	SB	Hybrid Simulation	Hybrid QML	Grover's Algorithm
Protein folding	✓											✓
Property prediction	✓✓ ✓✓	✓ ✓					✓			✓	✓	
Molecular generation		✓			✓✓ ✓	✓						
Conformation/optimisation		✓							✓			
Identification/screening			✓	✓	✓	✓						

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Drug Discovery Stage	VQE	QAOA	QSVM	QNN	QGAN	QCNN	QSVC	QSVR	SB	Hybrid Simulation	Hybrid QML	Grover's Algorithm
Drug-target interaction	✓		✓	✓				✓				
Phytopharma modelling										✓		

Table 6 maps each algorithm to the drug-discovery stages in which it was applied. The synthesis shows that VQE is used primarily in property prediction. QAOA similarly appears in optimisation and property-prediction tasks. Machine-learning-based algorithms (QSVM, QSVC, QNN, QCNN) are primarily used for screening, classification, and drug–target interaction prediction, reflecting their application in analysing high-dimensional molecular descriptors. Generative models such as QGAN dominate molecular generation, where chemical space exploration is required. Table 7 shows the categorisation of the types of algorithms used in the empirical studies.

Table 7. Type of Algorithm

Type of algorithm	Number of Studies	Characteristics
Hybrid	13	Combines quantum algorithms with classical pre-processing or post-processing.
Quantum	1	Exclusively pure quantum
Quantum-inspired	1	Classical algorithms mimicking quantum behaviour.

In addition to the distribution of individual algorithms, the analysis of algorithm types provides insight into how quantum methods are being utilised. Three categories of algorithms emerged: hybrid quantum–classical, pure quantum, and quantum-inspired. Hybrid approaches overwhelmingly dominate, with 13 out of 15 studies adopting a hybrid pipeline. Only one study used a fully quantum algorithm, and one study used a quantum-inspired method. Hybrid quantum–classical approaches outperform fully quantum models primarily due to current NISQ-era hardware constraints. Classical optimisers manage error attribution and solution convergence, while quantum circuits address

combinatorial state exploration. This division compensates for noise levels and limited qubit counts that otherwise undermine fully quantum workflows. This suggests that hybrid quantum-classical approaches maximise the feasible quantum advantage while remaining operational in the current hardware. Taken together, the algorithm frequency distribution shown in Figure 5, the alignment of algorithms with specific drug-discovery tasks shown in Table 6, and the dominance of hybrid algorithm types shown in Table 7 illustrate how quantum algorithms are being practically deployed across the drug-discovery pipeline. These findings help answer Q2 by explaining the use of quantum algorithms in the drug discovery process, demonstrating clear patterns in how algorithm families are matched to task requirements and implemented primarily through hybrid quantum–classical workflows.

3.5. RQ2: How are the quantum computing algorithms utilised within the drug discovery process?

1) Variational Quantum Eigensolver (VQE)

VQE is a hybrid quantum-classical algorithm that seeks to find eigenvalues, with the computation workload split between the classical and quantum parts of the hardware [35]. VQE works by applying a quantum circuit to model the physics and entanglement of the electronic wavefunction and then optimising the parameters of the ansatz to minimise this trial energy, constrained always to be higher than the exact ground state energy of the Hamiltonian, which by virtue of the variational principle is always greater than or equal to the true ground-state energy of the Hamiltonian [36]. In other words, VQE computes the ground-state energy by minimizing the expectation value of a quantum circuit. VQE was applied by [23] to simulate the ground-state energy, and they reported greater precision than classical QM/MM models. [30], estimated molecular energy using VQE and recorded better accuracy than Density Functional Theory (DFT) and Hartree-Fock theory (HF). [32], also estimated molecular binding energies using VQE with higher accuracy than Hartree-Fock (HF). Lastly, [34] calculated the electronic structure using VQE and found greater accuracy with lower computational resources. Overall, VQE achieved better accuracy and precision in DFT/HF molecular energy calculations.

2) Quantum Approximate Optimisation Algorithm (QAOA)

QAOA is a hybrid quantum-classical algorithm for producing approximate solutions for combinatorial optimisation problems. It aims to maximise the number of satisfied clauses in max-satisfiability problems or to solve any polynomial, unconstrained, binary optimisation formulation. QAOA can find optimal parameters in drug design, such as identifying the most effective molecular configurations. It identifies low-energy configurations and optimal molecular conformations. [24] applied QAOA in molecular conformation and noted faster optimisation because the time-to-target factor was reduced for small molecules. [31] applied QAOA in property prediction and noted increased predictive performance for small molecules. Finally, [32] applied QAOA for structure analysis alongside VQE for energy estimation and reported efficient, accurate molecular geometries. Overall, QAOA offers improved predictive performance and accurate molecular geometry prediction, making it ideal for tasks such as optimisation and conformational analysis.

3) Quantum Support Vector Machine (QSVM)

QSVM exploits the parallelism and entanglement property of quantum mechanics to classify data points into well-defined, distinct categories. [37] reduce the computational burden associated with separating molecular features, and it applies to predictive models. [38] applied QSVM to predict molecular interactions and the identification of drug candidates, noting improved accuracy and scalability compared to classical support vector machine and neural network algorithms. QSVM can process high-dimensional molecular descriptors and outperforms classical SVR in prediction tasks.

4) Quantum Neural Networks (QNN)

QNNs represent the crossover of quantum computing with deep learning. Quantum-enhanced feature spaces enable fast, efficient data operations over quantum data, thereby capturing complex patterns and correlations that are not available to classical architectures [39]. QNNs to facilitate the process of target identification, molecular docking, compound optimisation, protein-ligand interactions, and binding affinity predictions and speed this process up by exploiting quantum parallelism, entanglement, and superposition in pattern recognition and simulation of molecules[40]. [25], [38] integrated a QNN with QSVM for molecular interaction predictions and reported improved accuracy over classical NN models.

5) Quantum Generative Adversarial Network (QGAN)

GANs discover drug candidates by generating molecular structures that satisfy chemical and physical properties and bind the receptor for the target disease [41]. Quantum GANs can offer several opportunities, such as stronger repressibility, learning speedup, the ability to learn richer representations of molecules, the ability to search exponentially growing chemical space with increasing qubit count, and the ability to sample from distributions that may be hard to model classically [41]. As such, [26], [28] achieved novelty by generating molecules with improved drug-likeness, with [28] reporting a +30% drug-likeness score. [33] also used QGAN and QCNN to increase accuracy over classical GAN/CNN for screening and molecular generation.

6) Grover's Algorithm

Grover's quantum search algorithm provides quadratic acceleration over classical solutions [42], [43], [44]. Grover's algorithm is applied to search in unstructured data by scaling the number of search iterations, thereby polynomially accelerating the search [45]. The unique capabilities of Grover's algorithm were utilised by [22], who accelerated and optimised protein folding.

7) Quantum Support Vector Classifiers (QSVC)

QSVC elicits patterns in the data by embedding classical inputs into high-dimensional, complex Hilbert spaces, thereby efficiently producing atypical patterns that could yield a quantum advantage in training speed, prediction accuracy, and classification [46]. This algorithm was used by [29] for ADME-Tox prediction, and it was observed that increased predictive power was achieved, resulting in better classification with an AUC-ROC of 0.80-0.95 across various ADME-Tox datasets.

8) Simulated Bifurcation (SB)

SB is an algorithm that uses parallelism for optimisation problems. [24], [47], [48], have used QAOA and SB and observed faster convergence of molecules as the time to target factor is reduced, hence SB worked in optimising the process.

9) Hybrid Quantum Machine Learning (Hybrid QML)

Integrating classical computing with quantum computing addresses the bottlenecks in quantum hardware and computationally intensive challenges [49]. Hybrid QML was used

by [27], and increased speed and accuracy were observed for binding affinity prediction to gain a +6% increase in prediction over classical methods.

10) Hybrid Simulation

A hybrid QM/MM simulation combines the power of QM with accuracy and MM with speed for structure-based drug design and calculation of properties in general [50]. In improving complex interaction modelling, [21] used a hybrid simulation.

11) Quantum Support Vector Regression (QSVR)

QSVR is for property prediction instances, regression tasks with the inclusion of predicting continuous values, such as binding affinities in drug-target interactions. It handles high-dimensional data and detects non-linear patterns. QSVR uses the concepts of quantum computing in conjunction with the classical SVR algorithm. First, it maps classical features to the quantum feature space to convert the input data into quantum states; then, quantum kernel computation exploits superposition and entanglement to accurately measure similarity. QSVR was utilised by [20], and he recorded a gain in prediction accuracy of 94-99% in drug target interaction.

12) Quantum Convolutional Neural Networks (QCNN)

QCNN will find the correlation between data by stacking the convolution layer and the pooling layer. Then, the convolutional layer learns new hidden representations by combining surrounding pixels, while the pooling layer reduces the size of the feature map, reducing the computational cost of learning and preventing overfitting. According to [33], [51] used QGAN and QCNN and noted increased accuracy over classical GAN/CNN in screening.

13) Categories of the algorithms

Overall, quantum machine-learning classifiers such as QSVM, QSVC, QSVR and QNN play a central role in early-stage prediction tasks, including screening, drug–target interaction modelling and ADME-Tox classification. Their advantage lies in quantum-enhanced feature extraction. Variational algorithms such as VQE and QAOA are used for energy estimation, conformational optimisation and structural modelling, demonstrating their suitability for tasks that rely on quantum descriptions of molecular states. Quantum generative models (QGANs) enable the exploration of chemical space and the creation of

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novel molecular structures. However, understanding how these algorithms are used also requires recognising the role of algorithm type, as summarised in Table 7. The dominance of hybrid quantum–classical approaches indicates that most practical implementations integrate quantum circuits with classical optimisation or preprocessing, enabling feasibility under NISQ hardware constraints. Pure quantum algorithms remain rare, as shown in this study. One study utilised a pure quantum algorithm, and quantum-inspired methods serve primarily as scalable approximations. This distribution shows that algorithm utilisation is shaped not only by computational purpose but also by hardware maturity.

14) Benefits of QC in drug discovery

Table 8 shows that quantum and hybrid quantum-classical algorithms consistently improve accuracy, speed, generative novelty, and efficiency in the drug discovery pipeline. The most frequently reported benefit is improved accuracy, followed by increased computational speed, enhanced generative novelty for molecule design and greater efficiency in resource utilisation.

Table 8. Benefits of QC in drug discovery

Ref	Algorithm	Description	Benefit
[20]	QSVR	Improved DTI prediction accuracy by 94-99%	Accuracy
[22]	Grover's algorithm	Accelerated protein folding	Speed
[23]	VQE	More accurate ground state energy estimations	Precision
[24]	QAOA, SB	Reduction of time-to-factor	Speed
[25]	QSVM, QNN	Improved accuracy of molecular interactions and drug candidate identification	Accuracy
[26]	QGAN	Generated molecules with improved druglikeness	Novelty
[27]	Hybrid QML	Increased speed and accuracy by 6% for binding affinity prediction	Accuracy Speed
[28]	QGAN	+30% druglikeness score in molecule generation	Novelty

Ref	Algorithm	Description	Benefit
[29]	QSVC	Better classification results with an AUR ROC of 0.80-0.95	Predictive power
[30]	VQE	Greater accuracy in molecular energy estimation and protein ligand binding	Accuracy
[31]	QAOA	Improved predictive accuracy and efficiency in molecule generation and property prediction	Accuracy Efficiency
[32]	VQE, QAOA	Accurate folding and structural analysis	Accuracy
[33]	QGAN, QCNN	Increased accuracy in screening and molecular generation	Accuracy
[34]	VQE	Higher accuracy with fewer computational resources	Accuracy Reduced computational resources

15) Benchmarking

Table 9 summarises the benchmark datasets, and Table 10 shows a comparison against classical methods. Benchmarking results across the reviewed studies show strong empirical performance of quantum and hybrid models. Dataset evaluations demonstrate high predictive accuracy on DAVIS (94.21%) and KIBA (99.99%), enhanced molecule generation on ZINC, faster optimisation on QM9 and improved drug-likeness (+30% QED) and binding-affinity prediction (+6% on PDBbind). ADME-related datasets such as HIA, CYP2D6 and DILI also reported strong AUC values of 0.80–0.95. Despite the promising performance, the interpretation of these results is constrained by dataset-related limitations. Many benchmark datasets, such as QM9 and ZINC, consist of relatively small, curated, or chemically constrained molecular spaces that may not fully represent real-world drug-like chemical diversity. Similarly, datasets like DAVIS and KIBA are biased toward well-studied protein targets, potentially inflating performance estimates and limiting generalisability to novel or less-characterised targets. ADME and toxicity datasets often suffer from class imbalance, label noise, and limited experimental validation, which can affect robustness despite high reported AUC values. These constraints highlight those current empirical gains, while promising, may not directly translate to large-scale

industrial drug discovery without further validation on more diverse, noisy, and clinically representative datasets. Table 10 shows algorithmic performance comparisons between classical baselines and quantum-enhanced methods.

Table 9. Datasets and their evaluation metrics

Type	Description
Dataset	Evaluation Metric / Result
DAVIS	94.21% accuracy
KIBA	99.99% accuracy
Zinc	Improved predictive performance, efficient molecule generation
QM9	Faster convergence of molecules (optimisation)
QM9 / PC9	+30% improvement in QED score (drug-likeness)
PDBbind	+6% improvement in binding affinity prediction
HIA	AUC 0.80–0.95 (ADME absorption prediction)
CYP2D6	AUC 0.80–0.95 (enzyme–substrate classification)
DILI	AUC 0.80–0.95 (hepatotoxicity)

Table 10. Algorithmic performance comparisons

Type	Description
Method / Baseline	Performance Outcome using QC-enhanced methods
Classical exhaustive search	Faster, optimised, accelerated search under the quantum model.
Classical molecular mechanics (MM)	Higher precision using QM/MM
DFT / Hartree–Fock	Higher energy-estimation accuracy using QC models
Hartree–Fock (folding analysis)	Accurate folding and structural analysis with QC
Classical GAN / CNN	QC-based generative and predictive models outperform classical models.
VAE baseline	No advantage over VAE

Algorithmic comparisons further show that QC-enhanced methods outperform classical baselines, offering faster, more optimised searches, higher precision than MM and DFT/HF, improved folding analysis, and superior generative and predictive capabilities. Together, these results demonstrate the diverse evaluation strategies used and consistently highlight QC's potential to improve accuracy, optimisation efficiency and molecular modelling quality in drug discovery. Quantum approaches outperform classical baselines largely due to superposition, which enables the simultaneous evaluation of multiple molecular configurations, and entanglement, which supports the modelling of complex molecular interactions that classical methods struggle to represent These allow more expressive molecular-state representations, and this advantage becomes particularly evident in conformational sampling and molecular energy estimation tasks, where classical heuristic approximations incur scaling limitations.

Findings from Tables 8, 9, and 10 help answer RQ3 by showing the specific mechanisms by which quantum computing enhances the identification of novel drug candidates. The tables present empirical metrics demonstrating improved accuracy, computational efficiency, and generative capability across the reviewed studies.

3.6. RQ3: How can Quantum Computing enhance the identification of Novel drug candidates

The evidence from the 15 papers studied shows that quantum computing outperforms classical methods in improving reliability and expanding the chemical space. Results show a strong empirical trend of improved predictive power as accuracy is an enhancement mechanism that occurs eight (8) times. This is shown in studies including [20], who attained a 94-99% gain in accuracy in drug-target interaction using QSVR, [27], who attained a +6% increase in the binding affinity prediction using Hybrid QML, [25], who recorded increased accuracy in molecular interactions and identification of drug candidates using QSVM and QNN, [30], who attained greater accuracy in molecular energy estimation and protein-ligand binding over HF/DFT using VQE, [31], who noted improved predictive accuracy in generated molecules that fit the target constraints, [32], who attained greater accuracy in protein folding and structural analysis over HF using the VQE and QAOA, [33], who noted increased accuracy over classical GAN and CNN in screening and molecular generation, and finally, [34], who attained higher accuracy while using fewer computational resources using VQE. Speed is another enhancement

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mechanism that was noted 3 times. [22] accelerated and optimised protein folding using Grover's algorithm, while [24] used QAOA and SB to reduce time-to-factor, hence faster optimisation, and [27] increased speed and accuracy for binding affinity prediction using Hybrid QML. Algorithms such as QAOA, simulated bifurcation (SB), and Grover's algorithm demonstrated significant speedups for structural optimisation tasks, while hybrid QML pipelines improved convergence in affinity-prediction workflows. Such speedups are particularly relevant to reducing drug discovery timelines. Another enhancement is increased predictive power, as noted by [31], who conducted an ADME-Tox prediction and reported better classification results using QSVC, with an AUC-ROC of 0.80-0.95. [23] attained high precision in the simulation of ground state energy using VQE, and [31] identified improved efficiency in molecular generation using QAOA. Finally, [36] reduced computational resources by using VQE to obtain an accurate electronic structure.

Across these 15 studies, quantum models consistently outperformed their classical variants for the same tasks. Examples include how VQE has repeatedly outperformed classical quantum-chemistry methods such as DFT and HF in higher-precision molecular-energy estimates [23], [30], [32]. In generative modelling, QGAN achieves a +30% improvement in QED score over classical GANs [28], demonstrating a superior ability to explore chemical space. Analogously, quantum classifiers such as QSVC and QSVM have outperformed classical SVMs and neural networks in ADME-Tox classification and drug-target interaction prediction studies, with QSVC achieving AUCs of 0.80–0.95 [29]. Collectively, the evidence shows that quantum computing enhances the identification of novel drug candidates by improving predictive reliability, speeding up search and optimisation processes, and enabling the generation of unique, biologically meaningful molecular structures, thereby extending the scope and speed of early-stage drug discovery. Moreover, the novelty gains recorded indicate that quantum models can explore chemical space beyond classical limits, enabling the identification of structurally unique drug candidates. Most improvements are realised in computation-intensive stages that depend on scalability, namely molecular conformation and generation, target interaction, and energy estimation. This is because QC leverages quantum parallelism towards the evaluation of multiple molecular configurations all at once, superposition to naturally encode complex electronic states, and entanglement to reduce search complexity.

Analysis reveals several limitations, with NISQ challenges related to limited qubit counts and hardware noise being the most dominant constraints, as identified in all 15 studies. The second most frequent limitation is Scalability, which was highlighted in 5 studies. Simulation dependence is another constraint identified in 3 studies [28], [30], [52]. Data encoding and molecular-representation challenges and dataset limitations, each with 2 mentions, [24], [33] and [28], [30] respectively. Less frequently observed but still relevant were algorithm/software immaturity, noted by [31], and limited molecular complexity, noted by [26], each occurring once. These findings help us answer Q4 by identifying the technological factors that restrict QC's practical integration into drug-discovery workflows. Table 11 presents the challenges noted by the authors of the 15 empirical studies utilised in this study.

Table 11. Author vs challenge

Author	NISQ Hardware	Scalability	Data Encoding	Dataset Limitation	Simulation Dependence	Algorithm/ Software	Molecular Complexity
[20]	✓	✓					
[21]	✓						
[22]	✓						
[23]	✓	✓					
[24]	✓		✓		✓		
[25]	✓	✓					
[26]	✓						✓
[27]	✓						
[28]	✓			✓	✓		
[29]	✓					✓	
[30]	✓			✓	✓		
[31]	✓	✓					
[32]	✓						
[33]	✓		✓				
[34]	✓	✓					

3.7. RQ4: How do current technological and technical limitations influence the application of quantum computing in drug discovery?

The reviewed studies clearly show that technological and technical limitations seriously constrain the application of quantum computing to drug discovery, with NISQ-related hardware constraints predominating. According to the challenge-frequency analysis, all 15 papers reported issues related to noisy, unstable, low-qubit-count quantum devices. This universal limitation, noted by authors like [20] and [22], predetermines that essentially all quantum algorithms used in the current research in drug discovery should run under the conditions of small coherence time, high error rates, and limited circuit depth, confining most research to hybrid or simulated environments, rather than actual quantum processors. The full quantum advantage thus becomes unrealised. Scalability remains one of the challenges for the practical application of QML models in drug discovery. Most evaluations are restricted to relatively small molecular systems, as increases in molecular complexity significantly raise computational resource requirements, limiting the feasibility of scalable implementations. Current quantum algorithms therefore, struggle to scale to larger, drug-like molecules or more complex biological systems, particularly under constraints imposed by limited qubit availability. As a result, encoding high-dimensional molecular structures often requires simplified representations, reducing the ability of model outcomes to generalise to realistic pharmaceutical scenarios. Collectively, these limitations confine the practical applicability of quantum computing to small molecules and early-stage tasks, narrowing the range of drug-discovery problems that can be realistically explored. Another challenge limiting the application of QC is simulation dependence, as reported by [28], [30], [52].

Many studies rely on simulators since hardware is too noisy or not scalable. Simulation is useful for prototyping, but it cannot fully reproduce the noise characteristics of real NISQ hardware. This makes it hard to translate the results into practical application. Data encoding and representation challenges make translating molecules into qubit representations very problematic. Most current encoding schemes are unable to handle large molecular graphs or protein structures, as they require circuit depths well beyond the reach of NISQ. The dataset limitations limit generalisability, as the datasets used are small. Algorithmic and software limitations mentioned by [29] identify that gaps in quantum software maturity lead to unstable or incomplete implementations. Finally, limitations in molecular complexity noted by [26] indicate that quantum generative

models often struggle with complex, drug-like structures beyond simple molecules, limiting the realistic exploration of drug-like chemical space. While the advantages of QC are clearly evident from the 15 studies, in practice, deploying QC across a complete pharmaceutical drug discovery pipeline is still in its infancy, as it faces many challenges related to noise, limited qubit counts, immature hardware, and scalability. These issues also highlighted research gaps, including the need for scalable systems, simulation dependability, challenging problems in molecular representation, and NISQ-era challenges such as decoherence, errors, and limited qubit counts.

3.8. Conceptual Framework

This conceptual framework provides a structured hybrid quantum-classical pipeline that incorporates the highest-performing quantum algorithms identified in this review. It addresses one of the key gaps observed, which is the absence of an end-to-end pipeline, by showing how hybrid quantum-classical algorithms can be used across the drug discovery pipeline. Figure 6 shows a conceptual framework for a hybrid quantum-classical drug discovery pipeline.

Algorithm-to-stage linkages were determined based on reported empirical performance across molecular simulation, screening, and optimisation tasks, with placement guided by task-specific suitability and demonstrated computational efficiency. These assignments reflect observed computational strengths, such as accuracy, stability, convergence efficiency, and scalability, within NISQ constraints.

The process starts with the Target Identification Phase, in which a biological component responsible for a disease is identified and assessed for druggability using classical bioinformatics and domain-specific knowledge. Once targets are validated, the workflow transitions into the Hit/Lead Discovery Phase. In this phase, QSVC performs molecular screening to classify compounds as favourable or unfavourable based on ADME–Tox profiles. This classification identifies high-priority molecules to narrow the chemical search. QSVC was chosen because it excels at precise, accurate classification [53], as shown by [31], who reported AUC-ROC values of 0.80-0.95 across various ADME-Tox datasets. De Novo follows to generate novel druglike molecules. QGAN is utilised as it has empirically shown to produce novel drug-like molecules and expand chemical diversity. Studies [26], [28], [33] demonstrated effective molecular generation using

QGANs, with [28] reporting a +30% improvement in drug-likeness. Quantum feature extraction is then performed using VQE to identify descriptors, such as binding potential and energy estimates. Collectively, this phase aims to generate, screen and characterise molecules to identify the most promising chemical candidates for optimisation. VQE is assigned to this stage due to its superior accuracy and precision in molecular energy calculations compared to classical HF and DFT baselines, as reported in [23], [30], [32].

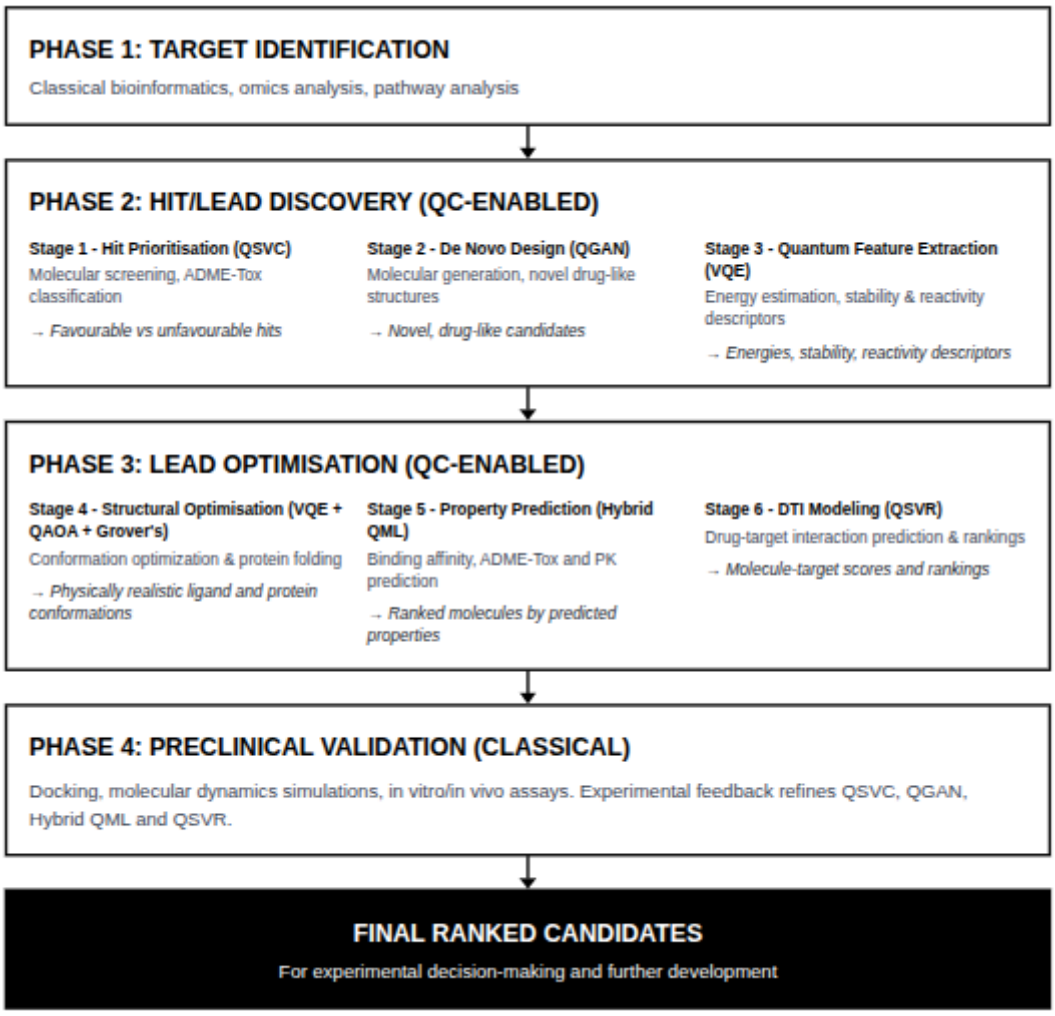

Figure 6. Hybrid Quantum-Classical Drug Discovery Pipeline Framework

The workflow then advances to the Lead Optimisation Phase, whose aim is to refine molecular structures, enhance predictive accuracy and prioritise the most promising drug-target interactions for pre-clinical testing. Structural optimisation uses VQE because VQE provides precise electronic structure and energy refinement [23],[30] and QAOA which demonstrated faster optimisation and accurate molecular conformation

prediction in small molecular systems [24],[31] to introduce conformational constraints that improve molecular recognition by a target receptor, while Grover's algorithm accelerates searches through protein-folding space [22]. This is followed by property prediction using Hybrid-QML to estimate binding affinity, ADME–Tox and pharmacokinetic behaviours, producing ranked molecular candidates. Hybrid QML is assigned here due to its demonstrated ability to improve binding affinity prediction, with [27] reporting a +6% accuracy gain over classical baselines. Drug-target interaction is carried out to predict the likelihood of a molecule binding to a specific protein target. This stage employs QSVR to perform regression in a quantum-enhanced feature space to enhance drug-target interaction prediction, thereby producing quantitative rankings of candidate-target pairs. QSVR is employed for quantitative drug–target interaction prediction, as it has been shown to model continuous binding-affinity values in quantum-enhanced feature spaces effectively, achieving prediction accuracies of 94–99% in drug–target interaction tasks [20].

Finally, the workflow proceeds to the Preclinical Validation Phase, whose aim is to experimentally validate predicted candidates and confirm which molecules are viable for further development. Classical validation methods such as molecular docking, molecular-dynamics simulations and in-vitro assays evaluate whether predicted binding interactions, stability and ADME–Tox behaviours hold in practical settings. The Final ranked candidates proceed for further development.

The classical components of the framework support all quantum-enabled stages. Classical data preparation curates, cleans and standardises chemical libraries, protein structures and bioactivity datasets, followed by the computation of descriptors required for quantum encoding. The orchestration layer coordinates the workflow, schedules quantum calls and integrates quantum outputs with classical computations. The validation and feedback module sends top-ranked candidates to docking, molecular dynamics simulations, and in vitro assays, with experimental results used to retrain and refine the quantum models.

Implementation of the proposed framework in pharmaceutical R&D should follow a hybrid deployment strategy that integrates quantum workflows into existing classical pipelines. Classical infrastructure can support data preparation, feature extraction and

initial filtering, while quantum algorithms are selectively applied to computationally intensive tasks such as optimisation, screening and energy estimation. A cloud-accessible NISQ platform will enable prototyping without requiring in-house quantum hardware. An orchestration layer should manage data flow and integrate quantum outputs with classical modelling tools. Experimental feedback from docking, molecular-dynamics simulations and in vitro assays can then be used to iteratively refine the quantum models under current hardware constraints.

3.9. Implications

1) Technical Implications

The findings show that progress in the NISQ era will continue to rely on hybrid systems rather than fully quantum pipelines as hybrid quantum–classical approaches dominate current applications. This means that organisations must remain grounded in hybrid architectures to manage expectations realistically and advance error-corrected hardware, scalable quantum algorithms, and more expressive molecular-representation schemes to support end-to-end quantum-integrated drug-discovery pipelines. Second, the concentration of strong empirical results in molecular generation, property prediction, structural optimisation, and drug–target interaction indicates that quantum computing is presently most impactful in computationally intensive, quantum-mechanically structured tasks. This suggests that pharmaceutical organisations should prioritise quantum deployment in these bottleneck areas to gain improvements in accuracy, novelty generation, and predictive reliability, rather than prematurely attempting full-pipeline quantum adoption.

2) Policy Implications

The geographic concentration of studies highlights the need for national research agencies to establish quantum-ready innovation hubs, hardware-access programmes and specialised training pipelines to reduce global disparities, particularly in underrepresented regions such as Africa and South America. Policymakers must also develop ethical, governance, and data security frameworks to regulate quantum-generated molecular data and ensure the transparent, responsible use of quantum-assisted decision tools.

3) Industrial Implications

Pharmaceutical companies should integrate quantum resources into existing infrastructure through hybrid QC-classical pipelines, rather than standalone quantum models. Organisations should prioritise QC in early-stage bottlenecks, where the review showed the strongest returns in screening, molecular generation, structural optimisation, and property prediction.

4) Limitations of the Study

This study noted several limitations, including a limited database scope of four databases, which may have omitted relevant studies from other repositories. Second, the study was limited to English-language papers. Third, the study only utilised empirical papers. Fourth, out of the 1291 papers, only 15 met the inclusion-exclusion criteria, meaning that all relevant work was not exhausted.

3.10. Future works

Based on the patterns identified in this review, a number of clear directions emerge for future research. First, significant advancements are required in quantum hardware, particularly in error correction, qubit scalability, and noise mitigation, to enable more chemically realistic simulations. This includes improving quantum feature encoding, quantum kernels and hybrid QML architectures. The improvement will strengthen the ability to encode larger drug-like molecules and enhance scalability. Second, dependence on simulation must be reduced. Since most studies tested quantum algorithms on classical simulators due to NISQ limitations, future work should focus on experiments on real quantum hardware, with noise-aware training, error mitigation, and hardware-specific optimisation to better capture accurate representations of large biomolecules, protein–ligand systems, and conformational landscapes.

Third, the review identifies a critical absence of standardised benchmarks. Future work should develop open biomedical quantum datasets and unified benchmarking frameworks to enable reproducible, comparable, and rigorous assessment of quantum vs classical methods. Finally, geographic concentration in QC research indicates the need for broader global participation. Policy initiatives, funding schemes, and quantum innovation hubs will be essential to expand the discipline beyond its current regional clusters and ensure equitable scientific progress.

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Overall, while quantum computing has already demonstrated tremendous potential for the enhancement of accuracy and speed in early-stage discovery tasks, due to technological constraints, it currently has a limited impact. However, ongoing progress in hardware, algorithm design, and hybrid integration strategies positions quantum computing for an increasingly transformative role in the future of drug discovery.

4. CONCLUSION

This systematic literature review analysed 15 empirical studies published between 2020 and 2025 on quantum computing applications in molecular design and drug discovery. Findings show that QC provides significant benefits in tasks including molecular property prediction, molecular generation, structural optimisation, and drug–target interaction prediction with algorithms such as VQE and hybrid QML improving accuracy, novelty generation, predictive reliability, and computational efficiency. These results demonstrate that quantum computing enhances existing computational workflows while also introducing novel generative capabilities that expand the chemical space explored during drug discovery. Despite these advances, this review identified a clear gap in the current literature: no study has yet proposed or implemented an end-to-end quantum-integrated drug discovery pipeline, as existing works remain fragmented and focused on isolated tasks. To address this gap, this review introduced a conceptual hybrid quantum–classical framework that synthesises empirical findings and maps validated quantum algorithms to specific stages of the drug discovery pipeline. The framework provides structured guidance on how current quantum methods can be realistically deployed under NISQ constraints, bridging fragmented empirical efforts into a unified, system-level workflow. However, fully quantum end-to-end drug discovery pipelines remain impractical due to NISQ-era hardware constraints, including hardware noise, limited qubit, scalability limitations, and a heavy reliance on workflow simulations. As a result, current implementations predominantly adopt hybrid quantum–classical approaches rather than fully quantum workflows. Future research should therefore prioritise the development of error-corrected and fault-tolerant quantum hardware, scalable and qubit-efficient quantum algorithms, improved molecular encoding strategies, and large-scale validation on real quantum devices beyond simulation environments, as these represent key milestones for enabling practical end-to-end quantum pipelines. This review, therefore, concludes that while quantum computing holds strong potential to accelerate early-stage

drug discovery, its broader impact will be realised progressively as these hardware and algorithmic milestones are achieved, with hybrid quantum–classical architectures remaining the most practical pathway for integrating quantum computing into pharmaceutical R&D.

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